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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past 10 decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences 15 based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based 20 techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

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The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and form a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases o disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

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effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

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As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers. than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3×25) . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as omithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

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Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

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The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3)

35 appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

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The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

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4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

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The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

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In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., Gene 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and Current Protocols in Molecular Biology, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylguanine, 2,2-dimethylguanine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

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PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

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The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1350 or (b)

polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1351-2700.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

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The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

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The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

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The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WT), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

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In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) Current Protocols in Molecular Biology, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

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The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
include, without limitation, those described in: Measurement of Human and Murine Interleukin 2
and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in
Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991;
deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988;
Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse
and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol
1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci.
U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J.,
Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp.
6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin
9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology.
J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

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Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce 15 large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem'cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

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Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

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Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals 15 models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

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A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

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Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cisDDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin,
Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

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In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

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4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

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Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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ANTI-INFLAMMATORY ACTIVITY 4.10.15

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Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

LEUKEMIAS 4.10.16

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia). 30

NERVOUS SYSTEM DISORDERS 4.10.17

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

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- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
 - (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

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Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

increased survival time of neurons in culture; (i)

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- increased sprouting of neurons in culture or in vivo; (ii)
- increased production of a neuron-associated molecule in culture or in vivo, e.g., (iii) choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., 15 depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

OTHER ACTIVITIES 4.10.18

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

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The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

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comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing. dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

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For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, tale, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

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administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

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Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity.

Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

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The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about $0.01 \mu g$ to about 100 mg (preferably about $0.1 \mu g$ to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications.

Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the 10 invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab} and $F_{(ab)2}$ fragments, and an Fab expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG1, IgG2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

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indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, 35 synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

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After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

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The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

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Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 Fab Fragment's and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_{v} fragments.

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., <u>J. Exp. Med.</u> 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

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Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include 212 Bi, 131 I, 131 In, 90 Y, and 186 Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem.

56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the

4.16 DIAGNOSTIC ASSAYS AND KITS

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The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

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For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

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Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

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Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviII normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviII**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviII** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviII** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

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5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

PCT/US01/03800 WO 01/57188

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of 15 component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-1350. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

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TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927
addit or ant			976 1233 1319
adult brain	GIBCO	ABD003	41 49 74 101 111 120 132 141-142 151
			217 225 238 271 317 404 446 469 503
			513-514 535 550 564 573 666-669 798
			898 910 927 976 1067 1083 1085 1178
			1254
adult brain	Clontech	ABR001	39 216 238 327 356 535 927 1056 1121
		·	1178-1180 1199 1251
adult brain	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145
			147 188 197 208 225 227-239 250 300-
			303 312 316 328-331 340 357-362 374
		•	380 384-391 408 414 446 448 464-467
			483 488 495-496 505 512 521 535 550
		ł	566 571 577 585 590 594 598 634 641
	ŀ		658 666 683 725 742 764 767 786 801
			805 810 823 826 829 831 836 841 887- 923 927 934 943 950-951 963 976 995
			1000-1001 1006 1026 1034 1048 1057-
			1067 1086 1088 1090 1118 1120 1122-
			1128 1142 1162 1181-1192 1199 1204
	(1218-1219 1225 1232 1253 1267 1271-
			1306 1342 1347 1349-1350
		ADDOLL	49 238 1219
adult brain .	Clontech	ABR011 ABR012	74 238
adult brain	BioChain	ABR013	868 1268
adult brain	Invitrogen		49 117 138 191 217 252 291 305 535
adult brain	Invitrogen	ABT004	566 596 663 670 746 798 816-819 876
			892 898 922 943 963 1034-1036 1121
	Charlesons	ADP001	41 74 101 138 211 238 304 537 582
cultured	Strategene	ADIOUI	740 798 883 943 976 1067
preadipocytes	Clontech	ADR002	49 74 101 111 120 127 151 215 238
adrenal gland	Cioniech	ADROCZ	240-247 316 330 363-364 404 414 534-
			535 833 924-940 950 963 976 1001
	,		1003 1067-1070 1118 1156 1193-1200
			1325
adult heart	GIBCO	AHR001	38 49 71-72 74-77 79 92 99 101 111
. addit ficart	GIBCO		118 129 132 138 151 158-163 182 195-
		į	203 215 217 238 264 269 353 384 398
			408 434-439 446 504 512-513 519 537
			562-573 577 611-614 616-619 658 661
			671-672 722 734 757-773 815 828-835
			874 891 898 919 926-927 976 988
			1021 1037 1041 1062 1067 1071 1080
- 9-			1083 1093 1122 1131 1185 1201 1254
			1308 1331 1335
adult kidney	GIBCO	AKD001	41 49 51 71-74 78-85 94 100-101 103-
			107 111 119-120 138 151 157 215 217-
	1		
	1		218 238 250 264 294 304 384 404 440
			446 454 477 504-505 509 514 518-519
			446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653
·			446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859
	·		446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859 877 909 918 927 956 963 976 1067
	-		446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859 877 909 918 927 956 963 976 1067 1074 1083 1095 1178 1302 1331 1335
adult kidney	Invitrogen	AKT002	446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859 877 909 918 927 956 963 976 1067 1074 1083 1095 1178 1302 1331 1335 11-12 41 49 111-112 215-217 294 316
adult kidney	Invitrogen	AKT002	446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859 877 909 918 927 956 963 976 1067 1074 1083 1095 1178 1302 1331 1335 11-12 41 49 111-112 215-217 294 316 446 487 564 575 844 868 910 927 976
adult kidney	Invitrogen	AKT002 ALG001	446 454 477 504-505 509 514 518-519 535 537 564 574-583 620-627 639 653 673-675 705 753 789 831 844 851 859 877 909 918 927 956 963 976 1067 1074 1083 1095 1178 1302 1331 1335 11-12 41 49 111-112 215-217 294 316

rissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS: 518 537 545 549 580 582 592 594 634
			640 651-652 676-678 725 851 873 .18
			952 976 1042 1067 1076 1083 1152
			8 111 121 151 180-182 188 215 537
lymph node	Clontech	ALN001	545 549 651 679-682 789 804-810 868
•			873 927 952 976 1042 1059 1335
			8 64 79 111 186 215-216 238 446 514
young liver	GIBCO	ALV001	519 537 564 653 683-684 698 753 798
,			519 537 564 653 683-684 698 755 796
			813 833 840 858 927 976 1038-1039
		J	1051 1085 1224 1245 1256
adult liver	Invitrogen	ALV002	40 71 292-293 305 384 468-469 496
			505 657 675 714 753 832 844 941-942
			976 1040 1076 1256 1293
adult liver	Clontech	ALV003	976
adult ovary	Invitrogen	AOV001	8 32 36 38 41 49 51 71 74 79-80 101
	}	}	104 111 120 122-125 138 140 143-149
			151 188-190 207-212 215-217 238 264
			316 384 409 440 445-446 496 504 512
			514 518-519 535 537 549-550 564 566
		(571 580 582 600 618 638 657 667 681
			685-697 699 705 722 735-744 761 771
			815 833 842-865 868 875-876 918 926-
			927 950 952 963 976 1023 1042 1048
			1051 1059 1072 1076 1083 1117 1120
			1124 1131 1144 1174 1224 1268 1331
			1335
adult placenta	Clontech	APL001	102 217 238 537 641 700
placenta	Invitrogen	APL002	663 851 1048
adult spleen	GIBCO	ASP001	8 45 74 111 132 140 151 185 217 238
		•	294 414 446 477 504 514 534 545 549
			592 722 873 883 952 976 1041-1042
			1083 1093-1094 1152 1224
testis	GIBCO	ATS001	72 107 111 113 126 140 151 183 215
			238 446 497 537 642 701-706 811 877
			927 962 976 1083 1117 1131
adult bladder	Invitrogen	BLD001	41 151 191 402-405 409 414 496 545
			592 607 706 873 952 1178 1329-1335
вопе татом	Clontech	BMID001	8 58-62 65-68 74 79 108 111 116 137
			147 151 164-174 213-215 238 305-307
			374 404 446 460 466 516 519 534 538-
			541 544-546 549-554 566 584 586 592
		· '	596 607 610 628-629 643-645 652 707-
		j	708 774-789 844 866-871 873 919 927
			952 963 976 998 1034 1042 1064 1083
	1		1085 1120 1132 1152 1225 1229 1268
	•		1307 1310
bone marrow	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132
			210 317 510-511 545 549 581 598 628
J	10		638 724 766 789 844 860 868 873 919
			927 952 963 968 976 1042 1111 1141
			1160-1161 1229 1266 1346
bone marrow	Clontech	BMD004	111 238 282 549 1083
	Invitrogen	CLN001	52 260 264 299 494 536 545 564 592
			844 873 877 952 976 1042 1152 1268
adult colon		1	1336-1337
adult colon	RioChain	CVX001	49 51 129 132 151 205 207 238 332-
	BioChain	CVX001	49 51 129 132 151 205 207 238 332- 335 365-367 392-401 440 466 470-471
adult colon	BioChain	CVX001	49 51 129 132 151 205 207 238 332- 335 365-367 392-401 440 466 470-471 518 537 597 629 832 877 927 976 1006
adult colon	BioChain	CVX001	49 51 129 132 151 205 207 238 332- 335 365-367 392-401 440 466 470-471 518 537 597 629 832 877 927 976 1006
adult colon	BioChain	CVX001	49 51 129 132 151 205 207 238 332- 335 365-367 392-401 440 466 470-471

T' Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Tissue Origin	Strategene	EDT001	32 40-41 49 74 79 101 111 120 132
endothelial cells	Suategene	DD 1001	138 151 204-206 215-217 238 269 316
	1	-	414 433 505 510 513 550 555 580 582
	{ (596 675 722 745 798 814 836-841 851
			918 976 1041 1043 1073 1083 1131
			1331
		EPM001	525-532 927
Genomic clones	Genomic DNA	EPMOUI	323 332 72.
from the short arm	from Genetic		
of chromosome 8	Research		47 525
Genomic clones	Genomic DNA	EPM003	47 525
from the short arm	from Genetic		}
of chromosome 8	Research		525 927
Genomic clones	Genomic DNA	EPM004	323 921
from the short arm	from Genetic		
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM005	531
from the short arm	from Genetic	Į.	
of chromosome 8	Research		74 100 000
esophagus	BioChain	ESO002	74 138 238
fetal brain	Clontech	FBR001	441-442 927
fetal brain	Clontech	FBR004	215 893 927 1001
fetal brain	Clontech	FBR006	48 61 101 120 132 138 140 147 208
terat orani	0.02.5		225 271 317 319 336 359 368 405-414
			519 550 571 594 686 715 722 764 824
	ļ		829 836 859 909 927 943 947 963 1057
4	[1067-1068 1104 1135-1140 1162 1206-
	· .	1	1207 1235 1268 1288 1307-1308 1319
			1338-1350
fetal brain	Clontech	FBRs03	111 446
fetal brain	Invitrogen	FBT002	41 51 120 151 192-194 264 504 512
IEIAI DIAIII	111VIII OBOII		535 683 761 798 820-827 844 876 909
1	j		963 976 1026 1048 1083 1144 1302
fetal heart	Invitrogen	FHR001	446 566 761
	Clontech	FKD001	51 74 111 127 140 151 184 294 537
fetal kidney	Cionicon	1112001	550 630-631 1319
C . 11:1	Clontech	FKD002	111 976 1083
fetal kidney	Invitrogen	FKD007	238 974
fetal kidney	Clontech	FLG001	463 566 976 1074 1083 1093
fetal lung		FLG003	41 238 330 407 415-416 537 573 844
fetal lung	Invitrogen	TEGOOS	859 1048 1083 1116 1192
	- C. L bio	FLS001	8 14 34-35 37 41 43 49 51 54-56 63-64
fetal liver-spleen	Columbia	TESOU.	69-71 74 77 79 87-90 101 107 110-111
l	University	. [114 120 128-131 138 140 147 150-155
			197 210 215 217 225 238 312 367 384
İ			414 440 446 460 468 483 496 504-507
	1	1	511-515 518-519 523 533-535 537 541
	1	1	544-545 547-550 555-560 564 566 571
	1	{	577 582 585-586 598 636 646-647 649
	1		652 664 698 709-710 714 722-723 731
			735-736 746-753 761 784 798 823 829
ļ		1 .	832 844 851 858-859 868 873 876 898
1			927 943 949 952 963 976 984 1002
	*		1021 1023 1040 1042 1044 1050 1083
1			1021 1023 1040 1042 1044 1030 1030
			1217 1251 1254 1256 1302 1308 1311
1		}	
			1319
	Columbia	FLS002	8 36-37 41-46 49 54 64 71 74 79 101
fetal liver-spleen	Common		
fetal liver-spleen	University		111 120 129 147 207 210 215-216 238
fetal liver-spleen			250 330 353 359 366 383-384 414 478
fetal liver-spleen			250 330 353 359 366 383-384 414 478 505 508-509 511 515-524 534-535 537 544-545 564 566 571 577 591 598 638

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
11550C OTIGIN			663 671 698 714 722 725 727 751 798
			851 859 873 876 909 927 949 952 983-
	i		984 1002 1023 1042-1044 1085 1095
	Į		1131 1144 1178 1199 1233 1240-1270
			1331 1340
fetal liver-spleen	Columbia	FLS003	64 535 976 1256
terat tivet-spicon	University		
fetal liver	Invitrogen	FLV001	8 101 120 138 217 446 468 535 566
letal liver	III 41 III OBOM		580 722 730 749 844 918 943 976 1051
			1256 1331
C. Ilian	Clontech	FLV004	537 926 1256
fetal liver	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421
fetal muscle	WAITLOBEIL	Philodox	425 535 537 577 598 614 836 857 1141
•	1		1208 1268
	7	FMS002	537
fetal muscle	Invitrogen	FSK001	13-26 32 41 51 89 107 111 147 151
fetal skin	Invitrogen	rskooi	225 264 316 405 422-429 488-494 496
		\	519 534-535 537 566 675 732 859 876-
		}	877 898 947 949-950 963 976 1001
			1062 1076 1083 1117 1144 1165 1268
		}	1281
			537 812
fetal skin	Invitrogen	FSK002	
fetal spleen	BioChain	FSP001	87 549 27-33 41 49 151 215 238 248-249 301
umbilical cord	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301
			316 446 495-503 519 521 534-535 537
		1	582 634 691 877 883 927 944-950 963
			976 1001 1075 1142-1143 1171 1218
		<u> </u>	1243 1308
fetal brain	GIBCO	HFB001	41 49 57 79 87 103 111 120 132-135
Tour ordin			138 145 151 188 197 207 215 238 264
ļ .	Ì		271 294 316 367 414 440 446 466 504
			513-514 535 542-543 550 564 571 596
1			635 648-654 675 711-715 722-723 798
		1	832 872 876 883 927 976 1095 1144
į			1168 1171 1178 1211 1335
тасторнаде	Invitrogen	HMP001	238
infant brain	Columbia	IB2002	49-50 77 81 89 105 111 136-138 140
man orani	University		151 161 175-179 185 216-217 264 295
	O.M. vo.c]	299 308-310 371-373 462 476 504 511-
		}	513 533 537 564 566 571 655-657 662
{			683 716-720 723 752 790-803 829 832
	•		858-859 876 898 909 949 976 1045-
	İ	1	1047 1076-1087 1090 1093 1116 1122
	1	}	1144 1209-1213 1225 1233 1256 1319
			1341
	Columbia	IB2003	41 50 77 104 132 215 238 508 512-513
infant brain		152003	519 566 655 714 794 918 943 976 1067
1	University	1	1092-1093 1233
ļ	Calimitia	IBM002	311 472-473 753 1214
infant brain	Columbia	IDIMIO02	
	University	TD C001	51 111 376 474 790 876 949 1144 1204
infant brain	Columbia	IBS001	1221
	University	- X FD001	151 316 462 514 534 582 675 939 1131
lung, fibroblast	Strategene	LFB001	1-7 41 74 79 94 115 120 138-139 156
	Turkhanan	LGT002	215 217 269 280 296 337 374-375 384
	Invitrogen		
lung tumor	Invitrogen	1	213 217 209 280 290 337 374-373 304
	MAIROGEN		404 446 454 475-480 498 514 518-519
	Mythogen		404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705
	invitrogen		404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705 721-724 754-756 779 859 868 872-874
	invitrogen		404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705 721-724 754-756 779 859 868 872-874 876-877 919 927 949 951-952 959 976
	invitrogen		404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705 721-724 754-756 779 859 868 872-874

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Tissue Origin	IQ () I DOLLOG	1,1	1293 1311
lymphocytes	ATCC	LPC001	41 74 111 132 151 253 316 446 550
lymphocytes	11100		634 844 927 976 1085 1268
leukocyte	GIBCO	LUC001	8 11 41 74 86 91-98 101 109 111 120
leukocyte			147 151 212 215 218 238 252 288 312-
			314.316 338 359 408 427 443-447 505
			510 512 514 518 534 545 549-550 561
	ļ	}	564 566 571 577 580 582 587-609 615
	Į.		632-638 658-659 698 714 725-728 832
	1		836 841 859 866 873-874 882-883 918-
	{		919 927 943 952 963 976 1042 1076 1083 1090 1148 1152 1168 1195 1219-
• •]	· ·	
			1220 1224 74 100 215 232 238 339-341 446 545
leukocyte	Clontech	LUC003	657 660 729 873 883 927 952 963 1008
•			1042 1116 1120 1149-1150 1215 1222
			210 215 238 342 534 545 592 722 873
Melanoma from cell	Clontech	MEL004	919 929 939 952 976 1071 1118 1218
line ATCC #CRL		1	1235 1245
1424	<u> </u>	12040001	8-10 40-41 49 73 80 114 138-140 147
mammary gland	Invitrogen	MMG001	217 250-256 264 297-299 305 377-378
			398 446 481-486 505 512 537 545 549
			571 592 725 730-733 816 829 836 844
	[868 873 876-877 898 926 943 951-960
			963 976 995 1034 1042 1048 1054-
	1	1	1055 1076 1083 1091 1093 1116-1117
	1	1	1124 1152 1302
induced neuron cells	Strategene	NTD001	39 101 111 138 238 361 1225 1251
induced heuron cens	Bualogono		1319
retinoid acid induced	Strategene	NTR001	74 225 976
neuronal cells			200000000000000000000000000000000000000
neuronal cells	Strategene	NTU001	129 225 238 304 313 361 657 976
pituitary gland	Clontech	PIT004	976
placenta	Clontech	PLA003	38 976 111 188 238 257-258 564 724 961-966
prostate.	Clontech	PRT001	1067 1095
		777001	238 430-431 841 859 868 963 1001
rectum	Invitrogen	REC001	1116
	<u> </u>	CA7 001	8 151 402 432-433 446 496 868 952
salivary gland	Clontech	SAL001	976 1083 1120 1151 1184
	01 + 1	SIN001	8 101 147 215 259-266 446 462 505
small intestine	Clontech	311/001	545 592 660 789 836 866 873 927 952
	1	•	963 967-978 1042 1120 1152 1223-
			1224
skeletal muscle	Clontech	SKM001	238 302 927 943 992 1031
spinal cord	Clontech	SPC001	74 111 132 151 215-216 238 264 267-
Spinar cord	Cionicon		270 343-344 353 379 516 537 566 740
		1	828 927 976 979-994 1092 1153-1159
			1225 1250
adult spleen	Clontech	SPLc01	698 859 1042
stomach	Clontech	STO001	210 238 271-272 537 580 705 918 952
5.011111111			995 1171
thalamus	Clontech	THA002	61 219-220 273-276 312 315 330 596
			963 996-1007 1059 1093 1160-1162
thymus	Clonetech	THM001	8 120 151 208 221 316-317 353 639
	1		750 867 874 878-881 927 963 1023
			1083 1094-1096 1124
thymus	Clontech	THMc02	8 61 114 129 132 210 225 231 306 317-319 336 340 359 380 398 446 448-
1			463 512 519 545 554 587 598 698 724
I	ı	ı	1 403 312 317 343 334 307 370 070 124
1	1	l l	725 789 812 836 868 873 927 947 952

Contract Contract	RNA Source	Hyseq Library Name	SEQ ID NOS:
Tissue Origin	KNA Source	Trysoq Diorary Thans	976 1007 1042 1083 1085 1097-1116
			1122 1147 1177 1226-1229 1234 1311
			1313
thyroid gland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188
Highord grand	Ciontoen		210 217 222 253 264 271 277-286 294
			320-326 345-352 361 381-382 446 467
			483 514 534 549-550 564 578 602 649
			844 882-883 927 950 956 976 1008-
			1028 1076 1083 1117-1120 1142 1163-
			1175 1230-1238 1308
trachea	Clontech	TRC001	223-225 238 287 353-354 514
Hached	010111011		545 592 611 873 883-884 927
			952 1029-1031 1042 1151-1152
			1170 1176-1177 1239
uterus	Clontech	UTR001	151 226 288-290 355 537 877
uicius	Cionicon		885-886 976 1001 1032-1033
			1232

TABLE 2

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO: 1	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.	460	100
	1	77	Human secreted protein, SEQ ID NO: 7645.	111	51
2	G03564	Homo sapiens	Part of Major Yo paraneoplastic antigen	293	76
3	R26173	Homo sapiens	(CDR62) encoded by clone pY2.		
	1.29536	Homo sapiens	calcium channel L-type alpha 1 subunit	191	65
5	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	251	50
6	M11507	Homo sapiens	transferrin receptor	120	95
7	AF099100	Homo sapiens	WD-repeat protein 6	1941	93
8	Y92338	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-45.	245	82
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	91
10	AJ133798	Homo sapiens	copine VII protein	1127	68
11	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	99
12	X98330	Homo sapiens	ryanodine receptor 2	282	78
13	AL024498	Homo sapiens	d/417M14.2 (novel scrine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase))	293	100
14	AF045577	Pan troglodytes	olfactory receptor OR93Ch	191	36
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	93	39
16	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein	569	89
17	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	99	44
18	Y36203	Homo sapiens	Human secreted protein #75.	165	75
19	U15647	Mus musculus	reverse transcriptase	106	40
20	G02701	Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	544	100
21	Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 172.	1691	100
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 8111.	380	96
23	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	123	50
24	AF036329	Homo sapiens	gonadotropin-releasing hormone precursor,	284	90
25	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	96	32
26	S80119	Rattus sp.	reverse transcriptase homolog	100	34
20 27	U83303	Homo sapiens	line-1 reverse transcriptase	101	35
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	135	45

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
o:			eno vo 310, 8149	83	42
)	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	116	72
-	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	1	67
		Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	96	
	003272	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	58	32
2	G03224		Membrane-bound protein PRO1152.	2457	98
3	Y66688	Homo sapiens	Human secreted protein sequence SEQ ID	348	95
4	Y87071	Homo sapiens	NO:110.	182	48
5	U15131	Homo sapiens	p126	982	90
6	Y73464	Homo sapiens	Human secreted protein clone yl4_1 protein sequence SEQ ID NO:150.		
37	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	687	99
38	AC067969	amino acids	Homo sapiens ryanodine receptor 1 (skeletal)	386	66
39	AL031588	3338-4088 Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN,	493	76
			FGENES and GENEWISE)	110	51
40	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	228	68
41	AF132969	Homo sapiens	CGI-35 protein	220	88
42	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.		35
	X61048	Hydra sp.	mini-collagen	105	
43 44	M76546	Helianthus	hydroxyproline-rich protein	110	31
45	U82288	annuus Caenorhabditi	Rac-like GTPase	139	70
		s elegans	Human secreted protein, SEQ ID NO: 7558.	118	58
46	G03477	Homo sapiens		113	63
47	AF090942	Homo sapiens	PRO0657	90	59
48	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	72	56
49	AJ005560	Mus musculus	SPR2B protein		
	000450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	98
50 51	G02450 Y91649	Homo sapiens	Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.	973	94
			putative p150	105	38
52	U93563	Homo sapiens	putative p130	699	85
53	Y55927	Homo sapiens	Human STLK2 protein.	145	56
54	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	356	74
55	AB008175	Mus musculus	hepatic nuclear factor 1-beta short form		
	M68941	Homo sapiens	protein-tyrosine phophatase	165	
56	M68941			338	76
57 58	AL031600 AF011417	Homo sapiens Mus	putative pheromone receptor	143	55
59	AF167320	musculus Mus	zinc finger protein ZFP113	558	68
	1	musculus		263	96
60	U73036	Home sapiens	interferon regultory factor 7		69
61	X07984	Mus musculus	protein-tyrosine kinase	297	
-/^	7/00061	Homo sapiens	Human secreted protein clone cb98_4.	791	98
62	Y29861		repressor transcriptional factor	485	65
63 64	U35376 AF265555	Homo sapiens Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	785	74
L			APOLLON Human secreted protein, SEQ ID NO: 7964.	88	95
65	G03883 AF177390	Homo sapiens Manduca	antennal specific membrane protein AMP	274	54
١٠٠		sexta		614	100
67	AB040800	Homo sapien		213	26
68	AF030027	Equine herpesvirus 4	24		
		Tioms conics	s Human secreted protein, SEQ ID NO: 7046.	261	95
69	G02965	Homo sapien	· · · · · · · · · · · · · · · · · · ·	1144	98
70	W75770	Homo sapien		239	76
71	AB011135	Homo sapien	s KIAA0563 protein	813	78
72	AB014885	Halocynthia roretzi	HrPOPK-1		73
73	AF045454	Cavia porcellus	phospholipase B	955	
		21111000000		308	1 61

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
D	No.			Score	}
10:					
		musculus	gp210 (AA 1-1886)	413	84
15	Y00826	Rattus norvegicus		351	54
76	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240		1
17	Y38422	Homo sapiens	Human secreted protein.	468	76
78	Y14596	Homo sapiens	Human T-type voltage-gated Ca channel alpha-	1357	99
0	114390	Tiomo depiene	1-I (hCavT3).		
79	Y14591	Human	APM-1 protein	767	100
13	114371	papillomaviru			
		s type 68	dJ798A10.2 (KIAA0445 protein)	71	34
80	AL137802	Homo sapiens	protein arginine N-methyltransferase-like protein	359	65
81	AP000383	Arabidopsis thaliana			
82	L46815	Mus	DNA binding protein Rc	895	75
		musculus		315	96
83	G01600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681. A suppressor of cytokine signalling protein	538	171
84	Y53886	Homo sapiens	A suppressor of cytokine signaturing protein designated HSCOP-6.		1
85	AB029002	Homo sapiens	KIAA1079 protein	134	42
86 86	Y28678	Homo sapiens	Human cw272 7 secreted protein.	325	62
87	Y99368	Homo sapiens	Human PRO1326 (UNQ686) amino acid	156	48
07	177500	220	sequence SEO ID NO:100.	L	105
88	AJ225124	Mus	hyperpolarization-activated cation channel, HAC3	487	95
		musculus	cerebral cell adhesion molecule	290	. 56
89	AF177203	Homo sapiens	Duman G-protein counled recentor GRIR-2.	326	79
90	Y28280	Homo sapiens Homo sapiens	polycystic kidney disease-associated protein	1751	95
91	L39891	Homo sapiens	ion channel BCNG-1	953	99
92	AF064876 AF170723	·Homo sapiens	protein kinase STK10	401	53
93 94	X13292	Trypanosoma	GPI-phospholipase C (AA 1 - 358)	151	37
94 .	. \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	brucei		L	
95	Y34127	Homo sapiens	Human potassium channel K+Hnovl1.	661	99
96	X03638	Rattus	sodium channel protein I (aa 1-2009)	1775	92
		norvegicus	ubiquitin-specific protease	1995	99
97	AF134213	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	213	38
98	G00838	Homo sapiens	mytonic dystrophy kinase-related Cdc42-binding	675	48
99	AF021935	Rattus norvegicus	kinase		
100	AF279265	Homo sapiens	putative anion transporter 1	867	98
100	AF279263 AC007878	Homo sapiens	match to nuclear protein, NP220; note: sequence	160	60
101	ACOUTOTO	Monto suprons	difference at residue 58	<u> </u>	
102	U22829	Mus	P2Y purinoceptor	264	42
102	022025	musculus		1	99
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	516	99
	<u> </u>		Human secreted protein vb21_1, SEQ ID NO:20.	787	98
104	Y94990	Homo sapiens	Human signal peptide containing protein HSPP-	343	57
105	Y87342	Homo sapiens	119 SEQ ID NO:119.		
106	AF169312	Homo sapiens	hepatic angiopoietin-related protein	212	67
106	AF116657	Homo sapiens		74	52
107	AE000401	Escherichia	sialic acid transporter	587	96
100	ALOUGIO	coli		693	100
109	Y38395	Homo sapiens	Human secreted protein encoded by gene No. 10.	182	94
110	Y78801	Homo sapiens	Hydrophobic domain containing protein clone HP00631 amino acid sequence.	102	74
111	775575	Homo sapiens		464	85
111	Z25535 Y94939	Homo sapiens	Human secreted protein clone ye90_1 protein	274	51
	1	1	sequence SEQ ID NO:84.	100	
113	AF016365	Homo sapiens		301	71
114	AC007956	Homo sapiens	unknown	520	75
115	M83738	Homo sapiens	protein-tyrosine phosphatase	251	92
116	AL157952	Homo sapiens		484	91
1					

EQ D	Accession No.	Species	Description	Smith- Waterman	% Identity
10:	110.	1		Score	-
18	L41816	Homo sapiens	cam kinase I	407	62
19	AJ006710	Rattus	phosphatidylinositol 3-kinase	627	93
19	A3000710	norvegicus			<u> </u>
20	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPr	1646	94
21	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase {EC 3,1,3,48}	373	68
			oncostatin-M specific receptor beta subunit	262	88
22	U60805	Homo sapiens	Human truncated tankyrase-1.	111	35
23	Y44403	Homo sapiens	contains similarity to C2 domains	219	29
24	U88167	Caenorhabditi s elegans		693	90
25	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit	153	65
26	AB021861	Mus musculus	apoptosis signal-regulating kinase 2		97
27	AF305210	Homo sapiens	concentrative Na+-nucleoside cotransporter hCNT3	807	
20	M90360	Homo sapiens	protein kinase	220	73
28		Homo sapiens	alpha 1C adrenergic receptor isoform 2	574	86
29	D32202	Homo sapiens	IFI16b	496	67
30 31	AF208043 AF201734	Mus	testis specific serine kinase-3	800	87
		musculus	differentiation enhancing factor 1	159	74
32	AF112886	Bos taurus	phospholipase C-beta-1b	554	85
133	AJ278314	Homo sapiens	Phospholipase C-beta-10 Human secreted protein encoded by gene 73	1157	87
134	W74802	Homo sapiens	clone HSOEL25.	668	96
135	AB020335	Homo sapiens	Pancreas-specific gene	866	98
136	W80408	Homo sapiens	A secreted protein encoded by clone dt674_2.	5041	99
137	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)		
138	Y96736	Homo sapiens	DPO3434 a novel secreted protein.	891	100
139	AB024034	Arabidopsis thaliana	DNA-damage inducible protein DDI1-like	147	55
	11707900	Homo sapiens	Human GTPase regulator GRAF.	248	56
140	W97809	Homo sapiens	Human PLA2 protein.	125	46
141 142	Y51557 AF090113	Rattus	AMPA receptor binding protein	623	93
		norvegicus	Human RECK cancer-inhibiting protein.	641	82
143 144	W26642 U87306	Homo sapiens Rattus	transmembrane receptor UNC5H2	578	84
145	AF264014	norvegicus Homo sapiens	scavenger receptor cysteine-rich type 1 protein	727	92
			M160 precursor	140	40
146	W63683	Homo sapiens		513	81
147 148	M96264 D64014	Homo sapiens Escherichia	galactose-1-phosphate uridyl transferase HrsA	818	90
149	M83316	coli Escherichia	pppGpp phosphohydrolase	915	95
150	AL163279	Coli Homo sapiens	homolog to cAMP response element binding and	1261	99
			beta transducin family proteins	940	99
151	AF179867	Homo sapiens		392	61
152	R95332	Homo sapiens	ligand (clone 3TW).		
153	AF151859	Homo sapiens	CGI-101 protein	370	92
154	X66957	Homo sapiens	hexokinase type 1	489	81
	Y16355	Homo sapiens	alternatively soliced form	432	92
155	G00857	Homo sapiens		349	78
156 157	AF159455	Mus	zinc finger protein	352	74
		musculus	interleukin-1 receptor-associated kinase	537	76
158	L76191	Homo sapiens	1 ' l'ha a anible duel	670	98
159	AP001743	Homo sapiens	specifity Ser/Thr/Tyr kinase domain		74
160	AJ250425	Rattus norvegicus	Collybistin I	556	
1	G02885	Homo sapien	Human secreted protein, SEQ ID NO: 6966.	370	100

~ \	Accession No.	Species	Description	Smith- Waterman	% Identity
10:	No.			Score	ļ
	Z22968	Homo sapiens	M130 antigen	610	100
	AF181121	Homo sapiens	ATP-dependent Ca2+ pump PMR1	336	92
,	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	455	94
	AF160798	Rattus norvegicus	calcium transporter CaT1	700	96
66	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	327	45
	7740600	Homo sapiens	Human breast tumour-associated protein 68.	1072	99
67	Y48607 AB020741	Mus	NIK-related kinase	197	43
68	AB020741	musculus			
69	AF252293	Homo sapiens	PAR3	596	44
70	U59429	Cricetinae	diacylglycerol kinase eta	481	82
″ I	033123	gen. sp.		206	42
71	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	386	82
72	AF127085	Mus	semaphorin cytoplasmic domain-associated	507	82
<i>''</i> -		musculus	protein 3B	653	99
73_	Y27918 ·	Homo sapiens	Human secreted protein encoded by gene No. 123.		
74	G02979	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97 55 ·
175	U36488	Mus	embryonic stem cell phosphatase	168	33 .
.,,		musculus	·	1022	100
76	W95629	Homo sapiens	Homo sapiens secreted protein gene clone gm196_4.	255	93
177	AF289023	Homo sapiens	formiminotransferase cyclodeaminase form D	710	99
178	X04936	Homo sapiens	T-cell receptor alpha-chain (413 is 2nd base in codon)		
179	AF127481	Homo sapiens	non-ocogenic Rho GTPase-specific GTP exchange factor	175	80
180	G00978	Homo sapiens	Human secreted protein, SEQ ID NO: 5059.	517	94
181	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	671	96
182	AF110640	Homo sapiens	omban seven-transmembrane receptor	862	100 84
183	AB020854	Bos taurus	orphan transporter short splicing variant	766	38
184	AF169691	Homo sapiens	cadherin-like protein VR8	375 985	99
185	AF126372	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme		
186	L20966	Homo sapiens	phosphodiesterase	541	76 93
187	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	254	98
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	301	
189	Y66713	Homo sapiens	Membrane-bound protein PRO1309.	694	100 73
190	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	331	92
191	U36771	Rattus norvegicus	sn-glycerol 3-phosphate acyltransferase	707	· ·
192	R05935	Homo sapiens	Secreted GPIIb subunit of multiple subunit polypeptide (MSP)GPIIb-IIIa.	157	72
193	M92084	Theileria	casein kinase II alpha subunit	364	50
107	146645	parva Homo sapiens	Membrane-bound protein PRO1310.	448	90
194 195	Y66645 W95631	Homo sapiens		382	49
196	AF255614	Rattus	scaffolding protein SLIPR	680	99
197	AC021640	norvegicus Arabidopsis	putative phosphatidate phosphohydrolase	300	41
198	AF073967	thaliana Mus	olfactory receptor	316	43
170		musculus domesticus			
100	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	617	98
199	AF117948	Homo sapiens	nancreas-enriched phospholipase C	625	89
200	AF128625	Homo sapiens	COC42-binding protein kinase beta	636	94
201	AF128625 AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	1303	100
202 203	Y53021	Homo sapiens		701	99
	1 2000000	Homo sapien	SH2-B heta signaling protein	182	79
204	AF227968 S81752	Homo sapien		375	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			{ovarian cancer critical region of deletion}		
	U18315	Sus scrofa	parathyroid receptor	122	60
206 207	AF255342	Homo sapiens	putative pheromone receptor V1RL1 long form	170	96
	S52051	Rattus sp.	neurotransmitter transporter	715	94
208	W63683	Homo sapiens	Human secreted protein 3.	840	99
209		Homo sapiens	similar to Drosophila photoreceptor cell-specific	541	82
210	D79992	Homo sapiens	protein, calphotin.		
211	AF117948	Homo sapiens	pancreas-enriched phospholipase C	1348	99
212	U81035	Rattus	ankyrin binding cell adhesion molecule	471	69
212	001033	norvegicus	neurofascin		
213	AF154846	Homo sapiens	zinc finger protein	798	56
214	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	933	93
214	14 102///	musculus			
215	AL163303	Homo sapiens	putative gene containing transmembrane domain	523	89
216	U26595	Rattus	prostaglandin F2a receptor regulatory protein	563	78
210	020373	norvegicus	precursor		
217	G04095	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	98
218	X75756	Homo sapiens	protein kinase C mu	314	81
219	Y66723	Homo sapiens	Membrane-bound protein PRO1100.	770	98
220	D88577	Mus	Kupffer cell receptor	567	40
		musculus		1050	1,00
221	AF258465	Homo sapiens	OTRPC4	853	100
222	AF021935	Rattus	mytonic dystrophy kinase-related Cdc42-binding	636	96
		norvegicus	kinase		100
223	AL136527	Homo sapiens	bA215B13.1 (A kinase (PRKA) anchor protein 11)	693	100
224	AB032417	Homo sapiens	WNT receptor Frizzled-4	690	99
225	AF030430	Mus	semaphorin VIa	703	68
223	111030430	musculus	1 .		
226	AE000218	Escherichia coli	putative dihydroxyacetone kinase (EC 2.7.1.2)	297	39
227	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	2080	100
227	AB024573	Mus	GTP-binding like protein 2	265	88
220	AB024313	musculus			
229	AF122924	Xenopus	Wnt inhibitory factor-1	316	40
223	AL 122724	laevis			
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.	229	100
231	X98260	Homo sapiens	M-phase phosphoprotein 11	265	92
232	R92754	Homo sapiens	Human growth differentiation factor-12.	682	95
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific	290	100
233	1.00		phospholipase-D.		
234	W69431	Homo sapiens	Human secreted protein cw1233_3.	235	97
235	Y08686	Homo sapiens	serine palmitoyltransferase, subunit II	859	81
236	AF118275	Homo sapiens	atrophin-related protein ARP	117	37
237	X81466	Mus	Embryo Brain Kinase	460	62
		musculus		1001	122
238	U64857	Caenorhabditi s elegans	similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor (TFPI)	284	33
239	AJ250840	Mus	serine/threonine protein kinase	739	63
240	AJ223472	musculus Mus	transcription elongation factor TFIIS.h	222	38
		musculus	Human secreted protein clone rb649_3 protein	353	52
241	Y94906	Homo sapiens	sequence SEQ ID NO:18.		
242	AF169301	Homo sapiens	Na+/sulfate cotransporter SUT-1	591	99
	L22022	Rattus	orphan transporter v7-3	667	93
242	1.22022	norvegicus			
243			potassium channel	1043	98
243	AF016191	Rattus	1	.	
		norvegicus		645	98
	AF016191 AF097366	norvegicus Homo sapiens	cone sodium-calcium potassium exchanger	645	98
244		norvegicus Homo sapiens Homo sapiens	cone sodium-calcium potassium exchanger Human secreted protein clone pp325_9.	497	98
244	AF097366	norvegicus Homo sapiens	cone sodium-calcium potassium exchanger Human secreted protein clone pp325_9. Not4-Np		

SEQ	Accession	Species	Description	Smith-	%
D ID	No.	Species		Waterman	Identity
NO:	140.	ł i		Score	1
110.	 	sexta	protein SCLP		
250	AF192756	Kaposi's	Orf73	134	34
250	1	sarcoma-			
	1	associated			
		herpesvirus			
251	AB022694	Homo sapiens	MOK protein kinase	209	83
252	W55045	Homo sapiens	Neural adhesion molecule (ethb0018f2 product).	469	100
253	L46815	Mus	DNA binding protein Rc	251	67
233	1240013	musculus	D.11.0		1
254	W68505	Homo sapiens	Human acid sensing ionic channel.	173	82
255	AF070066	Mus	Citron-K kinase	1201	98
233	AF070000	musculus	CIRON AR ALIE-ST	1	
256	G02491	Homo sapiens	Human secreted protein, SEQ ID NO: 6572.	460	100
	Z12841	Oryctolagus	Phospholipase	368	80
257	Z12841	cuniculus	1 Hospitonpase		1
060	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1857	99
258		Mus	L-periaxin	430	72
259	AJ222968	musculus	C-benavin	""	
	1 1250000	Homo sapiens	serine/threonine protein kinase	861	100
260	AJ250839		AMP-activated protein kinase gamma 3 subunit	758	98
261	AJ249977	Homo sapiens		198	40
262	AF141386	Rattus	SLIT-2	1.50	1.0
		norvegicus	37. 27-07	335	62
263	AF022859	Homo sapiens	neuropilin-2(a0) Ig superfamily receptor LNIR precursor	387	91
264	AF160477	Homo sapiens	Ig supertamily receptor Living precursor	636	99
265	Y44662	Homo sapiens	Human 14273 G-protein coupled receptor	030	1 "
			(GPCR).	204	56
266	U27269	Mus	sodium glucose cotransporter	204	50
		musculus	CITY	159	75
267	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	209	39 .
268	AF127389	Rattus	putative taste receptor TR1	209	39 .
		norvegicus		215	95
269	X98296	Homo sapiens	ubiquitin hydrolase	129	26
270	X78482	Streptococcus	Fc-gamma receptor	129	20
		pyogenes		109	26
271	AB009883	Nicotiana	KED	109	20
		tabacum	00000	899	97
272	AF137367	Mus	VPS10 domain receptor protein SORCS	099	"
		musculus		460	86
273	L34938	Rattus	ionotropic glutamate receptor	1 460	1 80
		norvegicus		188	74
274	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent	100	/*
	İ		Expressed Protein LIKE PUTATIVE protein)	ļ	
·		<u> </u>	(isoform 1)	173	94
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	1/3	34
	·		APOLLON COST	140	56
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	
277	L40380	Homo sapiens	thyroid receptor interactor	430	61
278	AB046851	Homo sapiens	KIAA1631 protein	283	96
279	AC008075	Arabidopsis	Contains PF 00069 Eukaryotic protein kinase	157	43
		thaliana	domain.	1	+
280	M83738	Homo sapiens	protein-tyrosine phosphatase	181	73
281	AK024397	Homo sapiens	unnamed protein product	439	91
282	AF141326	Homo sapiens	RNA helicase HDB/DICE1	497	84
283	AF156530	Mus	ETS-domain transcriptional repressor PE1	605	76
		musculus		1	
284	Y29336	Homo sapiens	Human secreted protein clone cs756_2 alternate	647	100
١ - ٠			reading frame protein.	1	
285	Y73402	Homo sapiens	Human secreted protein clone yc25_1 protein	300	90
203	1,3402	- Como capiono	sequence SEQ ID NO:26.	1	
284	AF016411	Homo sapiens	KCNA3.1B	137	100
286	W89253	Homo sapiens	Human ALP.	688	97
287		Bos taurus	differentiation enhancing factor 1	750	96
288	AF112886		host cell factor homolog LCP	367	44
289	AF113131	Homo sapiens	plexin-related protein	698	100
290 291	U52111 AF026504	Homo sapiens	SPA-1 like protein p1294	603	89
		Rattus	1 3FA-1 HKC 010WH U1474		

SEQ D NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
<u>\U:</u>		norvegicus			\- <u></u> -
92	AF102854	Rattus	membrane-associated guanylate kinase-	124	53
92	AL 102054	norvegicus	interacting protein 2 Maguin-2		ļ
93	X99211	Drosophila	ubiquitin-specific protease	143	38
.93	Α,5,2,11	melanogaster			
.94	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	185	94
.74	134343		sequence SEO ID NO:92.		
95	Y94890	Homo sapiens	Human protein clone HP02798.	108	59
96	AF019767	Homo sapiens	zinc finger protein	154	96
90	Y28568	Homo sapiens	Secreted pentide clone bd577 1.	568	84
98	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	182	97.
.90	134343	1101110 2007-11111	sequence SEO ID NO:92,		<u> </u>
299	B08906	Homo sapiens	Human secreted protein sequence encoded by	605	69
299	D00900	Troing seprens	gene 16 SEO ID NO:63.		
00	R58890	Homo sapiens	Human-32 cadherin-related molecule.	212	97
	AF022859	Homo sapiens	neuropilin-2(a0)	277	100
01	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
02		Homo sapiens	Human receptor tyrosine kinase.	228	97
03	Y44297 D32050	Homo sapiens	alanyi-tRNA synthetase	192	80
304		Homo sapiens	protein kinase related to Raf protein kinases;	428	72
305	U43586	LIOUIO SEPICIES	Method: conceptual translation supplied by		1
			author		
100	R54872	Homo sapiens	Human H13 viral receptor mutant 4.	280	95
306	D78572	Mus	membrane glycoprotein	199	41
307	אכאוע ן	musculus	Monorana B., capatan		
200	AT066614	Rattus	scaffolding protein SLIPR	639	88
308	AF255614	norvegicus	Sourcemb breast		
	S79463	Mus sp.	semaphorin homolog=M-Sema F	162	89
309	AF178941	Homo sapiens	ATP-binding cassette sub-family A member 2	736	100
310		Dictyostelium	calcium binding protein	151	36
311	U03413	discoideum		1	
210	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-	744	100
312	18/34/	FIGURE Sapiens	124 SEO ID NO:124.		
212	Z97055	Homo sapiens	draggn45 4 (putative GS2 like protein)	789 .	99
313 314	AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins;	197	38
314	AC004010	Tionio supieno	44% similarity to U42767 (PID:g1736918)		
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and	278	38
313	AL021332	110mic suprem	GENEWISE)		
316	1170209	Mus	polycystic kidney disease 1 protein	165	38
310	070203	musculus			
317	AF109643	Rattus	coxsackie-adenovirus-receptor homolog	223	38
317	AL 103043	norvegicus			
318	AF104923	Homo sapiens	putative transcription factor	138	84
319	AF104923 AF100287	Trypanosoma	activated protein kinase C receptor homolog	141	38
317	71.100201	vivax			
320	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	125	51
321	Y21591	Homo sapiens	Human secreted protein (clone CC332-33).	459	97
322	D26070	Homo sapiens		232	97
244	220070	1	recentor	<u> </u>	
323	Y27918	Homo sapiens		306	88
343	12/310	1105 544.546	123.		1 70
324	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	70
325	M19650	Homo sapiens		214	97
243	14113020	1105 500.000	3.1.4.37)		
326	W80396	Homo sapiens	A secreted protein encoded by clone bp646_10.	140	70
	X75756	Homo sapiens	protein kinase C mu	540	78
327	G02292	Homo sapiens	Human secreted protein, SEQ ID NO: 6373.	721	99
328	AF168990	Homo sapiens	I putative GTP-binding protein	877	99
329		Homo sapiens	ti t t t and a main a main all	581	80
330	S67984	Tiomo sapiens	region		
223	V12016	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	2823	98
331	X13916	Homo sapiens		1127	100
332	Y87330	Lionio sabiens	107 SEO ID NO:107.	1	
	Y28503	Homo sapiens		320	98
333			putative RHO/RAC effector protein; 95%	327	93

SEQ	Accession No.	Species	Description	Smith- Waterman	% Identity
D IO:	140.	}		Score	
0.			similarity to P49205 (PID:g1345860)		- (5
35	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-	1111	67
36	AF006466	Mus musculus	lymphocyte specific formin related protein	193	75
37	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	632	97
38	Y13443	Homo sapiens	Amino acid sequence of hSlo3-2.	516	100
39	Y07637	Homo sapiens	nutative GABA-gated chloride channel	189	100
140	Y05734	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
341	AE000497	Escherichia coli	L-idonate transcriptional regulator	928	98
342	D90855	Escherichia coli	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	769	99
343	D85613	Escherichia coli	membrane component	399	100
344	M93239	Escherichia coli	transmembrane protein	232	100
345	M60177	Escherichia coli	enterobactin	759	99
346	D90699	Escherichia coli	Sensor protein copS (EC 2.7.3).	638	97
347	D90843	Escherichia coli	CapB protein.	552	100
348	M13422	Escherichia coli	49 kd protein	1193	90
349	L10328	Escherichia coli	similar to drug resistance translocases	340	82
350	X69942	Mus musculus	enhancer-trap-locus-1	560	80
351	AF239613	Homo sapiens	apamin-sensitive small-conductance Ca2+- activated potassium channel	463	100
352	D90777	Escherichia coli	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (b- hydroxybutyryl-CoA dehydrogenase) (BhbD).	577	
353 .	D90863	Escherichia coli	similar to	311	98
354	Y52386	Homo sapiens	Human transmembrane protein HP02000.	133	58
355	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-	482	55
356	Y58637	Homo sapiens	Protein regulating gene expression PRGE-30.	119	51
357	AF119226	Homo sapiens	dual-specificity tyrosine phosphatase YVHI	1788	100
358	Y87219	Homo sapiens	Human secreted protein sequence SEQ ID NO:258.	165	93
359	J00132	Homo sapiens	beta-fibrinogen	233	70
360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	40
361	R28916	Homo sapiens	Type III procollagen (prior art).	108 649	65
362	U16655	Rattus norvegicus	phospholipase C delta-4	95	42
363	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	104	34
364	U47276	Gallus gallus	chicken brain factor-2	183	65
365	G03789	Homo sapiens		118	46
366	G04091	Homo sapiens		564	75
367	X98258	Homo sapiens		3387	99
368	AL021366	Homo sapiens	reverse transcriptase	92	59
369	U70932	Peromyscus leucopus		242	73
370	X86400	Homo sapiens	like	165	56
371	G03172	Homo sapiens		257	55
	U49974	Homo sapiens			99
372					
	X13916 AF234765	Homo sapiens Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	1182	78

220	- Aion	Species	Description	Smith-	%
SEQ	Accession	Species	2000.p.101	Waterman	Identity
ID I	No.	•		Score	<u>.</u>
NO:	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	221	67
376	G01984 G00669	Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	600	100
377	X52574	Mus	GTP binding protein	1456	91
378	A32374	musculus			
270	R69095	Homo sapiens	Anti-HIV Fab tat31 light chain.	68	37
379	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
380	AB002405	Homo sapiens	LAK-4p	530	43
381	U64830	Dictyostelium	protein tyrosine kinase	115	44
382	U0463U	discoideum	-		<u> </u>
202	G02916	Homo sapiens	Human secreted protein, SEQ ID NO: 6997.	618	98
383	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	617	93
384	AJ245822	Homo sapiens	type I transmembrane receptor	4560	100
385		Homo sapiens	KIAA0220	2148	98
386	D86974	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	142	50
387	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	99	59
388	G04072	Homo sapiens	envelope protein	197	51
389	M12140		NHP2 protein	461	77
390	AJ293309	Homo sapiens Homo sapiens	Human calcium binding protein 2 (CaBP-2).	181	94
391	Y42751		Human breast cancer related protein BCRB2.	241	66
392	W48351	Homo sapiens Homo sapiens	olfactory receptor protein	339	54
393	Y14442		Secreted protein clone da228_6.	957	100
394	W85607	Homo sapiens	Fragment of human secreted protein encoded by	171	34
395	Y76332	Homo sapiens	gene 38.	ì	·
		77	Human secreted protein, SEQ ID NO: 8011.	250	100
396	G03930	Homo sapiens	dopamine receptor D4	105	35
397	AB032904	Hylobates syndactylus	dopamine receptor 2.	1	
			stromal antigen 3, (STAG3)	861	.85
398	AJ007798	Homo sapiens	Human secreted protein sequence encoded by	1047	92
399	Y91405	Homo sapiens	gene 2 SEQ ID NO:126.		
		YYio-o	Human secreted protein clone cb98_4.	162	37
400	Y29861	Homo sapiens	similar to rat integral membrane glycoprotein;	527	78
401	D87002	Homo sapiens	accession number Z21513.		
		Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
402	AF100754	Gallus gallus	alpha-2-macroglobulin receptor	258	60
403	X74904	Mus ganus	ADP-ribosylation factor-directed GTPase	545	89
404	AF075462	musculus	activating protein isoform b		
	1.0000	Human	pol/env	162	30
405	X92887	endogenous	porchi		.
1	-	retrovirus K	}	l	
105	Y30162	Homo sapiens	Human dorsal root receptor 4 hDRR4.	325	72
406	AK022626	Homo sapiens	unnamed protein product	2833	99
407		Homo sapiens	ribosmal protein small subunit	264	92
408	L13802	Homo sapiens	Human secreted protein sequence encoded by	1788	89
409	Y91600	Trouse sabiens	gene 9 SEQ ID NO:273.		1
410	W88745	Homo sapiens	1 11 20 -1	2004	99
410	W 66 /43	Tiomo sapieno	HTSEV09.	J	
411	AB043953	Mus	Chat-H	2628	82
411	AB043933	musculus_	i de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	1	
410	7/06222	Homo sapiens	Human secreted protein HNTMX29, SEQ ID	1014	92
412	Y86233	LIOUIO Sapiens	NO:148.		
113	7710542	Pan	MHC class I A	265	71
413	U10542	troglodytes	MAIO GIABOTTO		
	A E166007	Homo sapiens	NY-REN-7 antigen	850	95
414	AF155097	Homo sapiens		88	48
415	G03203			266	89
416	Y57911	Homo sapiens		481	60
417	W27651	Homo sapiens		3077	87
418	Y76884	Homo sapiens	alpha tubulin	289	68
419	AF255559	Notothenia	aipna tuounii		
		coriiceps	Human secreted protein, SEQ ID NO: 6065.	209	74
420	G01984	Homo sapiens	A CDE Compiler	1446	96
421	AL109827	Homo sapiens	to rat sperm antigen 4 (SPAG4)))	1	
1 421			TO THE Sperm antigen 4 (SPAC4)))		
421				112	35
422	AC008075	Arabidopsis thaliana	F24J5.4	112	35

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			Alues margaret	1090	100
123	AF231705	Homo sapiens	Alu co-repressor 1	6268	97
124	AF234887	Homo sapiens	FLAMINGO 1 Extended human secreted protein sequence, SEQ	1961	99
25	Y35942	Homo sapiens	ID NO. 191.	635	98
26	AB009288	Homo sapiens	N-copine		
27	L12392	Homo sapiens	Huntington's Disease protein	16080	. 99
28	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
129	AJ293573	Homo sapiens	zinc finger protein Cezanne	542	87
130	Y84441	Homo sapiens	Amino acid sequence of a human RNA- associated protein.	2074	100
131	G02850	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
132	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	73	42
433	AF159296	Lycopersicon esculentum	extensin-like protein	613	48
434	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	44
435	X73874	Homo sapiens	phosphorylase kinase	3442	97
436	AF161426	Homo sapiens	HSPC308	268	74
	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
137		Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	168	56
438	G03798	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
439	X14766		beta-tubulin	311	95
140	X02344	Homo sapiens	activating signal cointegrator 1	1882	100
441	AF168418	Homo sapiens	zinc finger protein	795	54
142	L11672	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
443	G03203	Homo sapiens		2451	100
444	A52140	unidentified	HUMAN NDR	9356	99
445	X98330	Homo sapiens	ryanodine receptor 2	227	49
446	AF116712	Homo sapiens	PRO2738	576	99
447	AF245447	Homo sapiens	sphingosine kinase type 2 isoform	2630	94
448	AF133086	Homo sapiens	membrane-type serine protease 1		93
449	U87305	Rattus norvegicus	transmembrane receptor UNC5H1	817	
450	AF081249	Homo sapiens	JAW1-related protein MRVI1A long isoform	4568	99
451	AC005498	Homo sapiens	R31665_1	316	62
452	M60235	Homo sapiens	granule membrane protein-140	464	73
453	AB036706	Homo sapiens	intelectin	730	88
454	G00918	Homo sapiens	Human secreted protein, SEQ ID NO: 4999.	263	81
455	Y22634	Homo sapiens	Human cytokine inducible regulatory protein-1	192	67
456	Y36705	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	106	40 .
457	N91325	Homo sapiens	DNA encoding human growth hormone receptor.	3282	96
458	M19155	Plasmodium falciparum	S-antigen precursor	110	36
459	Y13377	Homo sapiens	Amino acid sequence of protein PRO257.	509	98
460	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	149	43
461	Y14482	Homo sapiens	clone HTDAD22. Fragment of human secreted protein encoded by	184	54
462	Y53005	Homo sapiens	gene 17. Human secreted protein clone pm749_8 protein	135	47
463	X84960	Triticum	sequence SEQ ID NO:16. low molecular weight glutenin	109	33
464	W19919	aestivum Homo sapiens		1781	-85
	AF189764	Mus	alpha/beta hydrolase-1	502	59
465		musculus		101	30
466	U93569	Homo sapiens		1172	99
467	Y41528	Homo sapiens	gene 77.	149	52
468	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.		
469	800000LA	Homo sapiens	PI3-kinase	5832	97
470	X70922	Mus musculus	neurotoxin homologue	118	47
471	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	75
	Y36705	Homo sapiens		72	57

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
ЙО:		1		Score	<u> </u>
110.	 		gene 62.		
173	G02313	Homo sapiens	Human secreted protein, SEQ ID NO: 6394.	328	100
74	Y07007	Homo sapiens	Breast cancer associated antigen precursor sequence.	1013	97
175	W93254	Homo sapiens	Human ESRPI protein.	943	80
75	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	236	65
76	1	Homo sapiens	Human secreted protein encoded by gene 44	202	60
77	Y02693		clone HTDAD22.	267	100
178	G01870	Homo sapiens	Human secreted protein, SEQ ID NO: 5951.	3427	92
179	AF102777	Mus musculus	FYVE finger-containing phosphoinositide kinase		
180	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	123	53
181.	W87701	Homo sapiens	A human membrane fusion protein designated	221	77
182	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
	AF210651	Homo sapiens	NAG18	124	59
183 184	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
185	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
186	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	149	73
407	Y76167	Homo sapiens	Human secreted protein encoded by gene 44.	627	100
487 488	AJ275213	Homo sapiens	stabilin-1	1244	91
188	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
190	L12392	Homo sapiens	Huntington's Disease protein	16081	100
190	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	197	66
192	J03799	Homo sapiens	laminin-binding protein	228	70
193	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	128	41
494	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	197	67
495	AC005175	Homo sapiens	R31449 3	889	94
496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	229	61
497	AB030237	Canis familiaris	D4 dopamine receptor	90	48
498	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
498 499	U70935	Peromyscus	reverse transcriptase	213	52
		maniculatus	skeletal muscle ryanodine receptor	26406	99
500	U48508	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
501	G03371		PRO1722	156	62
502	AF119851	Homo sapiens	PRO1722	116	50
503	AF113685	Homo sapiens Homo sapiens	WW domain binding protein-2	322	59
504	U79458	Homo sapiens	Human secreted protein CD124_3.	608	55
505	W29651	Homo sapiens	Secreted protein encoded by clone dh1135_9.	986	70
506 507	W85459 Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID	115	33
508	AL160175	Homo sapiens	NO:180. bA243J16.3 (similar to MYLK (myosin, light	184	92
509	U43360	Peromyscus	polypeptide kinase)) reverse transcriptase	97	62
	L	maniculatus	000 ID NO. 7070	117	63
510	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	1058	100
511	W79092	Homo sapiens	Human secreted protein dn740_3.	205	64
512 ·	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	2151	100
513	AJ133439	Homo sapiens	GRIP1 protein	259	42
514	AE003456	Drosophila melanogaster	CG6393 gene product		
515	Z17206	Xenopus laevis	p46XlEg22	128	40
516	AF104413	Homo sapiens	large tumor suppressor 1	1766	94
517	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	40
518 ·	AF151083	Homo sapiens	HSPC249	444	98
519	S80864	Homo sapiens	cytochrome c-like polypeptide	318	50
520	X92485	Plasmodium	pval	170	61
J2U	W27407	vivax	F	1	1

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
ID NO:	No.			Score	Identity
NO:	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	59
522	AF121857	Homo sapiens	sorting nexin 7	259	40
523	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	82	37
524	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	253	73
525	AF119851	Homo sapiens	PRO1722	162	57
526	Y27761	Homo sapiens	Human secreted protein encoded by gene No. 47.	154	57
527	G02707	Homo sapiens	Human secreted protein, SEQ ID NO: 6788.	70	86 86
528	U47924	Homo sapiens	C8	84	45
529	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	111	60
530	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284. Human secreted protein, SEQ ID NO: 8148.	92	65
531	G04067	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	75	29
532	G03267 G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	182	48
533 534	AF068286	Homo sapiens	HDCMD38P	861	100
535	U07707	Homo sapiens	epidermal growth factor receptor substrate	228	60
536	G01955	Homo sapiens	Human secreted protein, SEQ ID NO: 6036.	484	75
537	AF219232	Gallus gallus	qin-induced kinase	206	53
538	AF135022	Homo sapiens	mediator	128	100
539	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	141 853	59 39
540	AF016430	Cacnorhabditi s elegans	contains similarity to a BR-C/TTK domain		
541	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	408	66
542	M29487	Homo sapiens	integrin alpha subunit precursor	517	73
543	AF102530	Mus musculus	olfactory receptor F3		100
544	Y73431	Homo sapiens	Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.	386	
545	AE004833	Pseudomonas aeruginosa	probable TonB-dependent receptor	279	42
546	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	264 1772	67
547	Y69192	Homo sapiens	A human monocyte-macrophage apolipoprotein B receptor protein.		100
548	Y91493	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:166.	176	99
549	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	1953	88
550	AF044588	Homo sapiens	protein regulating cytokinesis 1; PRC1 Human secreted protein clone pe584_2 protein	1224	94
551	Y29332	Homo sapiens	sequence.	122	1
552	X98330	Homo sapiens	ryanodine receptor 2	24621	99
553	Y42782	Homo sapiens	Human UC Band #331 protein.	684	95
554	AB025258	Mus musculus	granuphilin-a	501	41
555	AJ010346	Homo sapiens	RING-H2	1468	100
556	W92388	Homo sapiens	Human TR-interacting protein S239a.	538	92
557	AF119851	Homo sapiens	PRO1722	175	59 32
558	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	183	J
559	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	319	93
560	D86214	Mus musculus	Ca2+ dependent activator protein for secretion	1010	<u> </u>
561	AF187325	Canis familiaris	melanoma antigen	287	55
562	AJ001981	Homo sapiens	OXAIL	2512	99
563	Z17238	Rattus norvegicus	glutamate receptor subtype delta-1	338	66
564	W30638	Homo sapiens	Partial human 7-transmembrane receptor HAPO167 protein.	371	100
565	AC005620	Homo sapiens	R33590 1	467	97
566	Y99358	Homo sapiens	Human PRO1772 (UNQ834) amino acid sequence SEQ ID NO:63.	1138	78
567	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1002	58
568	AF151043	Homo sapiens	HSPC209	798	100

SEO	Accession	Species	Description	Smith- Waterman	% Identity
D	No.	•		Score	Identity
10:				231	100
69	AF097518	Homo sapiens	liver-specific transporter	1532	100
70	AB035698	Homo sapiens	Misshapen/NIK-related kinase MINK-1	1064	100
71	Y07096	Homo sapiens	Colon cancer associated antigen precursor	1004	100
			sequence. dJ889M15.3 (novel protein)	735	55
72	AL031177	Homo sapiens	Membrane-bound protein PRO290.	254	45
73	Y66639	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
574	AB037108	Homo sapiens	This gene is novel.	836	100
575	D43949	Homo sapiens	Human breast tumour-associated protein 57.	108	50
576	Y48596	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	141	75
577	G00352	Homo sapiens	Neural thread protein.	140	65
578	R95913	Homo sapiens	unnamed protein product	201	70
579	AK025116	Homo sapiens	Human gene 52-encoded protein fragment, SEQ	77	70
580	Y86473	Homo sapiens	ID NO:388.		
581	AF196779	Homo sapiens	JM10 protein	450	100
582	AF188706	Homo sapiens	g20 protein	330	98
583	AB030234	Canis	D4 dopamine receptor	64	56
203	AD030234	familiaris		015	100
584	G02621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
585	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	268	62
			Antigen)	226	35
586	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	235	56
587	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	132	79
588	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	764	80
589	AF235017	Mus	2P1 protein	704	"
		musculus	La La La La La La La La La La La La La L	329	81
590	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	1 32	1
	<u> </u>		HPMBQ32. Amino acid sequence of a human secreted	110	43
591	Y30709	Homo sapiens		1	1
			protein. A human seven transmembrane signal transducer	1369	92
592	Y53875	Homo sapiens	polypeptide.	1	
		Homo sapiens	Human secreted protein clone dd119_4 protein	1112	97
593	Y53051	Homo sapiens	sequence SEQ ID NO:108.		
- 40.4	7105(50	Homo sapiens	Human secreted protein encoded by gene No. 92.	763	79
594	Y27658	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	156	58
595	G03798 AF151110	Mus	COP1 protein	2215	95
596	WE 121110	musculus		<u> </u>	
597	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	157	65
598	AF192499	Mus	putative secreted protein ZSIG37	143	40
390	FE 152455	musculus		 	76
599	AF119855	Homo sapiens	PRO1847	236	73
600.	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	88
601	Y00295	Homo sapiens	Human secreted protein encoded by gene 38.	567	74
602	AF184971	Homo sapiens	class II cytokine receptor ZCYTOR7	2015	96
603	AF061936	Homo sapiens	diacylglycerol kinase iota	773 1333	93
604	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	1333	33
			Antigen)	3915	100
605	AB033106	Homo sapiens	KIAA1280 protein	3916	99
606	X75756 ·	Homo sapiens	protein kinase C mu	5758	99
607	D86983	Homo sapiens		1377	199
608	W69341	Homo sapiens		339	82
609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	337	
		 	1 11	116	62
610	Y27868	Homo sapiens	107.		
<u></u>	1700000	Homo sapiens		2164	100
611	AF202636			218	82
612	AF090944	Homo sapiens		195	59
613	Y02693	Homo sapiens	clone HTDAD22.	<u> </u>	
	100000	Pottus	lens membrane protein	450	84
614	M87053	Rattus norvegicus	10110 HIGHIOLOGIC P. C. C.		
7	AC004020	Homo sapiens	FPM315	163	37
615	AC004232	Homo sapiens		205	79

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO: 517	Y91524	Homo sapiens	Human secreted protein sequence encoded by	821	99
			gene 74 SEQ ID NO:197.	2258	99
518	AJ245621	Homo sapiens	CTL2 protein Human secreted protein encoded by gene 75.	108	64
519	Y76198	Homo sapiens		3922	94
20	AF067864	Homo sapiens	transferrin receptor 2 alpha Transmembrane protein dppC	573	90
521	D90721	Escherichia coli		730	100
522	W75858	Homo sapiens	Human secretory protein of clone CS752-3.	733	100
523	Y94982	Homo sapiens	Human secreted protein vb12_1, SEQ ID NO:4.	637	83
524	AF034745	Mus musculus	LNXp80	94	46
	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, IPPPNMSLPLS (3x)		70
526	U79260	Homo sapiens	unknown	194	50
627	R95913	Homo sapiens	Neural thread protein.	99	100
528	G03450	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.		100
529	Y36281	Homo sapiens	Human secreted protein encoded by gene 58.	590	76
530	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	165	96
531	G02139	Homo sapiens	Human secreted protein, SEQ ID NO: 6220.	268	80
532	U16996	Homo sapiens	protein tyrosine posphatase	351	100
533	AF121857	Homo sapiens	sorting nexin 7	340	77
634	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899		
635	Y07090	Homo sapiens	Renal cancer associated antigen precursor sequence.	277	64
636	AB013382	Homo sapiens	DUSP6	414	76
637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
638	M95762	Rattus norvegicus	GABA transporter	924	89
639	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
640	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	137	79
641	AC008075	Arabidopsis thaliana	F24J5.4	121	33
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96 clone HAQBK61.	615	
643	AB015982	Homo sapiens	serine/threonine kinase	485	98
644	Y25806	Homo sapiens	Human secreted protein fragment encoded from gene 23.	162	
645	AF122904	Homo sapiens	membrane protein DAP10	474	100 38
646	AF233323	Homo sapiens	Fas-associated phosphatase-1	200	
647	W48804	Homo sapiens	Homo sapiens clone BK158_1 protein.	1203	99
648	AF257330	Homo sapiens	COBW-like protein	1440 233	73
649	Y36203	Homo sapiens	Human secreted protein #75.		$\frac{173}{78}$
650	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	173	100
651	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.		32
652	AB032909	Hylobates agilis	dopamine receptor D4	122	<u> </u>
653	AK021848	Homo sapiens	unnamed protein product	186	69
654	W73411	Homo sapiens	Human secreted protein encoded by Gene No. 15.	57	37
655	L22455	Rattus norvegicus	mu opioid receptor	116	34
656	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	110	45
657	G02345	Homo sapiens	Human secreted protein, SEQ ID NO: 6426.	459	97
658	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBO32.	291	75
659	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	65
660	Y91423	Homo sapiens	Human secreted protein sequence encoded by gene 11 SEQ ID NO:144.	333	96

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			Human secreted protein, SEQ ID NO: 7870.	168	68 .
61	G03789		A suppressor of cytokine signalling protein	375	43
662	Y53886	Homo sapiens	designated HSCOP-6.		
			Human GTP binding protein APD08.	629	100
563	W75771	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor	480	55
564	AL096770	Homo sapiens	(rhodopsin family) (olfactory receptor like)		
			(modopsin ramily) (oractory receptor rate)		i
			protein (hs6M1-21))	978	96
665	AB037734	Homo sapiens	KIAA1313 protein	192	84
666	W82841	Homo sapiens	Human cerebral protein-1.	182	87
667	W82841	Homo sapiens	Human cerebral protein-1.	757	68
668	AB030184	Mus	contains transmembrane (TM) region and ATP	131	00
		musculus	binding region	85	37
669	AB032919	Hylobates	dopamine receptor D4	63	13"
003		muelleri		746	81
670	AF107295	Rattus	outer membrane protein	/40	01
070	1	norvegicus			93
671	Z33642	Homo sapiens	leukocyte surface protein	394	93
672	W85608	Homo sapiens	Secreted protein clone du410 5.	261	
	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
673	AL035587	Homo sapiens	d1475N16.4 (KIAA0240)	2388	99
674	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	1134	53
675		Homo sapiens	Human secreted protein, SEO ID NO: 7878.	174	74
676	G03797	Bos taurus	pyruvate dehydrogenase phosphatase regulatory	1013	95
677	AF026954	Bos murus	subunit precursor; PDPr		
	<u> </u>	1.	receptor protein-tyrosine kinase	545	96
678	L11625	Mus	leceptor protoni-syrooms	_	
		musculus	dJ167A19.3 (novel protein)	745	100
679	AL031427	Homo sapiens	olfactory receptor	528	77
680	AJ133430	Mus	olizaciory receptor	1	
		musculus	Human secreted protein, SEQ ID NO: 6613.	179	70
681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	336	76
682	G03789	Homo sapiens	Human secreted protein clone yt14_1 protein	118	100
683	Y94943	Homo sapiens	Human secreted protein clone yer4_1 protein	1	1
			sequence SEQ ID NO:92.	100	37
684	U43360	Peromyscus	reverse transcriptase	1	-
	[maniculatus	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	162	60
685	G00885	Homo sapiens	Human secreted protein, SEQ ID NO: 4966.	590	100
686	AK001518	Homo sapiens	unnamed protein product	718	100
687	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	2405	99
688	Y92241	Homo sapiens	Human cancer associated antigen precursor	2403	1
		\ '	(MO-REN-46).	423	36
689	AC024792	Caenorhabditi	contains similarity to TR:P78316	723	"
		s elegans	V-	183	81
690	Y27868	Homo sapiens	Human secreted protein encoded by gene No.	105	1
	ŀ		107.	180	88
691	Y56514	Homo sapiens	Human Jurkat cell clone P2-15 AIM10 longest	180	1 00
]			OPF protein sequence.	1520	99
692	Y27795	Homo sapiens	Human secreted protein encoded by gene No. 79.	1539	98
693	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	428	89
694	U12465	Homo sapiens	ribosomal protein L35	308	
695	Y45272	Homo sapiens	Human secreted protein encoded from gene 16.	1517	99
	AF191838	Homo sapiens	TANK hinding kinase TBK1	1242	98
696	Y02693	Homo sapiens		275	75
697	102093	Tronio sapions	alone HTDAD22		
(00	1/07000	Homo sapiens		576	90
698	Y87280	Lionio sabiens	57 SPO ID NO:57.		
	1,00000	Tioms conicas	The state of the s	729	99
699	Y97999	Homo sapiens	ID NO:1.	1	
			- Islando	610	79
700	AJ006701	Homo sapiens	. 000	2357	100
701	AF209198	Homo sapiens	zinc finger protein 277	709	45
702	AJ298841	Mus	torsinA protein	1 '	
i		musculus	1	622	98
703	AK021729	Homo sapiens	unnamed protein product	920	51
704	Z46787	Caenorhabdit	similar to Glutaredoxin, Zinc finger, C3HC4	120	"
1	}	s elegans	type (RING finger)	589	98
705	G02882	Homo sapiens	Human secreted protein, SEQ ID NO: 6963.	707	1 70

EQ	Accession	Species	Description	Smith- Waterman	% Identity
5	No.	•		Score	Identity
o:			eno m NO. (592	125	58
06	G02501		Human secreted protein, SEQ ID NO: 6582.	121	95
07	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain	121	33
			ligand (clone 2DD).	125	39
08	G03002	Homo sapiens	Human secreted protein, SEQ ID NO: 7083.	516	98
09	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	131	59
10	M63577 .	Saccharomyc es cerevisiae	SFP1		85
711	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	467	
112	D21211	Homo sapiens	protein tyrosine phosphatase (PTP-BAS, type 3)	368	44
713	AF044033	Marmota marmota	olfactory receptor	615	83
71.4	G03561	Homo sapiens	Human secreted protein, SEQ ID NO: 7642.	251	100
114	AB033062	Homo sapiens	KIAA1236 protein	1380	100
115	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	73
7 <u>16</u> 717	Y96864	Homo sapiens	SEO ID 37 from WO0034474.	835	99
718	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	234	100
719	U47334	Homo sapiens	similar to chicken gamma aminobutyric acid receptor beta4 subunit	578	99
700	AB020598	Homo sapiens	pentide transporter 3	1096	100
720 721	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	570	74
	105045	Homo sapiens	insulin recentor-related receptor	6787	100
722 723	J05046 AF001958	Ambystoma tigrinum	electrogenic Na+ bicarbonate cotransporter; NBC	111	41
724	AF127084	Mus	semaphorin cytoplasmic domain-associated	5253	94
	1	Homo sapiens	GABA transporter	3114	99
725 726	X54673 AF016191	Rattus	potassium channel	370	100
727	AB029559	norvegicus Rattus	BATI	139	35
	<u> </u>	norvegicus	HGFH3 Human Growth Factor Homologue 3.	2186	97
728	Y28503 AJ011415	Homo sapiens Homo sapiens	plexin-B1/SEP receptor	729	56
729 730	Z93096	Homo sapiens	bK390B3.1 (manic fringe (Drosophila) homolog)	142	68
731	Z10062	Homo sapiens	cDNA encoding a human vanilloid receptor homologue Vanilrep1.	675	99
	177161202	Homo sapiens	HSPC264	492	94
732	AF161382 AB029033	Homo sapiens	KIAA1110 protein	3826	99
733 734	AE000493	Escherichia	putative transport protein	592	97
735	AL033379	Homo sapiens	dJ417O22.2 (novel 7 transmembrane receptor (rhodopsin family) protein similar to high- affinity lysophosphatidic acid receptor homolog)	2173	99
736	AF132599	Homo sapiens		245	56
777	X55019	Homo sapiens	acetylcholine receptor delta subunit	883	99.
737	X91906	Homo sapiens	voltage-gated chloride ion channel	1978	100
738 739	AB026116	Homo sapiens	organic anion transporter 4	1444	98
740	D00570	Mus musculus	open reading frame (196 AA)	83	24
741	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	118	40
742	U66059	Homo sapiens	V segment translation product	614	100
743	AF119815	Homo sapiens	G-protein-coupled receptor	2751	99
744	X16663	Homo sapiens	haematonoietic lineage cell protein (AA 1-486)	148	93
745	W67838	Homo sapiens		448	95
746	W57260	Homo sapiens	Human semaphorin Y.	2414	. 100
746 747	W21578	Homo sapiens	Alzheimer's disease protein encoded by DNA	968	65
748	Y94935	Homo sapiens	1 1 1010 1	622	100
		<u> </u>		314	85
749	AL022238	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	391	87

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
751	AB025258	Mus musculus	granuphilin-a	773	41
	144000	Homo sapiens	Human transmembrane protein HP02000.	900	99
752	Y52386		Human breast tumour-associated protein 47.	2527	99
753	Y48586	Homo sapiens	putative G protein-coupled receptor 92	694	100
754	AJ272207	Homo sapiens		979	68
755	M85183	Rattus norvegicus	vasopressin receptor		
756	AF190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	71
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
758	722535	Homo sapiens	ALK-3	439	98
759	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	564	97
760	W74902	Homo sapiens	Human secreted protein encoded by gene 175 clone HE8BI92.	1217	99
		VIana conione	Human secreted protein, SEQ ID NO: 7787.	223	88
761	G03706	Homo sapiens	KIAA0869 protein	4433	99
762	AB020676	Homo sapiens	unnamed protein product	2285	99
763	AK026992	Homo sapiens	glucocorticoid receptor AF-1 coactivator-1	573	100
764	AF173358	Homo sapiens		2019	89
765	AF268066	Mus musculus	netrin 4	1169	89
766	Y48585	Homo sapiens	Human breast tumour-associated protein 46.	309	45
767	AF230378	Mus musculus	interleukin-1 delta		
768	AF121975	Mus musculus	odorant receptor S18	268	62
769	AB008515	Homo sapiens	RanBPM	611	57
770	Y09945	Rattus norvegicus	putative integral membrane transport protein	458	50
771	AF226731	Homo sapiens	AD026	688	99
771 772	Y27132	Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
	X87832	Homo sapiens	NOV/plexin-A1 protein	1821	98
773 774	AB025258	Mus	granuphilin-a	500	41
		musculus	HSPC040 protein	232	93
775	AF125101	Homo sapiens	Human secreted protein, SEQ ID NO: 6896.	314	95
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	191	68
777	G02493	Homo sapiens	Sequence of pre-human atrial natriuretic peptide.	213	45
778	R03301	Homo sapiens	Sequence of pre-human arrial narriarede peptide.	232	100
779 780	AL357374 AF100346	Homo sapiens Homo sapiens	bA353C18.2 (novel protein) neuronal voltage gated calcium channel gamma-	1434	89
781	Y19566	Homo sapiens	3 subunit Amino acid sequence of a human secreted	103	52
	1		protein. Human secreted protein encoded by gene 10.	1098	93
782	Y36233	Homo sapiens	GTP-binding protein REM2	141	30
783	AF084464	Rattus norvegicus		2693	99
784	W49042	Homo sapiens	Human low density lipoprotein binding protein LBP-3.		91
785	AF238381	Homo sapiens	PTOV1	1904	
786	Y91870	Homo sapiens	Human apoptosis related protein.	547	100
787	Y71062	Homo sapiens	Human membrane transport protein, MTRP-7.	1062	94
788	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	8684	98
789	AL049569	Homo sapiens	dJ37C10.3 (novel ATPase)	2848	96
790	AF151848	Homo sapiens	CGI-90 protein	745	96
791	Y08639	Homo sapiens	nuclear orphan receptor ROR-beta	1421	95
792	Y41706	Homo sapiens	Human PRO381 protein sequence.	644	99
793	AF121228	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP95	1037	100
<u></u>			Human secreted protein, SEQ ID NO: 8153.	124	62
794 795	G04072 Y69384	Homo sapiens Homo sapiens	Amino acid sequence of a 14274 receptor	119	100
1	W40215	Homo sapiens	protein. Human macrophage antigen.	1358	99

SEQ ID	Accession No.	Species	Description .	Smith- Waterman Score	% Identity
NO:	470.50240	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
797	AF258340		FGF receptor activating protein 1	461	98
798	AF159615	Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
799	Y59863	Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
800	W70459	Homo sapiens		1913	93
801	L00073	Homo sapiens	renin	11963	97
802	P92219	Homo sapiens (human)	CRI protein.		
803	X15357	Homo sapiens	ANP-A receptor preprotein (AA -32 to 1029)	5199	98
804	W64473	Homo sapiens	Human secreted protein from clone EC172_1.	4018	95
805	AJ243874	Homo sapiens	olieophrenin-4	2067	100
806	G01731	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
		Homo sapiens	garp	1562	83
807	Z24680	Homo sapiens	glycoprotein-associated amino acid transporter	1364	90
808	AF171669		LAT2	1154	96
809	W70321	Homo sapiens	Secreted protein CC198_1.	855	99
810	W74843	Homo sapiens	Human secreted protein encoded by gene 115 clone HOVBA03.	·	
811	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
812	AF092135	Homo sapiens	PTD014	862	100
813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	784	100
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone gn114 1.	358	100
817	G01082	Homo sapiens	Human secreted protein, SEQ ID NO: 5163.	549	100
	AF151800	Homo sapiens	CGI-41 protein	1106	95
818	L00352	Homo sapiens	low density lipoprotein receptor	3980	100
819		Homo sapiens	IGF-I receptor	5832	99
820	X04434	Homo sapiens	Human secreted protein, SEQ ID NO: 7925.	572	100
821	G03844		TERA	396	48
822	AF212220	Homo sapiens	Human glycophosphatidylinositol-anchored	4897	99
823	Y50125	Homo sapiens	protein GPI-122.	2675	98
824	AF156778	Homo sapiens	ASB-3 protein	1105	100
825	AF096322	Homo sapiens	neuronal voltage-gated calcium channel gamma- 2 subunit		100
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded from gene 28.	1540	
827	AB032013	Homo sapiens	potassium channel Kv8.1	2435	95
828	Y13620	Homo sapiens	BCL9	5284	96
829	Y91474	Homo sapiens	Human secreted protein sequence encoded by gene 24 SEQ ID NO:147.	541	98
020	V64222	Homo sapiens	glypican	1625	87
830	X54232	Homo sapiens	acetylcholine recentor beta-subunit preprotein	2540	100
831	X14830		Human chondromodulin-like protein, Zchm1.	1002	100
832	Y71262 .	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	638	96
833	G03873	Homo sapiens	R29828 1	1389	93
834	AC003030	Homo sapiens	Human secreted protein.	964	87
835	Y38422	Homo sapiens	glycine-rich	85	36
836	U41557	Caenorhabditi s elegans		998	75
837	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))		60
838	AJ011415	Homo sapiens	plexin-B1/SEP receptor	1580	67
839	W80398	Homo sapiens	A secreted protein encoded by clone cw1543_3.	1105	
840	G00862	Homo sapiens	Human secreted protein, SEQ ID NO: 4943.	255	92
841	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
842	AF036717	Homo sapiens	FGFR signalling adaptor SNT-1	2629	99
	Y73446	Homo sapiens	Human secreted protein clone yc27_1 protein sequence SEQ ID NO:114.	1089	100
843			andmorran and mission	1 2 2 2	69
	000000	Vomo coniena	Human secreted protein, SEO ID NO: 6953.	357	0.5
844	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	1443	88
	G02872 AF151810 X83378	Homo sapiens Homo sapiens Homo sapiens	CGI-52 protein		

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
ID NO:	No.			Score	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
			to AF038969 (PID:g2827207)	170	17/
848	X99886	Homo sapiens	monocyte chemotactic protein-2	160	76 98
849	AC005587	Homo sapiens	similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)	963	
850	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
851	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
852	Y86217	Homo sapiens	Human secreted protein HWHGU54, SEQ ID NO:132.	1189	99
853	AF224741	Homo sapiens	chloride channel protein 7	3748	99
854	X17094	Homo sapiens	furin (AA 1-794)	3550	99
855	W78245	Homo sapiens	Fragment of human secreted protein encoded by gene 19.	1245	99
856	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	1926	100
857	Y41765	Homo sapiens	Human PRO1083 protein sequence.	3211	99
858	AF057306	Homo sapiens	transmembrane proteolipid	481	84
859	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone HLDRM43.	824	100
862 .	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived protein #375.	96	30
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	211	67
866	X54870	Homo sapiens	Type II integral membrane protein	1201	100
867	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
868	Y07894	Homo sapiens	Human secreted protein fragment encoded from gene 43.	388	88
869	J00123	Homo sapiens	preproenkephalin (1349	95
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:305.	1048	98
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	237	93
872 ·	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	960	94
873	AF161382	Homo sapiens	HSPC264	1124	99
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100 96
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573 171	56
876	M15530	Homo sapiens	B-cell growth factor	1652	99
877	W63681	'Homo sapiens	Human secreted protein 1.	1448	98
878	L27867	Rattus norvegicus	neurexophilin		100
879	Y10835	Homo sapiens	Amino acid sequence of a human secreted protein.	321	
880	W88991	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
881	AF118670	Homo sapiens	orphan G protein-coupled receptor	1971	100
882	AF208865	Homo sapiens	EDRF	528 209	72
883 884	Y18462 Y94950	Homo sapiens Homo sapiens	cathepsin L Human secreted protein clone dh1073_12 protein	348	100
005	APOTOCCI	Uarra arrive	sequence SEQ ID NO:106. HSPC005	404	100
885	AF070661 Y04315	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 23.	385	100
886 887	X92744	Homo sapiens	hBD-1	375	100
888	Y22496	Homo sapiens Homo sapiens	Human secreted protein sequence clone cn621 8.	994	94
889	Y41293	Homo sapiens	Human soluble protein ZTMPO-1.	4595 ·	99
890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	63
891	AF208856	Homo sapiens	BM-014	1012	99
892	U29195	Homo sapiens	neuronal pentraxin II	2002	98
893	X68149	Homo sapiens	Burkitt lymphoma receptor 1	1953	100
894	Y94914	Homo sapiens	Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	537	100
895	W61630	Homo sapiens	Clone HNFGW06 of EGFR receptor family.	326	63
896	M24110	Homo sapiens	G0S19-2 peptide precursor	481	100
897	Z68747	Homo sapiens	imogen 38	2018	99
898	AF186112	Homo sapiens	neurokinin B-like protein ZNEUROK1	619	100
899	AF225420	Homo sapiens	AD025	734	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			Sequence of human lipocortin.	1835	100
900	P60657	Homo sapiens	oncostatin M	1297	99
901	M27288	Homo sapiens Homo sapiens	Polypeptide with transmembrane domain.	749	100
902	W85737		Human secreted protein, SEQ ID NO: 5430.	650	99
903	G01349	Homo sapiens	Human secreted protein encoded by gene 4.	1133	99
904	Y00261	Homo sapiens	antigen NY-CO-3	771	99
905	AF039688	Homo sapiens		2544	100
906	AB007836	Homo sapiens	Hic-5	224	100
907	AB017507	Homo sapiens	Apg 12 unnamed protein product	1537	98
908	AK000056	Homo sapiens	Human secreted protein HFOXB55, SEQ ID	427	100
909	Y86299	Homo sapiens	NO:214.		99
910	AF231023	Homo sapiens	protocadherin Flamingo 1	7393	100
911	Y14134	Homo sapiens	Vascular endothelial cell growth inhibitor beta	1319	100
			protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding	1950	100
912	Z90420	Homo sapiens	CONA		100
913	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	1361	48
914	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	
915	U14971	Homo sapiens	ribosomal protein S9	886	90
916	AF172854	Homo sapiens	cardiotrophin-like cytokine CLC	1204	99
917	AC005525	Homo sapiens	F22162_1	1963	100
918	AF166350	Homo sapiens	ST7 protein	4711	99
919	Y87285	Homo sapiens	Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.	430	100
020	Y36131	Homo sapiens	Human secreted protein #3.	465	88
920		Homo sapiens	cytokine-like protein C17	724	100
921	AF193766	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.	357	100
922	Y95013	Homo sapiens	protein tyrosine kinase-receptor	5256	100
923	X75208	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	813	98
924	Y96202	Homo sapiens	down-regulated in gastric cancer	785	78
925	AB039886	Homo sapiens	Human secreted protein, SEQ ID NO: 7449.	55	50
926	G03368	Homo sapiens	Human breast tumour-associated protein 67.	539	100
927	Y48606	Homo sapiens	Human secreted protein #23.	668	100
928	Y36151	Homo sapiens	elongation factor Ts	1666	100
929 930	AF110399 AF210317	Homo sapiens	facilitative glucose transporter family member	2763	99
		<u> </u>	HTRM clone 082843 protein sequence.	931	100
931	Y73328	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
932	G01959	Homo sapiens	B-cell receptor associated protein	1469	100
933	U47924	Homo sapiens	Human secreted protein, SEQ ID NO: 7908.	529	93
934	G03827	Homo sapiens	mitochondrial ABC transporter 3	196	63
935 936	AB039371 X56385	Homo sapiens Canis	rab8	1064	100
930	A30363	familiaris		117	44
937	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	1	
938	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	1064	99
939	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	515	42
940	Y16630	Homo sapiens	Human Putative Adrenomedullin Receptor (PAR).	1904	99
941	AC005102	Homo sapiens	small inducible cytokine subfamily A member 24	627	99
042	1112004	Homo sapiens	T-cell receptor beta chain	1289	81
942	M12886	Homo sapiens		1049	98
943	AF226046		CEO	667	100
944	¥36078	Homo sapiens	ID NO. 463.	565	100
945	M22877	Homo sapiens	cytochrome c	551	93
946	W67869	Homo sapiens	L clone HHGDB72.	l	
947	W67859	Homo sapiens		283	100
948	W85726	Homo sapiens		789	100
. 4/1X				4236	100
949	AJ242015	Homo sapiens	eMDC II protein Human secreted protein, SEQ ID NO: 8156.	1 4230	99

EQ	Accession	Species	Description	Smith- Waterman	% Identity
2	No.	İ		Score	\
<u>0:</u>		Mama conione	candidate tumor suppressor p33 ING1 homolog	1314	100
1	AF110645	Homo sapiens	Extended human secreted protein sequence, SEQ	402	70
52	Y36111	Homo sapiens	ID NO. 496.		
			APC10	990	100
53	AB012109	Homo sapiens	transmembrane protein BRI	1405	100
54	AF246221	Homo sapiens	putative transmembrane GTPase	1883	100
55	AF054986	Homo sapiens	putative transmembrane G17 asc	1879	100
56	W74726	Homo sapiens	Human secreted protein fg949_3.	1581	100
57	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	1920	100
58	AJ222967	Homo sapiens	cystinosin	587	100
)59	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein.	387	100
ן פכי	1 33032	120410 0-7	cacuance SEO ID NO:110.		100
-	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	283	100
960		Homo sapiens	CGI-97 protein	1214	96
961	AF151855	Homo sapiens	diabetes mellitus type I autoantigen	250	65
62	U26592		dJ475B7.2 (novel protein)	3796	100
963	AL050306	Homo sapiens		2089	100
964	AF078859	Homo sapiens	PTD004 homologue of mouse dkk-1 gene:Acc#	1466	100
965	AB020315	Homo sapiens	homologue of mouse akk-1 gene. Accor		
-			AF030433	6580	99
966	X04571	Homo sapiens	precursor polypeptide (AA -22 to 1185)	993	99
967	AF146019	Homo sapiens	henatocellular carcinoma antigen gene 320	632	100
968	AF071002	Homo sapiens	mink related pentide 1: MIRPI		100
	AB021227	Homo sapiens	membrane-type-5 matrix metalloproteinase	3545	
969	AF180920	Homo sapiens	cyclin L ania-6a	1579	100
970		Homo sapiens	K-Cl cotransporter KCC4	5621	99
971	AF105365	Homo sapiens	ribocomal protein 1.26 homolog	739	100
972	AF083248		hyperpolarization-activated cyclic nucleotide	6295	100
973	AJ132429	Homo sapiens	gated cation channel hHCN4		
			Clone HTPEF86 of TM4SF superfamily.	454	100
974	W61619	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
975	AF155100	Homo sapiens		11763	99
976	AF275948	Homo sapiens	ABCA1	2552	100
977	AB026891	Homo sapiens	cystine/glutamate transporter	3348	99
978	AF117657	Homo sapiens	thyroid hormone receptor-associated protein		
• • •			complex component TRAP80	1570	92
979	AF044201	Rattus	neural membrane protein 35; NMP35	1370	1
		norvegicus		1170	99
980	AF119297	Homo sapiens	neuroendocrine-specific protein-like protein 1	1983	99
981	AF155652	Homo sapiens	potassium channel modulatory factor	1553	99
982	W88499	Homo sapiens	Human stomach carcinoma clone HP10412-	1555	177
702	17 00 123	1	encoded protein.	1000	98
002	Z56281	Homo sapiens	interferon regulatory factor 3	2012	
983	AB026125	Homo sapiens	ADTA	2160	100
984		Homo sapiens	to 1 months and add by	172	70
985	Y14482	LIOINO Sahiens	gene 17.		
	1	Homo sapiens	h-chemokine recentor CCR4	1895	100
986	AB023888	riomo sapiens	Human H1075-1 secreted protein 5' end.	712	100
987	W27291	Homo sapiens	juvenile hormone esterase binding protein	226	32
988	AF153450	Manduca	Juvenine normone escrips ormanic brasser	1	
		sexta	Human secreted protein, SEQ ID NO: 7778.	194	88
989	G03697	Homo sapiens		1486	100
990	AF204159	Homo sapiens	potassium large conductance carctum-activated	1	
			channel beta 3a subunit	558	99
991	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	327	40
992	AL031266	Caenorhabditi	VM106R.1	1 321	100
عرر ا	1.200.200	s elegans		4720	99
993	Y66749	Homo sapiens	Membrane-bound protein PRO1124.	4730	77
993	G01246	Homo sapiens	CEO ID MO: 5327	141	
		Homo sapiens	corin	5811	99
995	AF133845			4999	100
996	AF117756	Homo sapiens	complex component TRAP150		
L				284	93
997	W62066	Homo sapien:		725	100
998	Y87173	Homo sapien			
	1	1	NO:212.	1654	99
999	Y13379	Homo sapien			47
1000		Homo sapien	Human secreted protein vi3_1, SEQ ID NO.36.	1747	100
1 2000	AF190167	Homo sapien	s membrane associated protein SLP-2	1/4/	1.00

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	398	96
1002	W73420	Homo sapiens	Human secreted protein encoded by Gene No.	2150	100
1003			24.	742	100
004	X12791	Homo sapiens	19kD SRP-protein (AA 1 - 144)	642	100
005	M23323	Homo sapiens	membrane protein		98
006	X63745	Homo sapiens	KDEL receptor	326	
1007	Y35997	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 382.	824	99
008	AB032918	Hylobates moloch	dopamine receptor D4	92	35
1009	Y91680	Homo sapiens	Human secreted protein sequence encoded by gene 81 SEQ ID NO:353.	1372	99
1010	AL136125	Homo sapiens	dJ304B14.1 (novel protein)	825	98
011	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	379	98
012	Y17531	Homo sapiens	Human secreted protein clone BL205 14 protein.	818	97
	G00724	Homo sapiens	Human secreted protein, SEQ ID NO: 4805.	462	100
013		Naegleria	haem lyase	114	37
1014	AF288092	gruberi		3867	99
015	AB045292	Homo sapiens	M83 protein	644	100
1016 ·	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	1876	100
017	Y94873	Homo sapiens	Human protein clone HP02632.		100
018	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	589	
1019	X83425	Homo sapiens	Lutheran blood group glycoprotein	3054	99
020	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	100
021	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.	768	100
1023	AE000660	Homo sapiens	hADV36S1	573	100
1023	AF132965	Homo sapiens	CGI-31 protein	1550	100
	W92380	Homo sapiens	Human TR-interacting protein S103a.	1466	97
1025 1026	R66278	Homo sapiens	Therapeutic polypeptide from glioblastoma cell line.	830	100
	120000	77	S100P calcium-binding protein	476	100
1027	X65614	Homo sapiens	Human PRO704 protein sequence.	1323	100
1028	Y41741	Homo sapiens		806	100
1029	AJ001014	Homo sapiens	RAMP1	1354	99
1030	W63682	Homo sapiens	Human secreted protein 2.	766	100
1031	AK023007	Homo sapiens	unnamed protein product	2672	99
1032	W97900	Homo sapiens	Human SR-BI class B scavenger.		99
1033	Y82453	Homo sapiens	Human TGC-440 secretory protein SEQ ID NO:1.	639	
1034	Y73473	Homo sapiens	Human secreted protein clone yd178_1 protein sequence SEQ ID NO:168.	752	93
1035	Y86468	Homo sapiens	Human gene 48-encoded protein fragment, SEQ ID NO:383.	96	90
1036	U09813	Homo sapiens	mitochondrial ATP synthase subunit 9 precursor	698	100
1037	AJ242832	Homo sapiens	calpain	3699	99
1038	X66403	Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
1039	AJ242730	Homo sapiens	polyhomeotic 2	1310	100
1040 .	AF169968	Mus musculus	DNA binding protein DESRT	1453	80
1041	X52563	Bos taurus	permability increasing protein	383	29
1041	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	75	50
	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	60	53
1043			interleukin 8 receptor B	1850	100
1044	M94582	Homo sapiens	bG256O22.1 (similar to IGFALS (insulin-like	1704	50
1045	AL080239	Homo sapiens	growth factor binding protein, acid labile		"
1072	1.5165151	+	subunit)) HSPC040 protein	580	100
1046 1047	AF125101 W74809	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 81	176	100
		1	clone HMWDN32.		1.00
1048	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	2201	100
1049 ·		Homo sapiens	Secreted protein encoded by gene 134 clone HAIBP89.	1559	99
1050	AF097518	Homo sapiens	liver-specific transporter	2820	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO: 1051	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1052	Y21851	Homo sapiens	Human signal peptide-contianing protein (SIGP) (clone ID 2328134).	1643	95
1053	AL163815	Arabidopsis thaliana	putative protein	661	62
1054	Y76200	Homo sapiens	Human secreted protein encoded by gene 77.	262	100
	AJ276567	Homo sapiens	TC10-like Rho GTPase	1160	100
1055 1056	Y27620	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
1057	D14530	Homo sapiens	ribosomal protein	745	100
1058	AF132000	Homo sapiens	TADA1 protein	1132	100
1059	AL031778	Homo sapiens	dJ34B21.1 (novel BZRP (benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)	920	100
1060	AF227135	Homo sapiens	candidate taste receptor T2R9	134	33
1061	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
1062	Z11697	Homo sapiens	HB15	1088	100
1063	AF123757	Homo sapiens	putative transmembrane protein	819	99
1064	AF155135	Homo sapiens	novel retinal pigment epithelial cell protein	2932 936	99
1065	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.		100
1066	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	2575 770	85
1067	Y36087	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 472.	301	100
1068	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	l	100
1069	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	301	99
1070	W64535	Homo sapiens	Human leukocyte cell clone HP00804 protein.	2014	50
1071	X03145	Homo sapiens	pot. ORF III	148	91
1072	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	821 249	62
1073	X82200	Homo sapiens	gpStaf50	99	47
1074	G03213	Homo sapiens	Human secreted protein, SEQ ID NO: 7294.	506	55
1075	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	424	98
1076	G03187	Homo sapiens	Human secreted protein, SEQ ID NO: 7268.	332	76
1077	L25899	Homo sapiens	ribosomal protein L10	898	97
1078	Y91447	Homo sapiens	Human secreted protein sequence encoded by gene 48 SEQ ID NO:168.	290	89
1079	G01862	Homo sapiens	Human secreted protein, SEQ ID NO: 5943.	1376	92
1080	AB039723	Homo sapiens	WNT receptor frizzled-3	269	100
1081	AB020527	Homo sapiens	Na/PO4 cotransporter homolog	499	80
1082	L13802	Homo sapiens	ribosmal protein small subunit Human secreted protein encoded by gene 42	143	81
1083	W75098	Homo sapiens	clone HSXB125.	83	51
1084	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645. Human secreted protein, SEQ ID NO: 8144.	88	43
1085	G04063	Homo sapiens		124	64
1086	AF090942	Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598.	129	41
1087	G00517	Homo sapiens	CEO ID MO. 0172	126	36
1088	G04091	Homo sapiens Homo sapiens		364	82
1089	AF140631		CTO TO 10. 0144	114	32
1090	G04063	Homo sapiens	LMW G-protein	146 .	83
1091 1092	S72304 W88708	Mus sp. Homo sapiens		405	100
1002	W85612	Homo sapiens	Secreted protein clone fh123 5.	4358	97
1093 1094	Y53012	Homo sapiens	Human secreted protein clone pm514_4 protein	1013	99
1095	Y92345	Homo sapiens		409	100
1002	A. T. O. O. O. O.	Homo sapiens		147	60
1096	AF090942	Homo sapiens		166	58
1097	L24521	Homo sapiens	23 kD highly basic protein	490	70
1098	X56932 G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	35
1099 1100	Y02693	Homo sapiens		149	59

-000 T	Accession	Species	Description	Smith-	%
SEQ ID	No.	Species		Waterman Score	Identity
NO:				183	72
1101	AF119851	Trome oupsets	PRO1722 Human secreted protein, SEQ ID NO: 8167.	207	62
1102	G04086	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	91	52
1103	G04063	Homo sapiens	ribosomal protein L28	128	69
1104	X74856	Mus	ribosomai protein L26		1
		musculus	Human secreted protein, SEQ ID NO: 7870.	130	62
1105	G03789	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	48
1106	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	69	43
1107	G03040	Homo sapiens	HCF-binding transcription factor Zhangfei	744	99
1108	AF201951	Homo sapiens	high affinity immunoglobulin epsilon receptor	738	94
1109	AF201931	110mo sapiono	beta subunit		
1110	AF111108	Mus	transient receptor potential 2	223	79
1110	7111100	musculus			1-0
1111	AF119900	Homo sapiens	PRO2822	144	59 39
1112	Y16589	Homo sapiens	A protein that interacts with presenilins.	265 178	67
1113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	164	63
1114	Y02999	Homo sapiens	Fragment of human secreted protein encoded by	104	103
			gene 121.	1217	99
1115	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	130	40
1116	X51394	Хепория	APEG precursor protein	130	"
		laevis	neutral protease large subunit	442	65
1117	M27826	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	72	60
1118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	491	97
1119	G03602	Homo sapiens	Extended human secreted protein sequence, SEQ	244	97
1120	Y35906	Homo sapiens	I ID NO. 155.		
1121	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	65
1121	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	110	90
1123	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1124	AF212862	Homo sapiens	membrane interacting protein of RGS16	442	88 53
1125	W64469	Homo sapiens	Human secreted protein from clone CW795 2.	191	100
1126	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
1127	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	815	99
1128	Y84320	Homo sapiens	Human cardiovascular system associated protein	1 813	
L		<u> </u>	kinase-1. Human secreted protein, SEQ ID NO: 6186.	88	73
1129	G02105	Homo sapiens	Transmembrane domain containing protein clone	700	100
1130	Y32923	Homo sapiens	HP01512.		
1131	Y29817	Homo sapiens	Human synanse related glycoprotein 2.	260	91
1131	Y91644	Homo sapiens	Human secreted protein sequence encoded by	525	96
1132	131011	1101110 000	gene 43 SEO ID NO:317.	1	100
1133	Y91449	Homo sapiens	Human secreted protein sequence encoded by	542	100
1			gene 49.SEQ ID NO:170.	2399	93
1134	AB017908		4F2 light chain	312	55
1135	X51760	Homo sapiens		917	72
1136	Y99426	Homo sapiens	sequence SEQ ID NO:308.	1	
		Home series		102	50
1137	G03790	Homo sapiens Homo sapiens	NY-REN-36 antigen	768	91
1138	AF155106	Homo sapiens	1 1 1	117	50
1139	AL031055	TIOING Sahienz	transport proteins)	<u></u>	
1140	AF011359	Bos taurus	regulator of G-protein signaling 7	138	96
1141	Y70018	Homo sapiens		623	100
1,141	1,0010		(PPRG-12).	1,,,,	20
1142	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	38 48
1143	AB030235	Canis	D4 dopamine receptor	89	70
		familiaris	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	539	88
1144	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein	339	~
			sequence SEQ ID NO:50.	398	96
1145	X99962	Homo sapiens		168	79
1146	G03807	Homo sapiens		512	85
1147	G03712	Homo sapiens	t t to CDTD 1	705	76
1148	Y28279	Homo sapiens		247	36
1149	U13642	Caenorhabditi	CYOH 2 SHIMM TO REMINING TOTAL TOTAL		

~~	Accession No.	Species	Description	Smith- Waterman Score	% Identity
ю:			in a los registance protein		
			cerevisiae zinc resistance protein Human secreted protein, SEQ ID NO: 7519.	117	62
150	G03438		Human secreted protein, SEQ ID NO: 5084	181.	80
	G01003		Human secreted protein, SEQ ID NO: 5084.	198	63
	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	95	41
	X88799	Oryza sativa	DNA binding protein	155	96
	D85245	Homo sapiens	TR3beta		1
	R74272	Homo sapiens	Tumour suppressor protein, p53.	341	87
155 156	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.	99	41
ì			Human secreted protein, SEQ ID NO: 6658.	263	98
157	G02577	Homo sapiens	putative organic anion transporter	185	42
158	AF104334	Homo sapiens	Human secreted protein, SEQ ID NO: 5474.	173	57
159	G01393	Homo sapiens	Human secreted protein, SEQ 10 NO. 5474.	224	81
160	W75771	Homo sapiens	Human GTP binding protein APD08.	410	83
161	AF216833	Homo sapiens	M-ABC2 protein	1156	100
1162	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1136	
			PRO1722	230	70
1163 1164	AF119851 Y87252	Homo sapiens Homo sapiens	Human signal peptide containing protein HSPP-	113	31
, 104	- 0,		1 20 SECTID NO:29.	1220	82
1165	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	64
	AF269286	Homo sapiens	TICK	134	
1166 1167	Y14482	Homo sapiens	Fragment of human secreted protein encoded by	149	51
1168	D90789	Escherichia	Dipeptide transport system permease protein	411	90
		coli	DppC.	344	90
1169	R63783	Homo sapiens	TG0847 protein.	478	98
1170	Y45274	Homo sapiens	Human secreted protein encoded from gene 18.	347	96
1171	D64154	Homo sapiens	Mr 110,000 antigen	311	67
1172	AB026256	Homo sapiens	organic anion transporter OATP-B	60	52
1173	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.		59
1174	D87717	Homo sapiens	similar to human GTPase-activating protein(A49869)	178	
	<u> </u>	Homo sapiens	ribosomal protein	391	78
1175	M64716			285	67
1176	R08330	Homo sapiens		242	72
1177	L06505	Homo sapiens		276	88
1178	AJ251885	Homo sapiens		155	71
1179	G03258	Homo sapiens		282	90
1180	G01207	Homo sapiens	Human secreted protein, SEQ ID NO: 5288.	249	62
1181	AF181856	Rattus	tRNA selenocysteine associated protein	1 247	
		norvegicus		138	90
1182	AF161524	Homo sapiens	HSPG176	282	66
1183	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.		71
1184	Y02671	Homo sapiens	Human secreted protein encoded by gene 22	107	1
	1 000505	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	88	69
1185	G03797	Tiomo sapiens		118	46
1186	G03564 AB032905	Homo sapiens Hylobates	dopamine receptor D4	96	37
	1	concolor		292	78
1188	G00956	Homo sapiens	Human secreted protein, SEQ ID NO: 5037.	178	79
1189	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	324	76
1190	G03361	Homo sapiens	Unman secreted protein, SEO ID NO: 7442.	187	70
1191	AF117755	Homo sapiens	s thyroid hormone receptor-associated protein		
1192	Y70455	Homo sapiens	Human membrane channel protein-5 (MECHP-	202	67
1	1		5). s Human secreted protein, SEQ ID NO: 7133.	99	42
1193	G03052	Homo sapien		192	76
1194	G02607	Homo sapien		2001	98
1195	W29661	Homo sapien	- Lucro conjens C1542 2 clone secreted protein.	239	69
1196	Y14104	Homo sapien	s Human GABAB receptor 1d protein sequence.		90
	X61972	Homo sapien	a macronain subunit inta	149	
1197		Homo sapien	a Unman secreted protein, SEO ID NO: 4615.	145	51
1198 1199	G00534 Y86260	Homo sapien	s Human secreted protein HELHN47, SEQ ID	1089	89
	1		NO:175. s Human secreted protein, SEQ ID NO: 6688.	154	57

200	Accession	Species	Description	Smith-	%
EQ D	No.	Species	2 state page 1	Waterman Score	Identity
10:				404	50
201	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	202	49
202	M27826	Homo sapiens	neutral protease large subunit		61
203	Y73424	Homo sapiens	Human secreted protein clone yi4_1 protein	265	
204	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	625	98
205	7/2/202	Homo sapiens	Human secreted protein #75.	219	59
205	Y36203	Gallus gallus	AQ	205	57
206	U78111	Homo sapiens	putative G protein-coupled receptor	416	76
207	AF095448		PRO2829	127	75
208	AF116715	Homo sapiens	MaxiK channel beta 2 subunit	475	95
209	AF099137	Homo sapiens	hepatocellular carcinoma-related putative tumor	423	79
210	AF205718	Homo sapiens	CURREPORT	224	70
211	Y27868	Homo sapiens	Human secreted protein encoded by gene No.	117	44
212	G00719	Homo sapiens	Human secreted protein, SEQ ID NO: 4800.	351	73
213	G01009	Homo sapiens	Human secreted protein, SEQ ID NO: 5090.		70
214	AF090942	Homo sapiens	PRO0657	124	77
215	Y14427	Homo sapiens	Human secreted protein encoded by gene 17	99	
1216	G03905	Homo sapiens	Human secreted protein, SEO ID NO: 7986.	173	57
216		Homo sapiens	Human transmembrane protein HTMPN-21.	1173	100
1217	Y57897	Homo sapiens	hla-dr antigen alpha chain	454	78
1218	J00194	Homo sapiens	Secreted protein 76-28-3-A12-FLI.	470	92
1219	Y59709		EBV-induced G-protein coupled receptor (EBI-	725	100
1220	W81576	Homo sapiens	polypeptide. High affinity immunoglobulin E receptor-like	650	98
1221	W96745	Homo sapiens	protein (IGERB)	135	31
1222	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 160.	260	95
1223	Y00278	Homo sapiens	Human secreted protein encoded by gene 21.	568	90
1224	AF161422	Homo sapiens	HSPC304		95
1225	U14970	Homo sapiens	ribosomal protein S5	202	100
1226	G01733	Homo sapiens	Human secreted protein, SEQ ID NO: 5814.	610	56
1227	AF099973	Mus musculus	schlafen2	333	
1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	155	81
1229	AF217188	Mus musculus	YIPIB	801	63
1000	A E 10(012	Homo sapiens	soluble adenylyl cyclase	275	100
1230	AF176813	Homo sapiens	examic cation transporter	1704	100
1231 1232	X98333 W74955	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	212	53
1233	Y94940	Homo sapiens		526	100
1234	U76618	Mus	N-RAP	482	82
		musculus	1	380	97
1235	AF044924	Homo sapiens		417	100
1236	G01459	Homo sapiens		164	84
1237	AF000018	Homo sapiens		250	90
1238	W88633	Homo sapiens	HESEU04.		98
1239	W29660	Homo sapiens	Homo sapiens CH27_1 clone secreted protein.	697	
1240	AF004161	Oryctolagus cuniculus	peroxisomal Ca-dependent solute carrier	154	52
1241	Y92710	Homo sapiens	Human membrane-associated protein Zsig24.	709	97
1241		Homo sapiens	Human secreted protein vc34 1, SEQ ID NO:44.	908	88
1242 1243	Y95002 Y44905	Homo sapiens	t developed EDG 197	325	100
L				511	97
1244 1245	AF284422 Y53629	Homo sapiens	A bone marrow secreted protein designated	1888	93
1246	AB039371	Homo sapiens		389 168	97
		Homo sapiens		1 105	1 フブ

SEQ	Accession	Species	Description	Smith-	% Id
D D	No.	Орослов	•	Waterman	Identity
10:		}		Score	ļ
``			ID NO. 160.	559	90
248	AF072509	Rattus	glutamate receptor interacting protein 2	239	30
		norvegicus	A sim shored TP A AV	661	98
249	AF247042	Homo sapiens	tandem pore domain potassium channel TRAAK	1087	97
250	B08974	Homo sapiens	Human secreted protein sequence encoded by	100/	31
1			gene 27 SEQ ID NO:131.	858	59
1251	L15313	Caenorhabditi	putative	030	1 3
		s elegans	1 i alono i/217 2 alternate	278	75
1252	Y29338	Homo sapiens	Human secreted protein clone it217_2 alternate	278	1"
- 1			reading frame protein. Human G-protein receptor HPRAJ70.	211	92
1253	W01730	Homo sapiens	Human G-protein receptor Hr KA3 70. Human secreted protein, SEQ ID NO: 7155.	294	83
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	253	91
1255	G01818	Homo sapiens	Human secreted protein, SEQ ID NO. 3833.	222	54
1256	AF286368	Homo sapiens	eppin-l	87	93
1257	AF220264	Homo sapiens	MOST-1 Human secreted protein, SEQ ID NO: 6308.	281	78
1258	G02227	Homo sapiens	Human secreted protein fragment #2 encoded	81	94
1259	Y07970	Homo sapiens	from gene 26.	1	
		 	Tumor necrosis factor receptor 1 death domain	986	100
1260	R95332	Homo sapiens	ligand (clone 3TW).	1	
	1771465	Yyama sasiana	zinc metalloprotease ADAMTS6	172	36
1261	AF140674	Homo sapiens Homo sapiens	semanhorin V	237	67
1262	U28369	Homo sapiens	Renal cancer associated antigen precursor	288	71
1263	Y07049	Homo sapiens	sequence.		1
10//	Y36153	Homo sapiens	Human secreted protein #25.	187	80
1264	Y78114	Homo sapiens	Human cytokine signal regulator CKSR-2 SEQ	723 ·	93
1265	1/6114	110mo saprons	ID NO:2	l	
1266	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	191	100
1267	AF030558	Rattus	phosphatidylinositol 5-phosphate 4-kinase	859	95
1207	A 030330	norvegicus	gamma		
1268	U73167	Homo sapiens	candidate tumor suppressor gene LUCA-1	159	96
1269	AF190664	Mus	LMBR2	552	76
1205	1	musculus		820	98
1270	AL050332	Homo sapiens	dJ570F3.1 (homolog of the rat synaptic ras	820	98
			GTPase-activating protein p135 SynGAP)	131	95
1271	G02126	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	253	92
1272	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform .	1280	100
1273	AL035661	Homo sapiens	dJ568C11.3 (novel AMP-binding enzyme	1200	1,00
	i	}	similar to acetyl-coenzyme A synthethase	1	
			(acetate-coA ligase))	3523	61
1274	AF064748	Mus	S3-12	3520	
		musculus	TAXREB107	377	78
1275	D17554	Homo sapiens	Amino acid sequence of a human secreted	643	90
1276	Y30715	Homo sapiens	protein.	1 0.0	
	1	177	septin 2-like cell division control protein	707	100
1277	AF146760	Homo sapiens		281	46
1278	Y05069	Homo sapiens Oryctolagus	aorta CNG channel (rACNG)	267	85
1279	X59668	cuniculus	aura Crio dimino (i)		
1000	C01051	Homo sapiens	Human secreted protein, SEQ ID NO: 5132.	489	98
1280	G01051	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	120	43
1281	G03411	Homo sapiens		1635	100
1282	AF055084		odd-skipped related 1 protein	357	98
1283	AF117814	Mus musculus	Ode Sulphas services - Leaves	1	
1204	U87318	Xenopus	NaDC-2	535	60
1284	00/310	laevis		<u></u>	
1285	AF061346	Mus	Edp1 protein	452	68
1265	Ar001340	musculus			
1296	AB030182	Mus	contains transmembrane (TM) region	582	68
1286	7010C0GW	musculus			
1207	A13595	synthetic	immunosuppresive protein PP15	185	97
1287	W13333	construct			
1288	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1	837	100
	AF084205	Rattus	serine/threonine protein kinase TAO1	319	98
1289					

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			membrane associated guanylate kinase 2	523	100
290	AF038563	Homo sapiens	double-stranded RNA specific adenosine	468	100
291	AF034837	Homo sapiens	deaminase		
202	M15888	Bos taurus	endozepine-related protein precursor	937	87
292 293	AB010692	Arabidopsis	ATP-dependent RNA helicase-like protein	636	45
		thaliana	orphan G-protein coupled receptor	1570	100
294	AF209923	Homo sapiens	Human secreted protein encoded by gene 22	504	98
295	W67828	Homo sapiens	alama LICE A EA1	648	65
296	AC004832	Homo sapiens	similar to 45 kDa secretory protein; similar to CAA10644.1 (PID:g4164418)	575	70
297	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein		97
298	G02645	Homo sapiens	Human secreted protein, SEQ ID NO: 6726.	223	
	Y59440	Homo sapiens	Human delta3 fragment #4.	122	32
299 300	W70504	Homo sapiens	Leukocyte seven times membrane-penetrating	459	81
301	Y67315	Homo sapiens.	Human secreted protein BL89_13 amino acid sequence.	3916	99
			spermidine/spermine N1-acetyltransferase	174	96
302	M77693	Homo sapiens	Human secreted protein, SEQ ID NO: 5412.	254	69
303	G01331	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	747	99
304	G01491	Homo sapiens	Human secreted protein, SEQ ID NO. 3372.	602	98
305	AF148509	Homo sapiens	alpha 1,2-mannosidase	333	98
306	G01658	Homo sapiens	Human secreted protein, SEQ ID NO: 5739.	332	98
307	Y90899	Homo sapiens	D1-like dopamine receptor activity modifying protein SEQ ID NO:1.	348	52
308	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein		
	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	147	66
1309	AF063243	Bos taurus	ribosomal protein L30	296	90
1310 1311	AF224494	Mus musculus	arsenite inducible RNA associated protein	688	70
			HTRM clone 2709055 protein sequence.	1154	100
1312 1313	Y73342 Y99419	Homo sapiens Homo sapiens	Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.	1145	78
			sequence SEQ ID IVO.202.	433	97
1314 1315	AF116667 W75100	Homo sapiens Homo sapiens	PRO1777 Human secreted protein encoded by gene 44	807	97
			clone HE8CJ26.	789	100
1316	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	2607	98
1317	AB041533	Homo sapiens	sperm antigen	1 ====	
1318	U19617	Mus musculus	Élf-1	806	92
1319	U82598	Escherichia coli	ferric enterobactin transport protein	768	100
1320	D90892	Escherichia coli	SORBITOL-6-PHOSPHATE 2- DEHYDROGENASE (EC 1.1.1.140) (GLUCITOL-6- PHOSPHATE DEHYDROGENASE) (KETOSEPHOSPHATE	709	100
1321	W67847	Homo sapiens	REDUCTASE). Human secreted protein encoded by gene 41	601	92
1341	110.04.		clone HPBCJ74.	1	
1322	AJ276101	Homo sapiens	GPRC5B protein	466	93
1323	AJ276101	Homo sapiens	CPRC5B protein	504	97
	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1584	100
1324		Rattus	pyridoxine 5'-phosphate oxidase	1277	89
1325	U91561	norvegicus		1	
	17105500	Homo sapiens	NADH-cytochrome b5 reductase isoform	1606	100
1326 1327	AF125533 Y32206	Homo sapiens	Human receptor molecule (REC) encoded by	1531	90
	l		Incyte clone 2825826.	657	85
1328	AF151048	Homo sapiens	HSPC214	1645	100
1320	Y10530	Homo sapiens	olfactory receptor	4314	99
		Homo sapiens	quanine nucleotide exchange factor		99
1329	LAFIXO6KI				1 77
	AF180681 AF111856	Homo sapiens	NaPi-3b		
1329 1330			NaPi-3b	2171	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			Human secreted protein encoded from gene 45.	1380	96
1334	Y25755	Homo sapiens	Human secreted protein encoded from gene 43.	4742	99
1335	AF152325	Homo sapiens	protocadherin gamma A5	639	81
1336	X74070	Homo sapiens	transcription factor BTF3	1931	95
1337	AF095927	Rattus norvegicus	protein phosphatase 2C		
1338	G03877	Homo sapiens	Human secreted protein, SEQ ID NO: 7958.	621	100
	AL008582	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	626	100
1339 ·	1	Homo sapiens	leukemia inhibitory factor receptor	5820	99
1340	X61615		A carcinogenesis-inhibiting protein.	7528	97
1341	Y01519	Homo sapiens	ethanolamine kinase	2372	100
1342	AF207600	Homo sapiens		1167	97
1343	U54807	Rattus norvegicus	GTP-binding protein		
1344	AC020579	Arabidopsis thaliana	putative phosphoribosylformylglycinamidine synthase; 25509-29950	3283	51
			Secreted peptide clone pe503_1.	944	100
1345	Y28576	Homo sapiens	Human secreted protein encoded by gene 58	1171	100
1346	W74787	Homo sapiens	clone HHFHN61.		-
1347	M55542	Homo sapiens	guanylate binding protein isoform I	2636	87
1347	AF183428	Homo sapiens	28.4 kDa protein	1329	100
	U70669	Homo sapiens	Fas-ligand associated factor 3	167	24
1349 1350	AF295530	Homo sapiens	cardiac voltage gated potassium channel modulatory subunit	562	99

TABLE 3

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence 337	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion TPSLIHQAPTPCPAGLWG/PPNGHYHGS*PGC
	1351	A	2	33/	-	HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAGRLPGPAWSWHASGAAPA OPGPL*LLVPGSSGLPDPRDP
2	1352	A	2.7	-100	366	IRNSSIRPMKERETKLSAKHMITCSASYDIRGL QIETT\YHHTPIRMAKIQKT/GHHQC**ECGAT GTLIHGWWGCKVVEPLGKTVWQIPK
3	1353	A	40	3	314	. HASAHASVVLKDNSELEQQLGATGAYRARA LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVVDTH\RTPI*R SCNYTLALILFL
4	1354	A	74	2	292	TASALFSCPDGGSLAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQQARQSPG*RTNPE/ALQWVLPVSDGWH VLPLP
5	1355	A	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRISAHPP NAGGEVSNGPKRKLTLMLNFSLPSSGLNAGA FYALSTLLNRMVIWHYPGEEVNAGRIGLTIVI AGMLGAVISGIWLDRSKTYKETTLVVYIMDT GGAWWCYTFYLGTGDTCG*CFITAGVTMGFF MTGYLPLGFEFAVEL\SYPESEGISSGLLNISA QVFGIIFTISQGQIIDNYGTKPGNIFLCVFLTLG AALTAFIKADLRRQKANKETLEN EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A
6	1356	A	81	97	376	YLRVPFIRILLNAR*IRKAYKRMSLEIKLLI/RE *CI_FOEMGLSLOWLYSARGDFFRATSRL
7	1357	A	93	2	872	TLSSACLIGDAWKELTIVAGAVSNQLLVWYP ATALADNKPVAPDRRISGHVGIIFSMSYLESK GLLATASEDRSVRIWKGGDLRVPGGRVQNIG HCFGHSARVWQVKLLENYLISAGEDCVCLV

				5 1:4:4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Accordic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
,			ļ	peptide	1	/=possible nucleonide deletion, /-possible
		ì	1	sequence		nucleotide insertion
						WSHEGEILQAFRGHQGRGIRAIAAHERQAWV
		1		l .		ITGGDDSGIRLWHLVGRGYRGLG/DLGSLLQ
		ł		l		VP**ARYTQGCDSGWLLATAGSD*YRGPVSL
	1				Į.	*RRGQVLGAAARG*TFPVLLPAGGSSWSRGL
	}	Į	}	ı	1	RIVCYGQWGRSCQGCPHQHSNCCCGPDPVS
		1			į.	WEGAQLELGPAWL
	10.00	A	106	3	350	FSSLLSGRISTLRDETGAILIDGDPAACAPIIKF
8	1358	Α.	100	13	1	LLTEELHLRGVSIYVLRHEAQIYGITPL\VCAL
		1	İ	1	1	LI/CRRL*SDSCMRAALNDRGLYQVLILDGLV
				1		OCT GEVDSDSRKMVSTLT
			1	<u> </u>	186	QAWAIFKGKYKEGDTGGPAVWKTRLRCALN
9	1359	Α	115	49	100	KSSEFNEGPERERMDV
	1				1010	KGCRTQEKVDRTEVIRTCINPVYSKLFTVDFY
10	1360	A	123	2	1249	FEEVQRLRFEVHDISSNHNGLKEADFLGGME
		1		1		CILGQIVSQRKLSKSLLKHGNTAGKSSITVIA
		1	ł	Į.	1	EELSGNDDYVELAFNARKLDDKDFFSKSDPF
		ļ	1		1	EELSGNDD I VELAFNARREDDADI I SROUT
		1	1	1	ļ	LEIFRMNDDATQQLVHRTEVVMNNLSPAWK
	1	1	1		ĺ	SFKVSVNSLCSGDPDRRLKCIVWDWDSNGK
	1	1	1	1	1	HDFIGEFTSTFKEMRGAMEGKQVQWECNPK
	1	1	1	1	1	YKAKKNYKNSGTVILNLCKIHKMHSFLDYI
.37	1	i	1	1		MGGCQIQFTVAIDFTASNGDPRNSCSLHYIHP
•		l l		ì		YQPNEYLKALVAVGEICQDYDSDKMFPAFGF
			l		1	GARIPPEYTDSHDFAINFNEDNPECAGIQGVV
	1	1	1	1		EAVOSCE\PKAPTETGPTNICPHSSRKVAKERR
		l				SEGN*HQGRAFAIIFILVDPGQVGVYSQDMGP
	}	1	1	}		DNPGGHFV
		ــــــــــــــــــــــــــــــــــــــ	1		9	ACARKOLLGRTVFIWFVGOLLGGELKGYSKT
11	1361	A	147	614	1	NTTSSRPASSRG/TLSSSSSSSSSLTKDALPSSL
	ſ			ì		KSDSTTITSGLVFPFRSLCVNPAKSSVSESVSS
	1	1	1	1	1	KILLSSSVKYLE*KRTSCCFPDSSESKLSQLSS
	1	1	i	1	ľ	DERVSMGTSSRKPTNSSSSLGALKMSATS*G
		-	1	ì	i	SGSESPTPFFLTGLQSPPSTRPREPGLTTARNS
	· ·	1	- (1	1	TTLTRDC
						LIPSEPALDSLVDPRVRSRKQPFVIYPVYDTAL
12	1362	A	177	12	416	DTKIHFSLLDGNVGEPDMSAGFCPNHKAAM
		1				VLFLDRVYGIEVQDFLLHLLEGGFLPDLRAA
l	1	1		1	[ASLDT/AEIGAMDFLLS*LFTLCLMMFFFIYPF
		i i		Ì	Ī	
	1	- }		1		NLLTMNYY
13	1363	A	249	535	105	WITHRHLSPAPLIVCDQGTCVVSYYPQNIVQ
13	1303	1	1			MPDTQMEQGLN/HLFLDGNA*PHSVECYCPS
1	1	i	1	1	1	TFEIAIKITSFVLYFHRYRAPEVLLRSSVYSSPI
-	1	1	1	1		DVWAVGSIMAELYMLRPLFPGTSEVDEIFKIC
1		1	1	1		QVLGTPKKVSTLVPKLL
	1264		254	572	201	YLLTXIGNLMMLLVINADSCLRTXM*FFLGH
14	1364	Α	234	1 372		FFFI DICYSSVTAODAAEFPVS*KPILVWGYII
1	1	1			1	*SFFFIFSWGTNGCLLSAITYACYAAICHPLLS
1		1	1	1		TMVMNRPLCTATVNATNKMGFLNSQVN
1				100	68	THAKFLNKKFNIPKLVILPKLVYIVKAIPTKM
	1365	Α	257	425	00	AIFFLI ECDONIT/KLICENT*KNIAKNI*KRRV
15)				TETPIET*HPVKOMIKWO*LTAWLRNRGYKK
15	j				\ 	VOTENSET APSVCRNI VEDKCG
15		1		l		EOID TEED DE CODE CONTROL OF THE CON
15					1 401	I FCIFKI IEEDKOODDC 4 424 W INCHAINGEA
	1366	A	263	104	481	CANDILLOAD DELLA VI EEGAL CALADODADEE
15	1366	A	263	104	481	SKDVFSKPVNIFWALEESVLGVKARQPKPFF
	1366	A	263	104	481	SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV
	1366	A	263	104	481	SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDI SSPNETK YIISLDODSVVKLENWTDASRV
16					208	SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMV
	1366	A	263	104		SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMV VSSLAMKEMLTKTTM
16						SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMV
15		1			401	TFTPIET*HPVKQMIKWQ*LTAWLRNRC KQTPNSETAPSVCRNLVFDKCG FCIERTTEEDRGGDDCVVSVWTKQRNN
16			298	68	208	SKDVFSKPVNIFWALEESVLGVKARQPKPF AGNTFEMTCKVSSKNIKSPRYSVLIMAEKP GDLSSPNETKYIISLDQDSVVKLENWTDASI RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKM VSSI.AMKEMLTKTTM

		77.	CCC	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-			*	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	•	i	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	ł	amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	l	1	residue of	sequence	/=possible nucleotide deletion, \-possible
	l	Í	ļ	peptide		nucleotide insertion
	l		<u> </u>	sequence		IHLK*MFYTMSQKMP*PTINLILLLIIPGNLNIF
				1		KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR
	1	1	1	1		WK*DY*C/LQEVTDPIMEKGKKKKRTASFFK
	į.					WK*DY*CICQEY IDFINERORANGETTAGI P#
		1	1	Į.		GOPHOSTNALLRRCVR*RYHLS\TVETAGLP*
	}	1	1		ł	KNTGHIPGQPFLFKLVFKC*NVICI**QYKW*Q
]	1		}	NIGVKNKSFCPH*SSSPSL*FIGHHSRNF/CSFK
		1	1		İ	TEPHSVVQAGGQWRNLSSLQAPPPGLMPLSR
	i	Ì	ì	1		ISLMSSWDYRRPPQ
19	1369	A	302	3	445	NSPSRWAKIQMFEHTFCG*GCG/ER/NVHIHCS
19	1303	1.	1 302	1	1	WICRLRPLLWRAVREYLSKLKNAELSFDPGV
	1	1	1	1	}	SLLRIYAIDMPTSI*DEKEALLFAFLAFHE*HC
	1		1	1	1	KSRIWAVIO/CIHLWDWLRKL*CFHRMKFYA
		1		1	1	AV*NKPRHLLSHIWKDVONILLK
	1200	A	304	 	1339	FFFCGKEVPLFEONKHPGPRATTSPGA/HARA
20	1370	Ι ^	304	1.	1	LLSAGEFTAGVGLSP*AIHSFVWLCTFIQHGA
	1	1	1	1	1	GGPCHOPGGSPGPWMHTTOAGHLWEGAYPG
	1	1	1	Į.		GSSTWHOVPGOLGGSWGPRERSLLGSFIKCSP
	1	1	1		1	CPHPPGFRI.WMSPNOKPPTENPGVMGRVWR
	1	ł	1			I MPGESPLIWEAEGKEDHLSPEGOGHSE/PVA
	1	-1	1	i .	1	PLHSSLGNTVKP*PKNOKPKQNRSRHGQ\GF
	1	.1	1		ļ	MAGOGOSRPAAR*PPCPALTPASHSAGTWPP
	ł		1	ĺ	1	RICRTVPGGPCPSPSGFRSCRR*GFSA*TRSWP
	1.	ì		1	1 .	DAEPPSTPDTAPRCCTOSDTSSOGPO*S*WRR
	l l	1		}	1	CRALPGRICSAPAAGLRRARPRISESKRGNSP
	1	1		1	}	PASPAAASARCPSWGPSCPARPPSRPAAGTEP
[[1		1		AAPSRCTAWLRGEREPGPRPPGRRPRSGRGP
Ì	1	1	-		İ	VSFAPEVLSLPAVRQTKSWRWRNEEEITRPW
1	1	1	1	1	1	AT VRSRGG
·				 	1587	GSQVLPPPPSQDSATLPQDA*GPRAAPGQPVC
21	1371	Ā	326	799	1507	E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCLP
	1		1		1	HLSFSPRQGAAPDTEPSAWGPAPTGATGPGLP
\	i .	1		· ·		LRHVRLFSAGAPRGAATPCPPALLHGPAWPP
)	1 '	1	1	1		ARPMFRGHPPVRPLGPWGKVAAGPRALCLA
	1 .	1		į		GVPAVQGECATKPSG*GL*PAHLRGPPGPEVL
l		1				QWHWQLSAGRDPVPAEDPPL*EGPLGPGGPA
Į.		1	1			AAQAEPGADPEPEDKDQAAESRPAGAMSLSA
.)		1	-	1		AAQABIGADI BI BUKU QIB BUKU I GI BI BUKU I GI BI BUKU I GI BUKU I
	}					QGSGPVGGQGLR PHILENPHPEHSFPGAPLT*STLSWSILSPREPSP
22	1372	A	327	146	652	GAPCYPGHPHLENPHLEHLLTWRTVTWSTLL
1	1					DOADCOMERDON ENDS TWEEDING ENDOPOREDI
}	1	1		. [1	PGAPCYPEHPHLEHPLTWSTPHLEHPSPGEPL SCRTPTRSILHRDHPLP*CLSTEESPI*GWGSLP
1		1		İ	1	2CKI LI K2ITHKDULDA COCOCODO CAGA
1		l	1	1		APPSTPLVLDVAPPGPQPASSCPGRDSCYSVP
1		1		1		GTVVSP
23	1373	TA	348	397	2	CIVSSCQGTRKPCHLEDANKINKQSPTLEKIES
ا سا	1.575	1.,				LQESL*VKQ*LIVAEKYVQILHPRKKYFQRPL
1	1 .	1	l	1		NNEKRKMKKRKEEKKKCRERMQRRSKWRR
		1	1	1		EEKKE*RREE\EERKKEKEDRKERRKETSPRG
1		1]		SRRLLRD
1	1004	+-	362	170	352	GRAI DTA AGSPVOTAHGLPSDALAPLDDSMP
24	1374	A	302	170		WEGRTTAOWSLHRKRHLARTLLVSRVRGPQ
1 -			304	373	128	VI ITTILETGYLWKNRHSDO*KRTENPERDQH
			384	3/3	120	KYPKVDFCKSNSMKNRLCNKWHWTNWIFTD
25	1375	A	,		1	AD AA AD 1 AF TO THE TOTAL TOT
	1375	A		i		I KKINI NI KPHTKLIPNIKKN
				105	166	KKINLNLKPHTKLTPNIKKN EVENTNPEIESGTNI.TIWIRSI*RKSDEINORTK
	1375	A	397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK
25			397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI
25						EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIDANF
25	1376		397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF KSKATGYMVNI*KLIVVFLYANDEQLEIEMNK
25		A				EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIDANF

	000 10	144	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	De Aspertic Acid. F=Glutamic Acid.
NO: of	NO: of	поц	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	{		1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Į.		ì		Sequence	/=possible nucleotide deletion, \=possible
	ļ	1		peptide		pucleotide insertion
	l			sequence	407	TICTNKFNNLDEIK/FLERHKLSKLTQEEVENL
28	1378	Α	408	14	427	ITI KTSRETELVINK*VIPHKEKPGPDSFIGEF
	1	l	1		Ì	YQTFKEEL/IVILHKLFQTIKYGRILPNSVYETSI
	!	1				TLKPKPEKDL\KENYRPLPLSNIDAK\LNKTLA
			1		,.	NRI**HIR
		1	{	<u> </u>		IYSKMCMERQRLNN*ILKKNKVRGIAVPDVK
29	1379	A	434	395	128	VYYKPTVIK/TSWIL*KDSHIVEWNRLENLEID
		}	1		1	PN/IKRLILDKGAEATEWRKDSFFRQWQ
		1				FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS
30	1380	A	455	2	228	SWDYRYAPPRP\ANF*FLVETGFYYVAQAGL
50	1000	1	i	}	1	SWDYRYAPPRPANTYTLVEIGHT I VAQAGE
	1					KLLSPGDLPALAS
31	1381	1A	462	393	2	QLMFDKGVKNIH\WGWTPPFTK*YWKNWISI
31	1301	1 **				CRRMNLNPYLSRYIKINSR\KDLTVRPEPIKLV
		1	1	'		EENTGKTIQDTGLGK*FIAKTSKAQSTKTNK*
	1	}	}			KRQTRYIKLK\KKSTASKENNRVKRQPLE*EK
	1	1	1	1	\	IFAN
	1202	A	474	125	471	VKPYEIAVFLVKPIEYK*HLLSDPAIPLSGI*LK
32	1382	A	17/7	120	1	EIKAYT/RRICTPMFAAPVSVIA/RN*KQSK/CQ
	1	1	1	1	1	KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT
	1	}	1			ILRETDRIHKTTYDVISLI
	1	 	488	1825	2	KSACSFICSEEQPASPSPLKPGTYASET\RPRDP
33	1383	A	400	1025	-	HAAGPREDSSEAETERPEGA/DGSGTVVKGT
l	1]	-	1	1	PGSPAPPCSWGHGG\ETEGAG*CPAAPGTDLR
1	1	1	1	1		APGGSAGS*\GLPSAGGSRGRKGWRAAGRQP
!	İ	1	ì	ļ.		STR*GRPGRHGGRGE*AGHPEPRQSALQSAG
ł		1	1	1		I /ASSPERMGAALAEDGSGDSRGAGPKPUETP
1		1		1		PSVLSRS\GS*G*G*AASGTASSPRSHSSRLGPP
1	ŀ	1		1	\ .	SAGFHGLRCGOPPFAAAPPGPWPGTGRPAGG
	l l	1	1	1		AGSPPAAAGTAPPATRGAOSRRQNRTAGRNA
1	1	1		l l		SPOTA AGAGSPVOWALSRATG*TGETGSWC
1		1		i	[AGGTHOATHLTAAWVCPPTWSVRPGGSGPA
}	1				ŀ	AGLGR*GRHPAQSPPLPVPRG*PAWPQEAPSP
l		1			1	SPASSEVALSSGSCWPDQAPGPARGSPPAPLA
}	1	· l	1	1	1	PAWPAAGRGRQR*GRQSAHPPPRR*STAVSL
i		٠			1	SGTS*WRRSP*AGTRTQQC*SPWLVPACSSRP
1		1	1		1	L*RGTRRPSTQQSPQTTGTPGRSAGPGHPRS*
1		1	1	1	1	GGRSPAGTGHLGAQTVASPH*GHWPTALSCL
1	1	- 1	i	.1	ì	WASASPPGPEAPPQTGACIGTNCRYRAASAR
1	Ì	1	ì	1 .		RSSVAPACA*GWQ*AGSPPAVLRGPP*RVRER
1	1	1	1		1	CALLED DD A DDE
						GALTHRPRAPDE APGASVGRAQAAEG*RGGPTGRPPSALGVS/E
34	1384	A	497	422	2	AGRAGRAGEGRPVPPAYPLCKSAQTSGPPKA
1 .	1	1			i	RLS\PPLASCGGRGPPGGAACATCAPPAGPAR
1		-		•	i	KLSVPLASCOUKUPPOUAACATCAFFAOFAR
		}		ľ		SSRCRRSPPE*GPR*PSRPARPSPGSAASRRQ
		1	l	1		KLTPCRCQFRGLCA
75	1206	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN
35	1385	١^	303	1		TEL VVAVTDENIVGLEAALLAERRVLLIAS
1		1		1	j	KLSTLTSCDHAFCALLYPMRWEHVLIPTLPPH
	1	1			·1	II DVC+CPPLPRT
			- 	3	1631	PERSON VENT VCVSPTPGPHGRLATWL/PGLLA
36	1386	A	. 512	13	1031	FI GI A AGGOTL CPAGEL PGHARAQASGAPGS
		- 1		1	1	VI IAVPGRRRVHTCGPGPAAPSTRGECPPPAL
1	1	- 1			1	CUTEPARPRPV\PFAPAVPOEPGGQGHGAA/P
		1	- 1			PATGHSAPRGCPPARAAPTGSATPAPPPAACA
1		1	1	ì	1	AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT
				l .	1	ALHOW MOALLY ON THE LEGISLE
	1	ı	- 1	1 '	1	DOOLE LUDDE ADDANGEED ADADDDRI ALTA
			1		1	PGOHLLDRPGAPPAQGSGPAPAPPPRLAGPA
		i i				CDA ADPPOPPA ASWHSSLSKSSSSL\GWSPPLI
						PGQHLLDRPGAPPAQGSGPAPAPPPRLAGPA GPAAPPPGPPAASWHSSLSKSSSSL\GWSPPLF VGPGSLQ*TPPPQGPHLSGSCGGTSSWRGQR AAVARRLRSWNACGLSRVAGRSSASYPGRE

PCT/US01/03800

		14:	ero l	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	De A spartic Acid. E=Glutamic Acid.
IO: of	NO: of	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
uci-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence			ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			914	1	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			l l	amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				residue of	sequence	/=possible nucleotide deletion, \=possible
1				peptide		nucleotide insertion
- 1			ļ	sequence		GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD
			 			GRPSQSQ*PAGPPGWRGCCLRGW*P333G3D
i			1]		GPGPHPASTWLRAGKTGPSPPACGCA*LPPPS
• 1		Į	[1		VSAAPQSPRTRCPRGCAAAAGLCVLAAAGAS
			ļ			HGA\GLPGVRVHTQRVHIH*GAG/GCQTPRPR
-		Į.	ì		1	LRSLPVLGLPAPRCPVSAHPWHRRSGSSCHA
		ĺ		1		ARLVPRHPAPGCP**TG*\PLITGFPEP*A*GLP
		1		ì	1	NHQAVGLEASGALQAGHRDELPTMVQLLDH
		1	1	f	1	SPINVPLKGRPHAP
						EDI DI AAGA/RGAAEPRVAVSMAPDPSAKIH
37	1387	Α	620	828) 1	WEASPEMQSKCHQKGKNNQTECFNHVRFLQ
	()			RLNSTHLYACGTHAFQPLCAAIDAEAFTLPTS
		1	1			FEEGKEKCPYDPARGFTGLIIDGGLYTATRYE
		1			1	FRSIPDIRRSRHPHSLRTEETPMHWLNG*EDE
		1	1	1	ì	FRSIPDIRKSRHPHSLRTEBITIVITY DIG DDD
		Į.				AQDDGG*GTISSFLLPWPADHPTPKSPGEPVH
				1		SIPVCCQVRGQPQSGGKESPACLKSLSNCLTH
	1	1				VDAEFVFSVLVRESKASAVGDDDKVYYFFTE
	1	1	l l	l .		RATEKESGSFTQSRSSHRVARGIPPL
	1000	-	739	+1	427	FRAMVSSTI.KI.GISILNGGNAEVQ/QGNRGKG
38	1388	A	139	1 *		TOPECKEG*EVPV*LPVSPPLPRPLOKMLDYL
		1	1	1		KDKKEVGFFOSIOALMOTC\GEKVMADDEF1
	1 .	·•		}		QDLFRFLQLLCEGHNNDFQNYLRTQTGNTTT
	į			1		TNITICTVDYLLRLOESI
					1000	TLDLTGPLLLGGVPNVPKDFRGRNRQFGGCN
39	1389	A	767	1	1030	RNLSVDGKNVDMAGFIANNGTREGCAARRN
		1				FCDGRRQNGGTCVNRWNMYLCECPLRFGG
	i		}	1	İ	KNCEQGEWPASSIPPVTAAWEALLLDVPGTT
	1	1	1	1	1	KNCEQGE WPASSIPP VIAAWEALEDD VICE
	1	Į	1	× 1	Į.	VRGLHIQVRQPLVVYAAFTVDSHRPLQETVL
				1		RRAPAPASGVPSPSGVGWDR*AGPAEPSPSTF
	١.	1	1	ì	i	ATVIISVPWYLGLMFRTR\KEDSVLMEATSGO
			ì	1		PTSFRLQVTGAPCHQGTC*VGARGRDPMLSG
	Ì		1		}	I DVTDGEWHHILIELKNVKEDSEMKHLVIM
		Ì	1		1	TI DVCMDOVSWHI HI I WG*TLPPAOGKI GA
	1	i i	}	1	ļ	SEDKVSVRRGFRGCMQVRGGCGGRGEACPS
	1 '	į.	1			CAAPRI
	1	·			200	THE THEFT NEW KYILCS GMERLS TVMIPV
40	1390	A	801	69	399	PQIIYKFNA*Q\VILKFTW*E*GAKITILRKNKI
		- 1		1		RGLVLVPLSTC*VKYLLDKVLPHIKTYYEAR
		-	1	1	l l	KGLALALIC, AKITTEDIKATI TATAL
}		- }				VNKSVVLVQVTIM
41	1391	A	835	7	195	SMLKERKVFQFPSCLFFQYITWLGPPYHVLFI
" "	1371	1 .,				SSVTNFSIGAK*DILQSVMNCLYAKRIPCVT
10-	1200	A	841	1	415	CSTHASGYDKTPDFILOVPVAVEGHIIHWIES
42	1392	14	1 04,	1.		LA SECUE CHHAYL HDOFWSY WNSLKHIKI
		l		1		OGIGTVASNI SOL*TLNAPFPELLLFRSLAKT
Ì)	1	1	l	ł	FVLT*\RFGPGLVIYWYGFIQELDCNRERGIL
1	1	ł		1	1	KACEPTNIVTI.
					100	PALSPAPVPQKKGSPLPLDPCLGPSSWLLSV
43	1393	A	845	358	92	LGWPRL*PRRGPGDPGSLPATPPLLTPPHTLI
1 "	1				Ì	LOWLY LUCOL OF CONTEST OF
1		- 1				QRPMLPPSHAGLARPPPPEPISVP
144	1394		853	452	1	LPQYCFFPRLSPKSKLVKHSAL**PSALKPPT
44	1394	1 ^	""	\	i	SPRCIPRTSLYFTICC/PPALQL/SPIEDPPAIYR
1		1	1			PPTHMLRSASQPLNQAPTLVKGHPPSRFLQC
j		- 1		1	1	OVSCPPOPTLPREKPLPLHLRPPPRPAQPPLP
1	1	- [1		DI TESTERNVDPEIPERFR
					162	CVVPPTVFDNYSVOTSVDGOIVSLNIWD1A
45	1395	A	894	379	162	QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYO
				\ \ \	1	
1		1		1		WLSMSMGK TTKKTLISNNVSSRSLPILPELKAFSLAFNDP
}		1			366	TTKKTLISNNVSSKSLPILPELKAFSLAFNDF
46	1206		1 900	- 1 1	1 200	THE THE PARTY AT THE THE
46	1396	A	900	1	. 300	EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIF VFLFHQLNIT**CLHFFTMTTFIAIPFSFLFLG

		34.4	ero I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A coartic Acid. E=Glutamic Acid.
IO: of	NO: of	hod	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	1 1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	i				Schaorice	/=possible nucleotide deletion, \=possible
		Ì		peptide		nucleotide insertion
	l			sequence		D/KSLAMI.PRI.VSNSWPOVILPP
		Ī				QLQNLASRGCL*SQLLRRLRRENRLNPGGGG
47	1397	A	944	162	2	CSEIAP\CTPAWVTQRDFFRKKK
		l	l	<u> </u>		HFTPDRIAIVKNTRDSHCWRGC*EEGAPARC
48	1398	A	963	216	308	PRKRESWWGERLP/PRGFPPAAEDAPAPGWK
49	1399	A	967	466	1	GRKHASRTARAHVFHPIRQSIRSPVRGRPGDP
47	1377	1				GRKHASKIAKAHVFHFIKQSIKSI VIKGIG GEL
	1	1	1	,		RAAHTRSAGTRLQCKASRGG*GKGPAPTR*E
	1	l		Į.	1	GGPGSAPAPLPASSGCSLFPDSSPWTPPPPAPG
	1	į	1			AAAAQP**TPRCPAALRAGAHIGRVGRPY
	1	-	973	45	421	EKCIQALDVFVFCYIDHSSHCLMSCD*E/DQA
50	1400	A	1 3/3	177	1	LNFMPLEMEPKMSKLAFGCQRSSTSDDDSGC
	1	1	1	i		AT DEVAWVPPGLRPEOIOLYFACLPEEKYPI
		1	1	1	1	VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLSE
	1	٠	1		1	l E
					104	TOTOUR A ARSCI GCAAGHVPAPGLRLLPTVRG
51	1401	A	992	2095	194	DDCDDCDAAPGCVCY*SGESTFVSHVPQKMA
		1	1	1		WIDGS APPRICEHPLOSOTS PSDTVSSPQLSKEE
	1	ì	i			DGPGWEHPLSSSL*SLGQAGGNH*QPEELAG
	ŀ	ì		1		WEPRGPPSLAPSSPT/TMWTALVLIWIFSLSLS
	1					ESHAASNDPRNFVPNKMWKGLVKRNASVET
	1	1	1		!	VDNKTSEDVTMAAASPVTLTKGTSAAHLNS
	ı	1	1	1		VDNKISEDVIMAAASFVIETKOIOISE
•	1	1	1	l	1	MEVTTEDTSRTDVSEPATSGVAADGVTSIAPT
	l	1		1	ł	AVASSTTAASITTAASSMTVASSAPTTAASST
	j		- }	1	1	TVASIAPTTAASSMTAASSTPMTLALPAPTST
	· [i i			i .	STGRTPSTTATGHPSLSTALAQVPKSSALPRT
	İ	1	1	1	•	ATLATLATRAQTVATTANTSSPMSTRPSPSKH
	1	1)	1		A ADSTITA A SPVPPMRPOAOGPISOVS V DQL V V
		- 1	1			NITTNIKSTPMPSNTTPEPAPTPTVVITTKAQAK
	1		1		Ì	EDTASDVDVDHTSPIPEMEAMSPITQPSPMP I I
	- 1	ļ	1	1	i	OD A A COCTSOAPEOVETEATPGTDSTGPTPKS
	l l		1	1		L CCCTYMPATDSCOPSTOGOYMV/DHH*APIN
	İ	1		ļ		GRONSPSGGAVTRGDPFHHSLGFVCPAGL
	}	1	· ·		ì	*ELOFEGLHPGGLLNORDVCGLKNVKGAGA
1		1	l	1		WREAWPLPRPFLLPLRPNQVLPNSFGAIEEIC
	1	i i	1		Į	OMLKHI
						ESGEFLVSFTLKKPTNVFHHINGMKPFNK/LIF
52	1402	A	994	1	462	*SHTDIAFYKIQHPFMLKALTKWA*EGT*PDR
1 72	1	1	1	[1	*SHTDIAFYKIQHFMLKALIKWA EGCAILPI RYLH*SLRLNGEQLKTFPLRSGMR*G/CAILPI
1		.1				VLNAMLSIVPAVVPAGKTRHEKEITCPLIGQE
1	1				1	VLNAMESIVYAV VYAUKIKHEREITETEIGE
1		1	1	1		EK*FS*FVGDMNTCVENKKESKKLLE
-	1400	A	1011	1	630	PEVIQQSAYDSKADIWSLGITAIELAKGEPPNS
53	1403	I A	1,01,	J.*]	DMHPMRVLFLIPKNNPPTHCWRRLLESFKEV
	1	1	1		1	*LMLA*TKDPSI\RPTAKELLKHKFIVKNSKKT
	- 1	l		- 1		CVI TEL IDREKRWKAEGHSDDESDSEGSDSE
1		- 1		- 1	i	TODENNITHPEWSFTTVRKKPDPKKVONGALO
1	1	1		- 1	1	DI.VOTLSCLSMITPAFAELKQQDENNASKNO
1	1	- 1	1	1	Į.	ATEFI EKSIAVAEAAGPG
			L			TETDA * K A FOK TOH/CFMITTLKKLGIDGKYLN
54	1404	A	1016	1	222	TIKAIDDRHTVSTILNVEKLKAFL*RSGTRQR
"	1			1		
1						PISGSGARI HASVDGDEGSDDVYYYYTPAILRELQALNT
55	1405	A	1033	3	366	HASYDGUEGSDDY I I I I I I I I I I I I I I I I I I
55	1405	^	1000	1		EAAEHRPEEDRMLSEDPWRPAHMIKGYMPL
l	(1		HNIPHTEVIDVTGLNQSHLYQHLNKGTPMKT
1		- 1	1	1		OND A AN VIWHVLEOLEILROINQUSHUPU
					429	CVI TI OTR SPSK PLS\RKLMDWEVVSKNSISE
56	1406	A	1044	5	429	DDI ETOCO ACROPPVTPNOSOETPVDGKPLA
-		١	ì	1		DDNOCOVNID VHIHYI HI OYYLDRHISATLPI
1	ĺ		1	1	1	SSSGIPTPIAVITDALTDLVELILGQPCSEESGI
Ţ			1		1	I SANTIFICIA VII DOMIDDI DOME TO TO THE TOTAL TO THE TOTAL TO THE TOTAL
	1	- 1	1	1		APGTLFLLAL

			TOPO T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D-Accordic Acid F=Glutamic Acid.
IO: of	NO: of	hod	in in	nucleotide	location	r=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine K=Lvsine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	Į	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	i	Ì	1	peptide	1	/=possible nucleotide deletion, \=possible
	l	1		sequence		nucleotide insertion
57	1407	A	1050	11	430	GAYAFETNGFPIMLVLTTDKIEGDVGIAGLYD
) /	1407	\ ^	1.000			MHVISLPMAFLLRTLVRCTSYIIPVTHVLSTPV
		ì	Ì	į.		TCLRRREKDGVIVDVLSDTASNHNGFPVEEH
	ļ	1	l	1 -	1	ADDTHPARLQGPTLRSQPMGPLKHKAFEERA
•		1	i	l		NLGLVQRRLRLED LKHRDTPVVGANNRALSCTPLTSLTLCALCPI
58	1408	A	1058	258	419	LKHRDTPVVGANNKALSCIPLISLIECALCI
J 8	1700	1]	PCLGCPTXATCRLYQTTVAVVF KAFSFTTSLIGHQRMHTGERPYKCKECGKTF
59	1409	IA-	1064	3	425	KAFSFTTSLIGHQRMHTGERFTRCKEGGRAFSQC KGSSSLNNHQRIHTGEKPYKCNECGRAFSQC
39	1 ****	1				SSLIQHHRIHTGEKPYECTQCGKAFTSISRLSR
	1	1	1		1	HHRIHTGEKPFHCNECGKVFSYHSALIIHQRIF
	1	1	1		1	HHRIHTGERPHICNECORVISTIONE
	l	1				TGEKPYACKDVGK GGPPGPFLAHTHAGLQAPGPLLAPAGDEGDL
60	1410	A	1065	204	419	LLLAVQQSCLADHLLTASWGGK/DPIPTKALO
00	1	1			1	
		1		\		EGQEGLPLTV RHSRAHLCQPFHLVMRDLLQLGQDIPQGCHT
61	1411	A	1079	3	383	LEENHLIHRDIAARNCLLSCAAPTRAATIGDF
••		1	1	1	1	GMARYIYRTRYYQLGDRAL/LPRKWMPPEAI
	1	1	1	1	1	LEGIFTYNTDSWTFGVLLWEIFSLGYMPYPG
	1	1	1	(1	TN
		1 _	. i	J	1	VVEFLWSRRPSGSSDPRPRRPASKCQMMEER
62	1412	A	1080	1	859	AND MUMAKI SIKVI LOSALSLGRSLDADHA
				1		DI OOFFVVMEHCLKHGLKVKKSFIGQNKSFI
				ì	1	CDI DI VEKI CPEASDIATSVRNLPELKTAVOL
	1	1	- 1	1	1	GRAWLYLALMOKKLADYLKVLIDNKHLLSI
	•	1	1	1	ľ	EVEDEAL MMEEEGMVIVGLLVGLNVLDANL
	1	1			1	CLKGEDLDSOVGVIDFSLYLKDVQDLDGGK
	1			1	1	HERITOVI DOKNYVEELNRHLSCTVGDLQ11
		1		l		IDGLEKTNSKLQERVSAATDRICSLQEEQQQ
	1	[1		DEONE! ID
			1002	2	615	SSEAKHKRIHTGEKPFICLECGKAFTSSTTLT
63	1413	A	1083	12	012	LIDDILLTGERPYTCEECGKAFROSAILYVHRK
	1	- (1	1		HTGEKPYTCGECGKTFROSANLYAHKKIHI
		- [1	1		FKPVTCGDCGKTFROSANLYAHKKIHI U\L\
		į.			İ	VKCKECGKAFKSYYSILKHKRTHTRGMSYE
l		1		1	1	DEC/ORSLN/RSSILSNHKIIHNEEK/PLKCEKC
		1	1		}	KAFNHTSICCRHKKN
			1084	946	1	KKODI SSSI TDDSKNAOAPLALTESHLATLA
64	1414	Α	1084	1 240	1	SSSOSPEATKOLLDSGLPSLLVRSLASFCFSH
		}	1	1	1	SSESTAGSIDISODKLRRHHVPQQCNKMP118
	1	1 .	1		1	I VADII REI TEVGNSHIMKDWLGGSEVNPLV
ł	1	l l	1]	}	TALLFLLCHSGSTSGS\HNLG\AQQDQCKISF
1	İ	j	- 1		1	FFSWLTTGLTTQQRTAIEWATVAFFLQCIS
1		1		1	1	LIPANIOKI MAOVI CELFOTSPORGNIPISON
1		1]		1	SIGRIBIRI FI OLMILEDEK VTMFLQSPCPLYK
1	1	1	1	{	-	RINATSHVIOHP\MYGAGHKFRTLHLPVS11
		- 1		- 1		envi prventpsitakLiskOkDDkkkk
	-	+-	1087	103	324	DDAFFEVHTEMIVG/RVONIHLFTLQVLEDK
65	1415	A	108/	103	1	LFTMSVGSSLWSTYLIHVMALP/DRELLKPN
	1		1	·		SVALHKLSNALV
L		_+-	1005	- 3	493	UETCSVTHIVSFSLPFLNPSHPASTPGHTENE
66	1416	A	1095	,	175	PSI_VWFDRGKFYLTFEGSSRGPSPLTMGAQ
		- 1	-	1		TI DVA A A FTETVNA YFK GADPSK CIVKII GI
1		- [1	l l	1	LACA SEPAGITRHEANNPSPAALTERVINESK
			1	1	1	HVLPNPQLLCCDNTQNDANTK\EFWVNMP
		ı	ı	3		HALPINEGEDECEDIATE
		.				MITH K
		<u> </u> -		52	356	MTHLK I KI TSI GFIIGVSVVGNLLISILLVKDKTLHR
67	1417	A	1098	57	356	MTHLK LKLTSLGFIIGVSVVGNLLISILLVKDKTLHR PYYFLLDLCCSDILRSAICFPFVFNSVKNGS WTYGTLTCKVIAFLGVLSCFHTAFMLFCISV

PCT/US01/03800

			· · ·		N 12 1 1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	[in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	Iocation	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ì	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence	ľ		914	ng to first	acid residue	Q=Glutamine, K=Arginine, S=Serine,
	1	ļ		amino acid	of peptide	T-Threonine, V-Valine, W-Tryptophan,
	İ	1	İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	Į.	i	1	peptide		/=possible nucleotide deletion, \=possible
	1	ì	1	sequence	l .	nucleotide insertion
	+		-	· · · · · ·		RYL
68	1418	A	1106	1	1326	MGKISATGINMGTKCSWALVWHLESYDPKH
00	1410	^	1100	1 .		YEREGMQDWKTASGQSEEATQQSSQKPQPH
1	l		İ	(YTTYQSSSFLKYSSESHLLAWRENSSEGSFQF
	1	ł	ļ	1	{	PGRSRARPPRTROORRGAAAGPGRGAVRLG
	1	1	ì		}	HPQSAAQPQLRAAARIPESPAAFPAQPRPGSA
1	-	1	l	1.		RNSDASGPASLSRTLGRASSPRPPQAPDVTAP
	1	1	ì	Ì		SPAALAPRAARGGSRAAALAGAEAEEPLRTL
1	Į.	1	l	ļ		APRPTRAAAPPPPPPPPPPPLPPGAPPPPVRCVSR
ŀ	1	-		ļ	l	RARAPPWR/PAATGPPP\RPVAPSRKLGSARAP
	1 .				J	APALQIRKGTSSGLPGRGGGSGPGNNLSSVA
Ì	1	1		1	Į.	GNWRGSSFAVERPGMAKYQGEVQSLKLDDD
	1	ĺ		1	ì	SVIEGVSDQVLVAVVVSFALIATLVYALFRNV
1		1		1	Į.	HQNIHPENQELVRVLREQLQTEQDAPAATRQ
i	Ī	ļ		<u>}</u>	1	QFYTDMYCPICLHQASFPVETNCGHLFCGSLT
	1	}	1	1		
				<u> </u>		PNSIW FDTARLHEFGTSITQIFAVDNREDLQKWMEA
69	1419	A	1107	2	466	FWQHFFDLSQWKHCCEELMKIEIMSPRKPPLF
	1	1	ł		1	FWOHELDISO WHICCERTING WHILE
1	1.	1 .	}	1	1	LTKEATSVYHDMSIDSPMKLESLTDIIQKKIEE
	1	1	1		1	TNGQFLIGQREESLP/SS/CGPHSLMVTIKWSS
1						RKRY/SYPASEPLHDEKGKKRQAPLPPSDK
70	1420	IA	1111	698	23	ALRRLHYVRATKVFLSFRPFWREEHIEGGH
1 "	1					SNTDRPSRMIFYPPPREGALLLASYTWSDAAA
	1	1	1	1		AFAGLSREEALRLALDDVAALHGPVVRQLW
	ì		1	1		DGTGVVKRWAEDQHSQGGFVVQPPALWQT
Į	1	1		ł		EKDDWTVPYGRIYFAGEHTAYPHGWVETAV
1	l	1	1	1	i	KSALRAAIKINSRKGPASDTASPEGHASDMEG
	1	1	ł		1	QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL
	1	1	1			QNTTHTRTSH
71	1421	A	1119	2	385	QKQTLQNGYLDSSMDILYLGSLPPELQVSSDE
/ '	. 1421	1 **		1		PPGPPEQAGLSQFHLEPETQNPETTEEIQSS/LQ
1	1	1	1	1	1	QEAAAQLPQLPEVVELSSTKA\EAPALPSQSL
ļ		1	1	ì	1	EGVHSSTEQKAPAQQLPAFEEILAPLLIHHE
72	1422	1 _A	1127	1	906	HAQYVGPYRLEKTLGKGQTGLVKLGVHCIT
1/2	1422	1^	112/	1.	1	GOKVAIKIVNREKLSESVLMKVEREIAIL\RLI
-	1		1]	EHPHYLKLHGVYENKKYFPPDELTSGPSMLA
1	(1	1	1		OVSPHGKLSARRSWDLLSGFPRYLVLEHVSG
1	1		1	1	1	GELFDYLVKKGRLTPKEARKFFRQIVSALDFC
}	J	1	1	1	1	HSYSICHROLKPENLLLDEKNNIRIADFGMAS
1	}	j	1	1	1	LOVGDSLLETSCGSPHYACPEVIKGEKYDGR
1			1	1	1	RADMWSCGVILFALLVGALPFDDDNLRQLLE
1	1		1	1	1	KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR
ŀ				1	1	LSLEQIQKHPWYLGGNFIS
L			1	 		LRNALDVLHREVPRVLVNLVDFLNPTIMRQV
73	1423	Α	1128	1	802	FLGNPDKCPVQQAMLEPLGSKTETLDLRAE
1				1	1	MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG
1	ł	1		1	ſ	SDFLCTEWKASNSVPTSVHQLRPADIKVVAA
	-	1	1	1	1	LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG
		-		1	1	GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG
1	1	1	1	1 .	1	GUGNELITI ILINILAATAT ILLGISISI WEG
	-	1	1	1		TAGLNVAAEGARARDMPAQAWDLVERMKN
		1	Ì]		SPDINLEKDWKLVTLFIGGNDLCHYCENPEA
1	1	J	1	1		HLATEYVQHIQQALDILSE
74	1424	A	1139	60	480	FREPCLLVPGDHQPLREASWLA/LPPIGLWGT
17	1727	''		1		DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG
	- 1	1	1	1		VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE
		1	1	1	1	EQPAADAAVAKGEF/QGEQIAPVPAVIAAHPE
		ı	1	1	1	AADPAPVHTTAHPKGA
75	1407		1147	2	413	PFPHOHPOEP\KGSCWPQSALRGQCPGPVLGV
75	1425	A	114/	1	1 ""	TTTSDLCSLQVPVSSHRNPLLDLAAYDQEGR
						1,

			LODO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=A sportic Acid, E=Glutamic Acid,
NO: of	NO: of	hod		nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine K=Lysine L=Leucine.
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ	1	1	peptide		/-possible nucleotide deletion, \-possible
	Ì	1	ļ	sequence	i	nucleotide insertion
	 	+	 			RFDNFSSLSIQWESTRPVLASIEPELPMQLVSQ
	Ì	1			Į.	DDESGQKKLHGLQAILVHEASGTTAITATAT
		}	}	1		GYQESHLSSAR
76	1426	A	1155	38	410	PIISAPAQDDPILLSFIHCLHANLLCVWRRDVK
70	1420	1.				PDCKEIWIFWWGDEPNLV\VQYIMNCMLWK
	1	1	1	i		KDSGKMAFPMNVGRC/FFKEIHNLLERCLMD
		Į.	1	1	1	KNFVLIGKWFVRPYYKDEKPVNKSEHLSCAF
	1		Ì			T RFPQGLEDVSTYPVLIEELLSRGWSEEELQGV
77	1427	A	1162	526	350	LRGNLLRVFRQVEKVQEENKWQSPLED
•		1				MAESASPPSSSAAAPAAEPGVTTEQPGPRSPP
78	1428	A	1171	1	1293	SSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQT
		1	1	1		TSPRNWCIKMVCNPWFECVSMLVILLNCVTL
		1	1		1.	GMYQPCDDMDCLSDRCKILQVFDDFIFIFA
	1			{		MEMVLKMVALGIFGKKCYLGDTWNRLDFFI
	1	İ	1			VMAGMVEYSLDLQNINLSAIRTVRVLRPLKA
]	j	1	1	TNR VPSMR II. VNLLLDTLPMLGNVLLLCFFVF
	1	1	1	1		FIFGIIGVQLWAGLLRNRCFLEENFTIQGDVAI
	1	1	-			PPNYVOPEEDDEMPFICSLSGDNGIMGCHEIPP
	1	ı	1	1	1	LKEOGRECCLSKDDVYDFGAERQDLNASGL
	1	109	1	1	1	CVNWNRYYNVCRTGSANPHKGAINFDNIGY
		1		1	ì	AWIVIFOVITLEGWVEIMYYVMDAHSFYNFI
	•	1	1	1	ł	YFILLIIVSVREPGLLGGSFSTAQSPKCQGDSF
	İ	1				GVAAESLLLRGWVLWLPGGG
	1	ا	1175	1	405	PNOFFKOMFPOLPGGPLGPIKAENDYGAYLN
79	1429	A	1175	,	1 403	FLSATHLGGLFPPWPLVEERKLKPKASQQCPI
{	1	Ì	1		1	CHKVIMGAGKLPRHMRTHTGEKPYMCTICE
١.		1			Į.	VRFTRQDKLKIHMRKHTGERPYLCIHCNAKF
1		1	1		1	VHNYDI KNHMR
80	1430	A	1182	25	198	EMNELSQQLSQQGGRGASQCPSPPAPTLPNP
80	1430	1^	1102			PLCQLQLQRVNTGLPTPPCHPGAGAA
81	1431	+A	1186	254	583	KTVLDVGAGTGILSIFCAQAGARRVYAVEAS
0,1	1431		1	1	ŀ	AIWQQAREVVRFNGLEDRVHVLPGPVETVE
}	l	1	1	l		PEQVDAIVSEWMGYGLLHESMLSSVLHARTI
]						VVKDGGFFLPXSSELFM
82	1432	A	1187	2	716	DFVDAARNLPLESTKSPAEPSKSVPSLE\DPR
, <u></u> .	1	1		1	1	SSQGLPSQGPVQNQGRRGEQRPKKF/TVIQHT SSFEKSDSLEQPSGLEGEDKPLAQFPSPPPAPH
		- 1		1		SSFEKSDSLEQPSGLEGEDRPLAQFFSFFFAFA GRSAHSLQPKLVRQPNIQVPEILVTEEPDRPD
1	1	1	1	1		WEDDERWEDEVTEEFOUROGEOTI AOFFVER
1		1				TEPEPPPKEPEKTEEFQWPQGSQTLAQFPVEK LPPKKKRLGLAKMAQSSGESSFESSVPLFRSF
	1	- [1	1	1	SQESNVSLSGSSRSALFERDDHGKAEAPSPSF
1	ŀ	İ		1	i	DMGPKPLGTHMLTV
1		1	_ L			ESPGLSKVLRTGAFAYPFLFDNLPLFYRLGLC
83	1433	A	1188	517	804	WGRGHGCGQEALSTSHGYHLFCALLTGFLF.
1	1		1		1	SHLPERLAPGRFDYIGHSHQLFHICAVLGTHE
1		- 1				1
	1				1	Q LGDVGFWVERTPVHEAAQRGESLQLQQLIE
84	1434	A	1192	45	476	GACVNQVTVDSITPLHAASLQGQARCVQLLI
		1				AAGAQVDARNIDGSTPLCECLRLGQHRVCE.
		-	1	1	1	LAVLRGQGQPSPVHSVPPARGLHXREFRMC
1	- {	l				GFLFDVGXNLEAHEFHFGEP
					1	KRSEEASAPPFPLGGTGAAPTRASLPEQILLP
85	1435	A	1194	69	410	SCLEARKSQPDEKLLSALHNSRTWN*EPRRS
1					1	HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT
		- 1		i	1	GRSPCPSLPGTTRTNSLL
1	1	1				LPSHTCGNPGRLPNGIQQGSTFNLGDKVRYS
	1436	A	1215	3	405	NLGFFLEGHAVLTCHAGSENSATWDFPLPSC
1 86				1	1	I NI ITHE PLEMA VI.IL PLANCE AND ALL WILLIAM DV
86	1	}	- 1	l l	ł	RADDACGGTLRG/AEWHHLQPPLPLG/ATK

PCT/US01/03800

Section Sect		ero m	344	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Nuc. a lucientide edide sequence USSN periode (USSN polymer) and the corresponding or periode (USSN polymer) and the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the standard process of the corresponding to the	SEQ ID	SEQ ID	Met			nucleotide	D=A spartic Acid. E=Glutamic Acid.
uence einde seq- uence 19/9/96 gence 19/9/96			noa			location	F=Phenylalanine, G=Glycine, H=Histidine,
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ERPGAERPSLLPNGKENSSGTPRVPPASPSSH		1	1	1			ERPGAERPSLLPNGKENSSGTPRVPPASPSSHS

			COPO	Th. 11-4-1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in			I=Isoleucine, K=Lysine, L=Leucine,
cotide	scq-	1	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi		O=Glutamine, R=Arginine, S=Serine,
uence	[[914 .	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
1	ļ	1	!	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ĺ	İ	}	residue of	sequence	/=possible nucleotide deletion, \=possible
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i	ł	1		sequence		nucleotide insertion
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94	1444	A	1261	3	385	KFSQWGLTKPKLSNASP/WISLVKKLMKKWS
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		1		i		DLOESISRIHRTIELMYSDKSMIQVPYRLHAV
	1.			1		LVHEGQANAGHYWAYIFDHRESRWMKYNDI
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	1	1	1	1		QKLRESETSVTTAQAAGDPKYLEQPSRSDFSK
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	1		1	}	1	YARLVKLAQEDTPPETDYRLHHVVVYFIQNQ
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98	1448	A	1304	118	453	SGPSSRATYLHRKEYSQNLTSEPTLLQHRVEH
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00	1449	A	1306	3	1660	CGYFCHTTCAPOAPPCPVPPDLLRTALGVHPE
99	1449	1^	1.300	1	****	TGTGTAYEGFLSVPRPSGVRRGWQRVFAALS

		16.	CEO T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A coartic Acid. E=Glutamic Acid.
O: of	NO: of	hod	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	•	Ì	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	`] .		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
]	}	}	peptide	1	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
	ļ					DSRLLLFDAPDLRLSPPSGALLQVLDLRDPQF
		ì	Ì	ļ		SATPVLASDVIHAQSRDLPRIFRVTTSQLAVPP
	ľ	1	l		1	TTCTVLLLAESEGERERWLQVLGELQRLLLD
	Ì	}		ļ.	ł ·	ARPRPRPVYTLKEAYDNGLPLLPHTLCAAILD
			1	ļ.	1	QDRLALGTEEGLFVIHLRSNDIFQVGECRRVQ
		1	1	ł	ł	QLTLSPSAGLLVVLCGRGPSVRLFALAELENI EVEVPKIPESRGCQVLAAGSILQARTPVLCVA
	1	l	Ì	l		VKRQVLCYQLGPGPGPWQRRIRELQAPATVQ
		1	}			SLGLLGDRLCVGAAGGFALYPLLNEAAPLAL
	1	1		İ	}	GAGLVPEELPPSRGGLGEALGAVELSLSEFLL
			1	į.		LFTTAGIYVDGAGRKSRGHELLWPAAPMGW
		}		}	}	GYAAPYLTVFSENSIDVFDVRRAEWVQTVPL
			1	1		KK\VRPLNPEGSLFLYGTEKVRLTYLRNQLAE
	1	1	1	1	1	KDEFDIPDLTDNSRRQLFRTKSKRRFFFRVSE
	1	į			}	EQQKQQRREMLKDPFVRSKLISPPTNFNHLV
	Ì	İ	1		1	LIVOPANGRPGARDKSP
					190	ST CVPGPVDTGTFAVMSVMVGSVTESLAPQA
100	1450	Α	1318	918	190	I NIDSMINETARDAARVOVASTLSVLVGLFQV
		1				CI CI THEGEVVTYLSEPLVRGYTTAAAVQVF
		1	1	1		VSOI KVVEGI HI SSHSGPLSLIYTVLEVCWKL
			1	1	l l	POSKVGTVVTAAVAGVVLVVVKLLNDKLQQ
	1	1	}	}		OI PMPIPGELLTLIGATGISYGMGLKHKI EAG
	[-	ì		ì	PPVAPNTOLFSKLVGSAFTIAVVGFAIAISLUK
	}	ļ				IFALRHGYRVDSNQVWVMRDV
101	1451	+	1353	220	445	DWPDLFTYPLIGSPKCFQSARPERMYRRTVR
101	1451	Α.	1333	1		SSHGNHALQEVLPRSGHGTEFTKQKHLEAAD
		İ				HGHPPARMSIFSR AHLLMLNLAL\TDLL\YLTSLPFLIHYYASGEN
102	1452	A	1363	542	2	WIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRY
102	1452	1		ł		CVIIHPMSCFSIHKTRCAVVACAVVWIISLVA
	}		j	1		VIPMTFLITSTNRTNRSACLDLTSSDELNTIKW
	1			1		YNLILTAILLCLPLVIVTLCYTTIIHTLTHGHAN
•				1		I VDGCI KOKARRI TILLL
					410	CUSTESSEDEIL PGDYLLGGLCPLHSGCLQV\C
103	1453	A	1371	2	410	SENERGYHLFOAMRLAVEEINNSTALLPNIIL
				1	1	CVOI VDVCSDSANVYATLRVLSLPGQHIMEL
			l		{	QGDLLHYSPTVLAVIGPDSTNRAATTAALLS
	,		i i		1	EL ADMITTEO
			- 1276 -	- 	432	NSRVEDRS/NMSLWTQNITVCPVRNVTRDGO
104	1454	A	1376	3	1,52	FGDWGDWOPCEHLDGDNSGSCLCRARSCUSI
		1	ı	1	1	DDDCGCI DCI GPAIHIANCSRNGAWIPWSSY
ļ		1	1	ł	1	ALCSTSCGIGFQVRQRSCSNPAPRHGGRICVC
١.	1 .	- (1	1		LEGRERECNENTPCPVPIF
105	1455	A	1379	12	396	GLGLLYLIFAAVEGVMRVIGGSNHLAVVLDI
105	1433	^	13/7	1-		IILAVIDSIFVWFIFISLAQTMKTLRLRKNTVK
Ì	ł	- 1	1		1	SLYRHFKNTLIFAVLASIVFMGWTTKTFRIAN
1	1	1			1	CQSDWMERWVDDAFWSFLF\SLILIVIMFLW
1 .		1]	RPSA CLADILA ERCHI ERWICH
106	1456	A	1383	1	432	EDGHGGWSSRCLVDHAEEGHREPWKRLCIV QRGGHEIRFAFYFPGHPLLSPQICLAPETPPRO
100	1470	1"	1.2.2			QRGGHEIRFAFYFFGHPLLSPQICLAFETFYRG CPPVSSLHFISLQ/RLPRDCQELFQVGERQSG
1		1		1	-	FEIQPQGSPPFLVNCKMTSGTFWTCRTDSRV
	1]]	- 1	1	FEIQPQGSPPPLVNCKM15G1FW1CK1D5K4
		1				QNANPSNAAHSEDQPTP QNANPSNAAHSEDQPTP QNANPSNAAHSEDQPTP
107	1457	-	1386	719	558	FFFVTRSHSVAQAECSGVFTAHRSLDLVGSS
10,	1457	11				YPALSLQSSWDHRHTWLIFAFL RVAISLLCAAIFISFMVQSAGKRWPTGVMLN
108	1458		1397	631	2	VVVLFAFLYSWPIQALLPTYLKTDLAYNPH
1,00	1450	1				VANVLSFSGFGAAVGCCV/GGFLGDWLGTR
1	1	- 1	1	· I	1	AYVCSLLASQLLIIPVFAIGGANVWVLGLLL

				B 0 7 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	•	in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		
	'		1	sequence		nucleotide insertion
						FQMLGQGIAGILPKLIGGYFDTDQRAAGLG
	l	i	i	1		FTYNVGALGGALAPIIGALIAQRLDLGTALAS
		1	į		i	LSFSLTFVVILRNRRPGKSLVR
	1.150	 	1402	15	387	VLVALPDT\VTSETVVTEVLGHRVTLPCLYSS
109	1459	A	1402	1.5	1	WSHNSNSMCWGKDQCPYSGCKEALIRTDGM
		ì		ļ	1	RVTSRKSAKYRLQGTIPRGDVSLTILNPSESDS
	į	l	i	[CVVCCRIEVPGWFNDVKINVRLNLQRASTT
		<u> </u>	 	<u> </u>	350	TUPDI SSI I TROSONOFREROLKKLISLRDWM
110	1460	A	1421	3	330	I ARE APPYGVE ATCA * SLLSC * YCVILL FPCSCF
	ì	ì				FFHSPDALFSLLLLSCYFPSYCFFYYLFFSSSPL
ł	Į.	1	1	1	į	CLLLASSPFPLFILLASL
}		1		l		FTSTMTKPFEKESEQPA*ATLAFGAQTSTTAD
111	1461	A	1426	2	344	QCALKPDLSYLNNSSSSSSTPATSAGGGIFGSS
1111	1	}				QCALKPDLSYLNNSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
ļ		1		1	1	TSSSNPPVATFVFGQSSDPVSSYGFVNTAESST
1	{		1	1	1	SDSLLFSQDSKLATTS
<u></u>	1462	A	1434	46	372	TTSWTTSCTRSCT*SGASSGPGWTPRTTWWR
112	1402	1	1737	1.0		SRRSSQRTCSRACSGAWSRTW*RSS*TSSSSC
Į.				1	•	STSCSSSSSRSCGRPGGPLGARGVHITSCLNSC
			1			MCCCTTCCTTCTF
Ì		1	- -	3	292	HEDIMTHYDRLVDE*ALNAGKQRYEKMISG
113	1463	Α	1439	13	2,72	MANI CEIVENII IDETKKGELLRGOISEMLKI K
ł	1	1	1	ł	1	CIETTET I SNELTVCVLLEYVSFYLFOSCINFYL
ì	}				1206	KQQAVPEPHSSTTTPQEQEQNWYGQDLLNLQ
114	1464	A	1463	1	396	LODTEVILL PCHKTGPAVAKDTPEPVKKEPIVE
				1		ATSQGP*SPFSEEPPLPPSNEEVPPTLPP*EPQS
	1	1	1	- {	1	EDP*KNA*LKQMHAATTHWQQHQQHQVGC
1	ł	1		1	1	
		1	1			QYHGIMQ AGSYPSMVWSCHWGVTQKRRAL*VYSFEEG
115	1465	A	1464	291	2	GRRKCGQYWPLEKDSRIRFGFLTVSNLGVEN
1 ***	1		1		ì	MNHYKKSTLEILNPEVNPGFFFLTLWKQGEN
1		1		1		
	1	1	Í	1		NYCN ACCEUNIAL O
116	1466	HA-	1465	667	337	LPPQRPA*TDSYSTCNVSSGFLAGQSHNIHLQ
110	1400	1 1	1			YWTKYQVWEWLQHFLDTNQLDANCIPFQEF
		ı		1		DINGEHLCSMSLQEFTRAAGTAGQLLYSNLQ
		i i		1	· ·	HLKWNGDSLFLCLSLPC
			1479	- 1 	381	CTSCCPKRVI VTERFPWONPLPVNRGQAQK
117	1467	A	14/9	1.	1	VI COSNICEOR VPI OAOKLVSSHKPGONQKHK
			1	i	1	OLOATSUPHPUCMPLNNTOKSKOPLPSAPEN
1)	1	1	1	1	NPEEELASDPNNEESL*RPWALEDFEIGRPLG
1	1	1		1		KCK
					205	TVI WI *GNPPFYEKNDGGLFELILRAKDEFNS
118	1468	A	1485	3	385	PVIJODMSDSAKHFIRPLTGRDP*KPFPCDQPL
				1		QHPWIEGHTCLDNNIHQAASEPINNNFAESKR
1	1	ļ	1		ļ	NLAFLATGVVRHMRKLFMGANLEGPGPTVS
1		- 1)	I
Ì		1		1		H CONTROL VENIA ATRIOL
119	1469	A	1486	1	398	GTTSKHH*LARSLIRGPFDHDLKPNAATRDQL
119	1407	1 ^	1	1		NIIVSYPPTKQLTYEEQDLGWKFRYYLTNQE
]	-	- 1	1	ì		KALTKFLKWVNWDLPQEAKQALELLGKWK
1	1	1		1	Ì	PMDVKDSLELLSSHYTNPTVRRYAVARLRQA
			1	1		DDFDLLMYI.
L					999	MGESPAV*GYFVLAGMNSAGLSFGGGAGKY
120	1470	A	1497	3	1 222	1 A EWA WHICVPS ENVWELDLKREGAL QSSK1
		1	1			ELDED AMEAMPL MADEKALHADEA LORAN
-	ì	- 1	[1	[RTSPLYDRLDAQGARWMEKHGFERPKYFVP
	-		1	l		PDKDLLALEQSKTFYKPDWFDIVESEVKCCK
1	.	1	1		1	EAVCVIDMSSFTEFEITSTGDQALEVLQYLFS
- 1	1	1	- 1	1	1	EAACAIDWOOLTELEILOIADAADAADAADAA
i i						
	-	- 1	1			NDLDVPVGHIVHTGMLNEGGGYENDCSIARL
						NDLDVPVGHIVHTGMLNEGGGTENDOSTA NKRSFFMISPTDQQVHCWAWLKKHMPKDSN LLLEDVTWKYTALNLIGPRAVDVLSELSYAP

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID.	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutarnic Acid,
IO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ed-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			{	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			'	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
}				peptide	1	/=possible nucleotide deletion, \=possible
1			1	sequence		nucleotide insertion
			 			MTPDHFPSLFCKEMSVGYANGIRVMSMTHT
			ì			GEPGFMLYIPIEYRWGFTMLSTLVSNS
121	1471	A	1498	3	306	AQFLLVGWDHIL*LIVL*TNLTELGRTTCDQN
121	14/1		1			WPNSPDVLNHGCFYMQCLSKDCTIGYVSRE
	,	i	1			MLVAHTHTVEEHTGTHLQYVSWPDHSVPDD
	ì		{			SSDFVEFEN
122	1472	A	1533	121	329	LGLFSFVWTEVLEEPKDFSCETEDFKTLHCT
122	1472	l				WDPGTDTALGWSKQPSQSYTLFES*VGSGYII
		1	1			DNFFLA DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE
123	1473	A	1547	111	408	RGHVEMIEKLTFLNLHTSEKDKGGNTALHLA
125	1	1		1		AKHGHSPAVQVLLAQWQDINEMNEKQQTPL
		ì	1	1		
		1	1		l	HVAADRG
124	1474	1 _A	1555	1	745	MTFDDDDKNTYGVALVWKKFQTQSLRLSDL HRKSHLWRGIVSITLIEGRDLKAMDSNGLSDP
124	1 ****	1		1	ì	YVKFRLGHQKYKSKIMPKTLNPQWREQFDF
	1 .	i	i	[HLYEERGGVIDITAWDKDAGKRDDFIGRCQV
		1			\	DLSALSREQTHKLELQLEEGEGHLVLLVTLT
]	}	1	1		ASATVSISDLSVNSLEDQKEREEILKRYSPLRI
	.	1	1	1	1	FHNLKDVGFLQVKVIRAEGLMAADVTGKSD
		1	}			PFCVVELNNDRLLTHTVYKNLNPEWNKVFTL
	1	ì	ì	ł		*VALVWKKFQTQSLRLSDLHRKSHLWRGIVS
	1	1		1		ITLIEGRDLKAMDSNGLSDPYVKFRLGHQKY
	1	1		ł	1	KSKIMPKTLNPQWREQFDFHLYEERGGVIDIT
	1	1		l l	Ì	AWDKDAGKRDDFIGRCQVDLSALSREQTHK
	1			ı	ł	LELQLEEGEGHLVLLVTLTASATVSISDLSVN
		1	1	ŀ	{	SLEDQKEREEILKRYSPLRIFHNLKDVGFLQV
		1	1			KVIRAEGLMAADVTGKSDPFCVVELNNDRLL
		ł	1		1	THTVYKNLNPEWNKVFTL
	1		<u> </u>			GGPAPNSRYAEP*KNSLAMT*AHADCENYVA
125	1475	A	1556	57	509	CGGLDNICSIYNLKTREGNVRVSRELPGHTGY
						LSCCRFLDDSQIVTSSGDTTCALWDIETAQQT
		1		l		TTFTGHSGDVMSLSLSPDMRTFVSGACDASS
		1		1		KI WDIRDGMCROSFTGHVSDINAVS
					178	KSEKSCVSSLAHFGTSCQRDYDAMVKLVETL
126	1476	A	1592	3	178	EMI PTCDLADOHNIKFHYAFALNR*ER
1					409	TESPLLVRPYLPYITKSELHAIMTAGFSTIAGS
127	1477	A	1612	1	497	VI GAVISEGVPSSHLLTASVMSAPASLAAAKI
1						FWPETEKPKITLKNAMKMESGDSGNLL*AAT
1		1	1	1	1 .	OGA SSSISI VANIAVNLIAFLALLSEMNSALA
1			1	1	1	WVGNMFDYPQLSFELICSYIFMPFSFMMGVE
}		1	- [1	1	WPDSFM
1				_	106	CCMNSKAOESVFKNVLCNPPALSEMPDVKA
128	1478	A	1619	286	486	EDEVDFRASSISEEVAVGSIAATLKMKQGPM
	1	1	1			TOAINR
					206	PTRGALRYWIFGRFLCNIWAAVDVRCCTATI
129	1479	A	1627	1	395	MGI CIISIDRYVGVSYPLRYPTIVTQRRGLMA
			1	- 1		I I CVW ALSI VIYIGPLLGWRHPAPEDETICQI
1		Į.				NEEPGYVLFSTPGSFYLPLAIMLVMN*RVYR
]	I.	- 1	1		AKTE
					100	DPRVRTKIVNRKTTIYEIODKTGSMAVVGKG
130	1480	A	1638	2	466	ECHNIPCEKODKLRLFCFRLRKRENMSKLMS
1	1	- 1	- 1	1		EMHSFIQIQKNTNQRSHDSRSMALPQEQSQH
1	ı	1		ļ		KPSEASTTLPESHLKTPQMPPTTPSSSSFTKVT
1	1	1	- 1	1	1	KDKDIK*LLFNLYSSVEILPEVLHLKT
						LAEGGDVFDCVLNGGPLPESRAKALFRQMV
122	1481	A	1651	607	3	AIRYCHGCGVAHRDLKCENALLQGFNLKLT
1 141	,	1	(I	AIRYCHUCUVANKULACENALLQUITICADI
131	- 1	- 1			1	I DODAWIN DECIDE CONTOURS A VARE VIII
131						FGFAKVLPKSHRELSQTFCGSTAYAAPEVLQ GIPHDSKKGDVWSMGVVLYVMLCASLPFDL

		16.	CEO I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	İ	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	Į.		914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	} .]	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
	l	ì	1	peptide		nucleotide insertion
ì	1	í	1	sequence	<u> </u>	nucleotide insertion
	 	 				TDIPKMLWQQQKGVSFPTHLSISADCQDLLK
	ì	ł	1	1	i	RLLEPDMILRPSIEEVSWHPWLAST**KQWQV
	1	1				LSNKVGGESKPKKKK
130-	1402	A	1656	150	48	LVAKSLLYCGCLFFLLQLAKNVGNNSFNDIM
132	1482	^	1030	***		EANLTSPSPKPTPSSDM*VFLIY*TYFGAWHV
1		1)	ł	VDAQ
		 	1.00	3	406	RKHIKLLIQKLSDVP*ECQNNQL*KLTEICEKE
133	1483	A	1660	3	400	KKEFKKKMDDORPEKITEA*SKDKSPMEEEK
1	ł	1	1	1	1	TEMIRSYIQEVGRYIKRLEEAQSKRLEKLREK
1	1	1		Į.	}	HKEIROPILDEKPKGEGSSSFLSETCHEDTSWF
	}		1	l	1	1
	i	1				PNFTP PGSTHASARITIY*L*IILSNATEVDNNFSKPPP
134	1484	A	1666	1276	466	FFPAGAPPASSSSSSSSSSPPTVSTAPPLIPPPGF
137	1.0.	-	1			FFPAGAPPASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
1	1	1 .	ì	1	1	PPPPGAPPPSLIPTIESGHSSGYDSRSARAFPYG
ì	1		1	i		NVAFPHLPGSAPSWPSLVDTSKQWDYYARSS
1		1	1	1		SSSSSSSSSSSSPRDRDRER*RTRERERERDHS
	1	1		}		PTPSVFNSDEERYRYREYAERGYERHRASRE
1 .	i	ł	ı	\	1	KEERHRERRHREKEETRHKSSRSNSRRRHESE
1	l	ļ	1		1.	EGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE
	i		Ì	. [1	STEATPAE
		٠	1602		417	PTRPVNSSOAFALVYYTLGALGGNLIAHMGL
135	1485	Α	1673	1	717	GVRVWAGIGVLOSCESALTHYRLVANHVAS
1	1			1		DISLTGGSVVQRIRLPDEVENPGMNSGMLQE
1	l l	-		ļ		DLIQYYQFLAEKGDVQAQVGLGQLHLHGGR
	ł			Į.	ļ	GV*QNHQRAFDYFNLAA
	1	_				ANTSLSSAAVSAVSPPPCRTSTATTLPPPMPSF
136	1486	A	1678	525	9	FCVFPSPSMSPSPSEFLSCIASVSRVHSLSSSSS
1.00					1	GSSTASSLNFSAIMGSSSATASWVLSTASTPP
ľ	1	1	- [CPSALPSSPAQES*SLAASSSAWPVAGISPSGA
1		1	- }	1	ļ	CPSALPSSPACES SLAASSSAWF VACIOUS DOT
1	i	1	- 1	1		CTFPAGSASGAAKAPSPSWRCPSFRALFSLLD
	1	1				SSSLSL
137	1487	A	1680	1	2999	AHRDEIQRKFDALRNSCTVITDLEEQLNQLTE
137	1407	1,	1 2002	Ţ.		DNAELNNQNFYLSKQLDEASGANDEIVQLRS
1	}	- }	ł	ì	1	EVDHLRREITEREMQLTSQKQTMEALKTTCT
1			1	1	1	MLEEQVMDLEALNDELLEKERQWEAWRSVL
	1		İ)	1	GDEKSOFECRVRELORMLDTEKQSRARADQ
1	i	l		1		RITESROVVELAVKEHKAEILALQQALKEQK
1	1	1	1		1	I K A ESI SDKLNDLEKKHAMLEMNARSLQQK
ì	1		1	1		TETERFI KORI LEEOAKLOOOMDLOKNHIK
	ļ	- 1	- 1	1	1	I TOGI OF ALDRADLLKTERSDLEYOLENIQV
1 '	1	1	1	}	1	T VOLER VEMEGTISOOTKLIDELOAKMUUPA
	1	1		1	1	VYYYVPI OVNELKI ALEKEKARCAELLEALU
1		- 1	1	1		KTRIELRSAREEAAHRKATDHPHPSTPATARQ
	1	- [QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST
		1		,	1.	PEEFSRRLKERMHHNIPHRFNVGLNMRATKC
-{	1	ı		1		PEEFSKKLKERMININIPIKEN VOLINIKATKO
	1	l	1			AVCLDTVHFGRQASKCLECQVMCHPKCSTC
}	}		1 .	i		LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT
1	1	1		}	1	KEPSSSLHLEGWMKVPRNNKRGQQGWDRK
	1		- }	1	1	YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP
		i	1			DGDVSTHGAVGASELANTAKADVPYILKMES
		- 1		l		HPHTTCWPGRTLYLLAPSFPDKQRWVTALES
	1	1	1	1	1	VVAGGRVSREKAEADAKLLGNSLLKLEGDD
1		İ	1	1		REDMNCTLPFSDOVVLVGTEEGLYALNVLK
ì		1		}	1	NSLTHVPGIGAVFOIYIIKDLEKLLMIAGEERA
1	1	- 1		1	1	1 CLYDVKKVKOSLAOSHLPAOPDISPNIFEAV
1	[1			1	KGCHLFGAGKIENGLCICAAMPSKVVILRYN
- 1	ľ		1			ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK
	- 1	- 1	1 .	1	1	FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS
	- 1	- 1	1	1	1	LAFIDIME ALTERITOR COLLEGE TO CERECOLLING
1		- 1	1	Ĭ		NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDS

SEQ ID No.				650 T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
No.	SEQ ID	SEQ ID	Met	SEQ			De A spartic Acid. E=Glutamic Acid.
138			hod	_			F=Phenylalanine, G=Glycine, H=Histidine,
Sequence Sequence	nucl-	peptide					I=Isoleucine K=I.vsine L=Leucine.
138	eotide	seq-					M=Methionine N=Asparagine P=Proline.
	seq-	uence					O=Glutamine R=Arginine S=Serine.
	uence '			914 ·	ng to urst		T=Threonine V=Valine W=Tryptophan.
							V-Turocine X=Inknown *=Ston codon.
		ł	l			sequence	/
148			\				purposible interestion
138		ŀ	ł		sequence		NUCLEOUSE INSCITION
ISSGAIYLASSYQDKLRVICKGRLVKESGTE		 					YGKKSKIDDLKWSKLFLAFAIREFILFVIII
HHRGPSTSRR*PASPLPQYGGGRAFLGGRRR 138		ŀ	1	ł	ļ	ì	NSLEVIEIQARSSAUTPARATEDITAT RIEGITA
1488		ł	Ì				ISSUATILASS TOPLES TO CONTRACTOR AND CORPE
PLCCLGGAAGRL*ARSOKSGLRRRAHAGY POGPONSCP*CARPSGGGGPLPGFGGOVCS CWTRGCQTTARTAAAAAAAPGAAGRPFPGGGGVS CWTRGCQTTARTAAAAAAAPGAAGRPFPGGACP POGSCAASASQBAAPPPMCPGGRWAVAS PETRCPAAPGTRCRLLEAA 1889		ł	· ·				HHRGPSTSRR*PASPLPQTQQQRAFLQGRAR
PICCLIGATOR PICTURE	138	1488	A	1686	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV
CVTRGCOTTARTAAAAAAPGRARPPGRR	130		** .			i	PLCCLGGAAGRL*ARSGRSGLRRRRAMAUP
139		ì	1	1 .		ì	PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS
1489 A 1693 3 376			1	ł	l	Í	CWTRGCQTTARTAAAAAAAPGPAGRRPPGGA
1489			l	1			PQNGSCAASASQEAAAPPPMCPPGRRWAVAS
149		1	1	1		1	PPETRCPAAPGTRCRRLEAA
FEITKALGCAWFISLGCAWFISLGCAGEROIMMRLVDR	120	1490	+	1693	3	376	LPSMSNCTSCFRLQSRTES*IRQAGHLLGRNE
1490	139	1409	A	10,5	-		FIETKALGCAWFSLCYYLVLYFESSHKVDFVF
140	ł		İ	. .	1		IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR
140		1	1	1	ľ		RWAGIAKGVGTOKIIGRVHLGEQKALGL
140		1.400		1704	3	376	FRINKFIKELIMDGKNLIAATKSLSVAQRKFA
	140	1490	A	1704	13	3,0	HSLRDFKFEFIGDAVTDDERCIDASLREFSNFL
141		1	1	1	1		KNLEEOREIMVS*EGCKLISQLSRGKKIWIWK
141	1	1	1	1		{	LVLVEVVKHLSLGTVVHCNGKMRFPEP
141	L		 	1742	 	362	LITNKVFVARELSCLDVHLDSTGSTAVVADQ
MAAL*TELSGRLRSSKSNOWNGDNSTGYLTV PLRPLTIVKEVTMOPPANVRGLNWMG NNFSTLPRGS*PMSPRTTMGRRRQRRREHKSS LSLASSTVGPGGQIVHTETTTV*LCGDPLSGF GLQLQGGIPATETLSSPLVCFIEPDSPAERCG LLQVGDRVLSINGIATEDGTMEEANQLLRDA ALAHKVV QMLRNGGDQNTVPDYHFADRIRELL*PTEDQ KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA NELCEVNRKGGTSGDPCLPYTCVQGCKLQQA SDFIARQGTIQVPSAGEVECYKICSCGQSGL LENCMEMHCMDLPTDTSALVR PGRFRPPRLSQAGTDSGS*VPDSSFPSAPAEPL PYFLQEPQDAYIVKNKPVELRCRAFPATQIYF KCNGEWVSQNDHVTQEQLDEATGLRVREVH IEVSRQQVEELFGLEDYWCQCVAWSSAGTTK SRRAYVRI SRR	141	1491	A	1743	1 1	302	DKLELELVLKGSYEDTQTSFLGTASAFRFHY
PLRPLTIVKEVTMDVPAPNVRGLNWMG	ł	1 .	1	1	1.	}	MAAL*TELSGRLRSSKSNGWNGDNSTGYLTV
142	İ	İ	1	1	1	1	PLRPLTIVKEVTMDVPAPNVRGLNWMG
LSLASSTVGPGGQVHTHETTEVVLCGPLSGF				1-20	 . 	106	NNPSTLPRGS*PMSPRTTMGRRRQRRREHKSS
143	142	1492	A	1769	1	1 400	I SI ASSTVGPGGOIVHTETTEVVLCGDPLSGF
LLQVGDRVLSINGIATEDGTMEEANQLLRDA ALAHKVV		Ĭ	1	İ	1	i	GLOLOGGIFATETLSSPPLVCFIEPDSPAERCG
143	1	1	1	1	1	1	LLOVGDRVLSINGIATEDGTMEEANQLLRDA
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143				L		147	OMI.RNGGDONTVPDYHFADRIRELL*PTEDQ
NELCEVNRKGCTSGDPCLPYFCVQGCKLGQA SDFIARQGTLIQVPSSAGEVECYKICSCGSGL LENCMEMHCMDLPTDTSALVR	143	1493	A	1789	1 1	1 447	KNCIP*DTVLRPSALGNIVEEVTHPCSPGPCPA
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GIEGRLTADQLNSATACIFAAEVAIKESERFN GIPALSVPVAEPIRHAEALMQQALTLKRSDET RTVQQDTQPVKSVKTELKQALLSGISFAVPLI VAGGTQVA*AV*RQGISSLHDVQVRTWNS 149 1499 A 1880 611 24 GLNSENALSNEAMERGWQCLRLFAERLQDIP PSOIRVVATATLRLAVNAGDFJAKAQEILGCP	148	1498	A	10/3	1 300	1.	IAHTYMAAEYLEKAGRKLGVNVYVEKQGAN
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RTVQQDTQPVKSVKTELKQALLSGISFAVPLI VAGGTQVA*AV*RQGISSLHDVQVRTWNS VAGGTQVA*AV*RQGISSLHDVQVRTWNS GLNSENALSNEAMERGWQCLRLFAERLQDIP PSOIRVVATATLRLAVNAGDFIAKAQEILGCP	l	1	1		1		GIPAL SVPVAEPIRHAEALMQQALTLKRSDET
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149 1499 A 1880 611 24 GLNSENALSNEAMERGWQCLRLFAERLQDIP PSOIRVVATATLRLAVNAGDFIAKAQEILGCP		1		1	1		VAGGTOVA*AV*ROGISSLHDVQVRTWNS
149 1499 A 1660 OTT PROTEVVATATLELAVNAGDFIAKAQEILGCP	L:					124	GLNSENALSNEAMERGWOCLRLFAERLODIP
VQVISGEEARLIYQGVAHTTGGADQRLVVD	149	1499	A	1880	611	24	PSOTRVVATATLRLAVNAGDFIAKAQEILGCP
VQVIDOLENIA VQ	1		1		J	1	VOVISGEFEARLIYOGVAHTTGGADORLVVD
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SEQ ID NO: of nucleotide peptide sequence NO: of nucleotide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence No: of peptide sequence	PHTDYRPLIRDSNNYVLDEQTQQAPH
NO: of nucl- nucleotide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide uncleotide location corresponding to last amino acid residue of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide sequence NO: of peptide location corresponding to last amino acid residue of peptide sequence NO: of peptide sequence M=Methide Sequence N=Threat sequence NO: of peptide location corresponding to last amino acid residue of peptide sequence NO: of peptide location corresponding to last amino acid residue of peptide sequence NO: of peptide location corresponding to last amino acid residue of peptide sequence NO: of peptide location corresponding to last amino acid residue of peptide sequence N=Threat N=N=N=N=N=N=N=N=N=N=N=N=N=N=N=N=N=N=N=	alanine, G=Glycine, H=Histidine, ine, K=Lysine, L=Leucine, onine, N=Asparagine, P=Proline, nine, R=Arginine, S=Serine, nine, V=Valine, W=Tryptophan, ine, X=Unknown, *=Stop codon, e nucleotide deletion, \=possible e insertion ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD EHTDYRPLIRDSNNYVLDEOTQQAPH
nucle- sectide sequence USSN location corresponding or location corresponding or location corresponding or location sequence USSN location corresponding to last amino acid residue of peptide sequence M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid residue sequence I = Isoleuci M=Methi Q=Glutar T=Threor Y=Tyrosi /=possible nucleotid residue sequence I = Isoleuci M=Methi Q=Methi	ine, K=Lysine, L=Leucine, onine, N=Asparagine, P=Proline, nine, R=Arginine, S=Serine, nine, V=Valine, W=Tryptophan, ine, X=Unknown, *=Stop codon, e nucleotide deletion, \=possible e insertion ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD EHTDYRPLIRDSNNYVLDEOTQQAPH
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ng to first amino acid residue of peptide sequence y=Tyrosi /=possible nucleotid ryfADR1 Galaxi	nine, V=Valine, W=Tryptophan, ine, X=Unknown, *=Stop codon, e nucleotide deletion, \=possible e insertion ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD FHTDYRPLIRDSNNYVLDEOTQQAPH
amino acid residue of peptide residue of peptide sequence /=Tarreor y=Tyrosible sequence Ta	nine, V=Valine, W=Tryptophan, ine, X=Unknown, *=Stop codon, e nucleotide deletion, \=possible e insertion ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD FHTDYRPLIRDSNNYVLDEOTQQAPH
residue of peptide sequence Y=Tyrosi /=possible nucleotid rucleotid ryFADRI RYHSW	e nucleotide deletion, possible e insertion ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD FHTDYRPLIRDSNNYVLDEOTQQAPH
peptide /=possible sequence inucleotid IGGAST YFADRI RYHSW PITMET	e insertion ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD FHTTDYRPLIRDSNNYVLDEOTQQAPH
sequence nucleotid IGGAST YFADRI RYHSW	ELVTGTGAQTT*LFSLSMGCVTWLER NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD FHTDYRPLIRDSNNYVLDEOTOQAPH
IGGAST YFADRI RYHSW	NLGQENFDAAQKAAREVLRPVADEL KEVRGASVTVQALQEIMMAQGMDE WPVD FHTDYRPLIRDSNNYVLDEOTOQAPH
RYHSW	KEVRGASVTVQALQEIMMAQGMDE WPVD FHTDYRPLIRDSNNYVLDEQTQQAPH
DITMET	WPVD PHTDYRPI IRDSNNYVLDEOTQQAPH
RITMEI	PHTDYRPLIRDSNNYVLDEQTQQAPH
	PHTDYRPLIRDSNNYVLDEOTOOAPH
150 1500 A 1894 2 750 GRVDFI	TALL AND THE PROPERTY OF THE PA
130 1300 A 1001 -	LVDVDGNPHPTKYQRLVPGRENSAD
EHLIPQ	LGYVATSDGEVIEQIISLQTNDNDERS
PESSILI	OGMIRQLQQQQDQRMGADQDTIPRG
LSNGE	TPRRGFRRLSLDIQSPPNIGLRRSGQV
EGVRQ	MHQNAPRSQIATERDLQAWKRRVVV
PEVPLO	GIFRKLEDFRLEKGEEERNLYIIGRKRK
(KSDSVGLVSQSRPRTCRRKYP
151 1501 A 1900 141 785 GKTIQI	QTTMQNKYKTVQKQYKTIPKNKKA
121 1 1201 1 1 1 MEMOI	KKQFQDTCKVQTKQYKALKNHQLEV HKTILKTLKDEQTRKLAILAEQYEQSI
TPKNE	ASQALRLDEAQEAECQALRLQLQQEM
NEMMA	YQSKIKMQTEAQHERELQKLEQRVSL
ELLNA	EQKIEEELAALQKERSERIKNLLERQE
RRAHL	DMESLRMGFGNLVTLDFPKEDYR
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	DTQRDGLQNYEALLGLTNLSGRSDKL
152 1502 A 1915 2 377 LVRLL	KERALPDIENYMFENHDQLRQAATEC
RQKIFI	VLHKEVQERFLADGNDRLKLVVLLCG
MCNM	VUNAAAGALAMLTAAHKKLCLKMT
OVTT	VQIVAAAALIDI.ILLILILI
AVOR	RLEYLQIPPVSRAYTTACVLTSAAVQL
153 1503 A 1921 1 237 AYQSL	QLYFIPELIFKHFQIWRLITNFLFFVPFG
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VMCT VT
EMVE	GEGKMCINTEWGGFGDNGCIDDIKTK
154 1504 A 1526 2 VOTES	IDEGSI NPGKORYEKMTSGMYLGEIV
l l l ROILII	OLTKOGLLFRGQISERLRTRGIFETKILS
l l l l l l l l l oresti	RI ATTOVRRILOOLGLD
TRIAK	TEME AKKKYEKEL TMFONDFEKACQA
155 1505 A 1929 2 1 1 1 1 1 1 1 1 1	AN REKSTI FRIHKHOEIETKEIYAQKQ
l l l l lilkr	MDLLRGREAELKORVEAFESYQUELK
DDYII	RTYRLIEDDRINIQISGHWQESP
156 1506 A 1935 1 270 VTRKI	PIFIVDAFTARAFRGSPAADCLLENEL
156 1506 A 1555 1 DEDM	HOKIAREMNLSETAFIRKLHPTUNFAQ
l l l l l pecto	I INFTETTOLOILTSSILPSIL
LOS ESKA	INFKERTKSPKPAESPOSATKQLDQP1A
157 150/ A 1950 507 1 AVEV	VDAGNHWCKDCNTICG1MFDFF 1 HMLH
I I I I I I INKKH	TOGOFOKSSDFOKEELQQTFLPPEKQG
158 1508 A 1939 1 423 TTHRI	NVTAEPPCTSMPIYWMPDVPHRCTTA
1 1 28 1 208 A 1 227 1 NTCES	VDLTDYCAQNGFYCLVYGFLPYGSLED
RLHC	QTQACPPLSWPQRLDILLGTARAIQFLH
QDSPS	SLIHGDIKSSNVLLDERLTPKLGDFGLA
RFSRI	AGSSPIQSSM
159 1509 A 1974 3 401 HTST	ARLLLHRGAGKEAVTSDGYTALHLAAR
	ATVKLLVEEKADVLARGPLNQTALHL
	IGHSEVVEELVSADVIDLFDEQGLSALH
	GRHAQTVETLLRHGAHINLQSLKFQGG
	ATLLR
160 1510 A 1982 2 417 KFLK	DLEKQYNKEEPHLSEIGSCFLQNQEGFA
1 100 1 1210 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CONHPGACLELANLMKQGKYRHFFEA
	QQMIDIAIDGFLLTPVQKICKYPLQLAEL TQEHGDYSNIKAAYEAMKNVACLINER
LKYT	I CEHOD I SUITAW I EWATEL A VODILLER
	ESIDKIA
161 1511 A 1984 4 770 RETG	SVSLSPSOLEGAESYAVSPILYSSPDVKE TLQGQRHSHTGVKSTPGQSAAILMKLR
1 101 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ASKTLNANNMETLIECQSEGDIKEHPLL
SSHN	ADA I LIVANIANTE I DILOQUEDO DELLE EL

6710 ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID		hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	noa	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1		ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	}	1	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
	1	l	ł	residue of	sequence	/-possible nucleotide deletion, \-possible
	i	i]	peptide		nucleotide insertion
	1		l	sequence		ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS
					İ	ASCESEDSICULIBY KARRAY LSWIT CHICODEDTI B
	ł	1				PASDFSGALETDLKASLFDQPLSIICGDSDTLP
	ì		1]	RPIQDILTILCLKGPSTEGIFRRAANEKARKEL
			1		\	KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP
	1	1			i	RKLLSSDLFEEWMGALEMQDEEDRIEALK
160	1512	A	1986	864	501	LLNSGLFSAPDGSNLEMRLTRGGNMCSGRIEI
162	1312	^	1700	1 00-1	1	KFOGRWGTVCDDNFNIDHASVICRQLECGSA
		i	1	1		VSFSGSSNFGEGSGPIWFDDLICNGNESALWN
	i	1	ĺ	1	}	CKHQGWGKHNCDHAEDAGVICSSKD
	l				J	AVDLSIDESSLTGETTPCSKVTAPQPAATNGD
163	1513	A	2001	419	187	LASRSNIAFMGTLVRCGKAKGVVIGTGENSE
	1	ì				
ł	1	1				FGDIINLSTFVVHS
164	1514	A	2012	284	597	SLLCLFPGTSTVVCKPIVIETQLYVIVAQLFGG
1	1					SHIYKRDSFANKFIKIQAIEILKIRKPNDIETFKI
'		1	ì		ļ	ENNWYFVVADSSKAGFTTIYKWERETGFYSH
}	ł	l	1	1	[QSFTR
165	1515	A	2013	2	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY
103	1313	1 ^	2015	1 -	1	NVDLPFMYSITYAAFAIIATLLMLNLLIAMMG
1	l l	1	1	ł	}	DTHWRVAHERDELWRAOIVATTVMLERKLP
ļ	1		١.	1	•	RCLWPRSGICGREYGLGDRWILRVEDRQDLN
ł	1			1		RORIORYA
L					927	CCQREGLGLKAVVQILLSHGRNGLPGEPASS
166	1516	TA.	2019	2	927	QGLSAASSTPVFHLALQIDSAPDNIDWVEMLF
1		Ì				NKNMYTERLQNVMVLEQCFSDSSSLYRFLTY
Į.	1			l	İ	SYLLAFNYWLLLAPVTLCYDWQVGSIPLVETI
l	- {		1	[WDMRNLATIFLAVVMALLSLHCLAAFKRLE
1	l	1	1	1	1	HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER
	1	1				VLYMPSMGYCILFVHGLSKLCTWLNRCGATT
	1	1	}	1		VLYMPSMGYCILFVHULSKICT WEINGCOATT
				1	Į.	LIVSTVLLLLFSWKTVKQNEIWLSRESLFRS
1	1	1	1	ļ]	GVQTLPHNAKVHYNYANFLKDQGRNKEAIY
i			1		1	HYRTALNNNKAWDYLCWRFRKTLTDLP
167	1517	A	2025	696	71	AAASAASSLTVTLGRLASACSHSILRPSGPGA
107	1317	1 ^	2023	1		ASLWSASRRFNSQSTSYLPGYVPKTSLSSPPW
1		l l	1	ł	ľ	PEVVLPDPVEETRHHAEVVKKVNEMIVTGQY
1	1	1		1		GRLFAVVHFASROWKVTSEDLILIGNELDLA
1	į.	-		1		CGERTRLEKVLLVGADNFTLLGKPLLGKDLV
	- 1	1				RVEATVIEKTESWPRIIMRFRKRKNFKKKRIV
1	1	ì		1		TTPQTVLRINSIEIAPCLL
L						HLQVAARVFMPLQAVDSAPKPLKGQAQAPQ
168	1518	A	2046	2	366	RLOGAARVFMPLQAQVKAKASKPLQMQIKA
				1		PPRLRRAARVLMPLQAQVRAPRLLQVQSQVS
ĺ	1		1	1	}	KKQQAQTQTSEPQDLDQVPEEFQGQDQVLR
		1				LAQUACIQIDEI QUEDQTI EEI QOQDQTER
169	1519	A	2049	1	945	QNLEDREVLNGVQTELLTSPRTKDTLSDMTR
	1		1			TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI
	1		ł	l	l	EDNSRSKREGLFHENECIVKINNVDLVDKTFA
1		1	1	1		QAQDVFRQAMKSPSVLLHVLPPQNREQYEKS
1	1	1	1 .		1	VIGSLNIFGNNDGVLKTKVPPPVHGKSGLKTA
1		1			1	NI TGTDSPETDASASLOONKSPRVPRLGGKPS
1		1		ļ		SPSLSPLMGFGSNKNAKKIKIDLKKGPEGLGF
1		-	1	1		TVVTRDSSIHGPGPIFVKNILPKGAAIKDGRLQ
1				1		SGDRILEVNGRDVTGRTQEELVAMLRSTKQG
1	1			1		ETASLVIARQEGHFLPRELVMFRSQSH
	L					PVATHLTKILNSDEHAVVISSAKTLCETVKDF
170	1520	A	2050	363	1	VAKVEKTYDKTLENAVVADAVASKCSVLNE
			1	I	l	VARVERTIURILENAV VADA VASACSVENE
1		1	1	1	l l	KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV
	- [1	1		ESSSEESLGESKEQLGDDVTKPSSQKA
	1521	A	2055	139	675	IPSRPWLGRITGLDPAGPLFNGKPHQDRLDPS
1 171				,		TO THE PERSON OF
171	1321					DAQFVDVIHSDTDALGYKEPLGNIDFYPNGG
171	1321	' '				DAQFVDVIHSDTDALGYKEPLGNIDF 1PNGG LDQPGCPKTILGGFQYFKCDHQRSVYLYLSSL

		37.	000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	SEQ ID NO:	beginning	nucleotide	De Aspartic Acid. E=Glutamic Acid.
NO: of		nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1 1		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1 !			residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	ł		•		Sequence	/=possible nucleotide deletion, \=possible
				peptide	ĺ	nucleotide insertion
	<u> </u>			sequence	 	DESCTITAYPODSYODYRNGKOVSCGTSQKE
						SCPLLGYYADNWKDHLRGKDPPMTKAFFDT
			ì	1		AEESPFCMYHYFVDIITWNKNVR
		Į.		l	<u> </u>	LIQHKSAVEYAQSHLSLVSMCKESHKCSEPK
172	1522	Α	2056	3	361	MEWKVKIRSDGTRYITKRPVRDRILKERALKI
						KEERSGLTTDDDTMSEMKMGRYWSKEERKQ
	1	1		ł		KEEKSGLI IDDDIWSEWIGWGKI WSIZDZGG
	1	I				HLVRGKEQRRRREFMMRIRLKCLKES
173	1523	A	2060	1	387	GTRILSMQIPFVGFQPIRTSEHMAAAGVFALL
175	1323	1 **	2000	f -		QAYAFLQYLRDRLTKQEFQTLFFLGVSLAAG
	1	l	1			AVFLSVIYLTYTGYIAPWSGRFYSLWDTGYA
		ì	1	1 .		KIHIPIIASVSEHQPTTWVSFFFDLHILGCTFPA
	1			1		G
		 	2021	74	443	LLMGPKAKKSGSKKKKVTKAERLKLLQEEEE
174	1524	A	2071	\ '" ·	1	DDI KEEFEARI KYEKEEMERLEIORIEKEKW
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		1		}	1	OFTKI I SOWKHYIOCDGSPDPSVAQEMNI
				 	486	TAALTWSOPOEFWPMEMOPIVTDMVTVHWV
175	1525	Α	2083	139	480	AESSTVGWLCALFRVTHVGVGATGHGVVCG
			1			RRVLCGLPLPSPAPMPIMSLPEGESRKEREVQ
	1	1	1	1	ì	RLOFPYLEPGHELPATTLLAFLAAV
	1	1				EGSVNFKFGVLFAKDGQLTDDEMFSNEIGSEP
176	1526	A	2092	3	587	FORFLINLLGDTITLKGWTGYRGGLDTKNDTT
1				1		GIHSVYTVYQGHEIMFHVSTMLPYSKENKQQ
	.	1	1	1	ł	VERKRHIGNDIVTIVFQEGEESSPAFKPSMIRS
1	1	[1		VERKRHIGNDIV IIVF QEGEESSI AI KI SIMIKS
		1	ł	ł	}	HFTHIFALVRYNQQNDNYRLKIFSEESVPLFG
l	İ	1	1		l .	PPLPTPPVFTDHQEFRDFLLVKLINGEKATLET
1	1				1	PCI CONTINUOSPI (ICC
100	1527	TA	2103	44	427	GKGQVSLEGRPHRGPLCLGSWWPGSRVPGC
177	1327	^	2.05			CDGAWLAWACWVFGNDFPSPASAACSALLG
1				1	1	CSVSTACLCVPLCSGSPLAPFRRTAALQEGLR
ļ		ļ	-	1	1	RAVSVPLTLAETVASLWPALQELARCGNLAC
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178	1528	A	2104	12	107	DSTAASSEGAVVEIFCNHSVSNAYNFFWYLHF
	1	l l	1	ļ		PCCAPRLLVKGSKPSOOGRYNMTYERFSSSL
ĺ	ĺ		1		ł	LILQVREADAAVYYCAVEVPNTDKLIFGTGT
1.	ì	1		}		PI OVERNIONED
1	·				1212	PTRSSTRPPSLFVHASAKGGEKEEGDDGHYL
179	1529	A	2111	1	312	MRTESHTGLKKGGNANLVFMLKRNTEPKKG
1		1	1	1		SYHFDLERLRAAHILFEREQEHLAPGGISMPL
1	1	1		ì		
1]					PPPLPLPACLG TSIKRAIETTDVTRSFGWDSSEAWQQHDVQE
180	1530	A	2116	3	366	LCRVMFDALEQKWKQTEQADLINELYQGKL
100	1.555	1	}	1		LCKVMPDALEQX WAQTEQADEMEDT QOAD
		1	1	1	1	KDYVRSLECGYEGWRIDTYLDIPLVIRPYGSS
1		1.	<u> </u>		1	QAFASVVCTFHLTACVSLHRIHNSTVV
<u> </u>	1631	- A	2117	2	386	YGLGAHFGRLFIQAGINENDFYDGAWCAGR
181	1531	A	211/	\ ~ ·	1	ANDI OOWIEVDARRITRETGVITOGKNSLWLS
1			1	1		DWVTSYKVMVSNDSHTWVIGKNGSGDMIF
1	1	1	1	1		GNSEKEIPVLNELPVPMVARYIRINPQSWFDN
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					493	PTYTOVVII NI AVADLLLETLPFWAVNAVH
182	1532	A	2123	1	493	GWAT GKIMCKITSALYTLNFVSGMQFLACISI
		ŀ		1		DRYVAVTKVPSQSGVGKPCWIICFCVWMAAI
1		1		1		LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL
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						NIKIS
	1522	1	2140	3	561	NIKIS POAWHEAFKVRKEILTVICCLLAFCIGLIFVQ
183	1533	A	2140	3	561	NIKIS

		- T	050	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D-Americ Acid E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	- 1	in	location	corresponding	Introducine K=Lysine L=Leucine.
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O-Chitamine R=Arginine S=Serine,
ience			914	ng to first	of peptide	T-Threonine V=Valine W=Tryptophan,
	i '			amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
•	l			residue of	Sequence	/=possible nucleotide deletion, \=possible
	i '			peptide		nucleotide insertion
]			sequence	ļ	SPI MI I SI LIASVVNMGLSPPGYNAWIEDKAS
						EEFLSYPTWGLAVCASLDVFAILPVPVAFIGR
		į	1	1	1	RFSLIDDGAGPFCSAAYTTTGCRTPYL
		ļ.	1			HELTVAAADRGQPPQSSVVPVTVTVLDVND
184	1534	A	2145	3	538	NPPVFTRASYRVTVPEDTPVGAELLHVEASD
104	1331					ADPGPHGLVRFTVSSGDPSGLFELDESSGTLR
		l	1	}		LAHALDCETQARHQLVVQAADPAGAHFALA
	1	1	ł	j	1	PYTIEVQDVNDHGPAFPLNLLSTSVAENQPPG
		j	1	ł		PYTIEVQDVNDHGPAPPLNELSISVALINGITO
		1	ì			TLVTTLHAIDGDAGAFGRLRYHL
	1.535	A	2151	2	671	LDKLLDRMENYNIFNEYILKQVAATYIKLGW
185	1535	^	12131	1-	1	PKNNFNGSLVQASYQHEELRREVIMLACSFG
		}	1			NKHCHQQASTLISDWISSNRNRIPLNVRDIVY
	1	ì			1	CTGVSLLDEDVWEFIWMKFHSTTAVSEKKIL
		1	1	1		LEALTCSDDRNLLNRLLNLSLNSEVVLDQDAI
		1	1	1		DATES A PAPHORDI AWKI KUKWKILIA IN
		1	1	l		ROKTLEFDFAEPLILAFPIILYTAIDNPPLVREH
	1	1	1			l e
				12	400	GPMCDKHSAFAEKFHAGFIDYIVHPLWETWA
186	1536	A	2153	1 2	1 400	LITT AT DID A CIDIT VITLEDNENW VDSMLPQSPSPF
			1	1	- -	I DEONID DWOGI I ENLHVEL I LDEEDSEGFEN
		ر. ا	·· [ł		EGEGQTYFTSSKTLCGIVPQNTDSLGETGIHIC
1	1		i	ĺ		ALIDVED
	1	1			442	PAICED VASDSELENSSLLIMILPLRNATOEFUR
187	1537	A	2158	227	442	PGAVAYTCNPSTLGGWGGWITRSGVRDQPG
	-1	1		1		OUGCTPS
1		1		<u> </u>	404	AUT GGAWLTORSLGSWAAPGPARAAKEVYA
188	1538	A	2167	3	486	CECNICENDITURMETSEHLOLLSFYLGAVSF
,,,,				1	ĺ	AND TO THE PROPERTY OF THE PRO
1		1		ŀ	i i	MDDILAITGFNTCLSIVFSSGCARSSGSRNSKS
1		1		1		LRTPLGTICEGCDDSSIFSHLDHSSKWSSTYG
1	1			ì		
· ·	1.	- 1	İ			HSGA EFLSSNQITQLPNTTFRPMPNLRSVDLSYNKL
189	1539	A	2168	2	412	QALAPDLFHGLRKLTTLHMRANAIQFVPVRI
109	1333	**				QDCRSLKFLDIGYNQLKSLARNSFAGLFKLTI
1		ļ.	ł			LHLEHNDLVKVNFAHFPRLISLHSLCLRRNK
1	1	1		j		LHLEHNDLVKVNFAHFRLISCHSBEBIGG
1	1	ı		}		AIVVSSLDW
	1500	- 	2179	64	399	MRLNONTLLLESFGXXRPYTSEHAPTYHQW
190	1540	A	2113	١٠.		LAGUADET I DUCTTOEPI TI EHEYAMURI WEEL
1				1	1	AYECTFIVLDAEKRHAQPGATEESCMVGDV
1	1	ı		1		LEGITAL TALGETEVIJABL
			- 6.55	- 1	469	CLDD A A GIRHERNVI YINETHTRHRGWLAKK
191	1541	_ A	2190	1 '	302	I TOUR ETOERDVHKGMFAINVIENVLNSSA
				ì		
Ì	1	1		}	}	AVDIT OFMVATVSPAMIRLIGWVLLKLING
Į	1					FWNIQIHKGQLEMVKAATETNLPLLFLPVHF
1 .		- 1	- 1	ł	İ	OTT
						PSKXGGIRLLLTGTQLYGRFGSAIAPLGDLD
192	1542	A	2197	26	157	DGYNGEGREEPY
1 - 7 -		l l				EYFPNSIWRSLFSTMDLGDIGFYTYRILQALS
193	1543	A	2236	2	383	YTHSKGIMHRDVKPLNILCNSPRNKVILADV
173	1,343	1		1		GLAEFYHPMRKYSVHVATRYYKSPEILLDY
1	1	1	1		1	GLAEFY HEVILA 13 VIVALA 1 TROUBLES
1		- }			ļ	YYDYSLDIWAVGVILLELLTLKLHVFEGGDI
		}	- 1			EQ
			2241	105	409	RKGVGKMPTSEGRPGQERSDWVTSYKVMC
194	1544	A	2241	105	1	MOCHTIMOTOKNIGSGDMIFEGNSEKEIPVLN
}	1	1			į.	LPVPMGARYIRINPQSWFDNGSICMRMEILG
-	- 1	1		1		DI DIDRINIV
1					672	MGVASDWTKRIEYOPGSGSMPLFPSIHLETC
195	1545	A	2245	1	0/2	GAVSSLQIVTELQTNYIGKGCDRETYSEKSL
כפו ו						

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQID	SEQ ID	Met	SEQ	beginning	nucleotide	D-Acceptic Acid. E=Glutamic Acid.
IO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in USSN	location	corresponding	1-Teoleucine K=Lvsine, L=Leucine,
otide	seq-		1 - 1	correspondi	to last amino	M=Methionine N=Asparagine, P=Proline,
eq-	uence		09/496		acid residue	O-Glutamine R=Arginine, S=Serine,
ence			914	ng to first	of peptide	T-Threenine V=Valine W=ITYDtophan,
]		1	amino acid		V=Tyrosine, X=Unknown, *=Stop codon,
	ļ	i	1 1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	l	1 1	peptide	į	nucleotide insertion
		ļ		sequence		KLCGASSGIIDLLPSPSAATNWTAGLLVDSSE
	 					MIFKFDGRQGAKIPDGIVPKNLTDQFTITMW
	1	ļ	1		ì	MKHGPSPGVRAEKETILCYSDKTEMNRHHY
	1	1	1			ALYVHNCRLVFLLRKDFDQADTFRPAEFHW
	١.	}	1	1	1	ALYVHNCKLYFLLKKDFDQADITKI ADITI
	1	ł	1	1	1	KLDQQALAKVDGQPGKSITRQLQEMPVTIQG
	1	1		1		ISLKPS
	1	 	2256	1	396	FRGTPVSGLTNRDTLAVIRHFREPIRLKTVKP
196	1546	A	2230	1 '		GKVINKDLRHYLSLQFQKGSIDHKLQQVIRD
	1	1	1		1 .	AT AT AT DITIPOTTE APRINCEVPGVDYNF1SVEQF
		1	1		\	KALEESGALLESGTYDGNFYGTPKPPAEPSPF
	1	1	ł	l		ODDDA
	1					OF ATEICVE AT LEGYEVETEFLDPFORVIQPEE
197	1547	A	2259	43	594	TIT VENDI COSDNIPTRI MFAISFLTPLAVICY
	1			1	1	I WIIDDTOKTFIKFAFLAVSLALALNUVCINI
	1	1	1	i		KLIVGRPRPDFFYRCFPDGVMNSEMHCTGDP
	1	1	l	(DLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKI
	.	1	ì	1	Ĭ	HCFTESGRGKSWRLCAAILPL
	1	1	1	1		HCFTESGRGKS WRICEARINE
100	1548	A	2275	3	404	TCTTVVVIPRMLVDFLSESKTISLPECATQMF
198	1546	1	1275	1		FLGFASNNCFIMAAMSYDRYTAIHNPLQYHT
	1	1	l l			LMTRKICLQMMMASWMVGFLFSLCIIVTVFN
	1 .	1	1		ł	LSLCDLNTIQHYFCDISPVVSLACNYTFYHEN
	1	1	i	1	•	AIFVLSA
				 	375	LTQMFFIHALSAIESTILLAMAFDRYVAICHP
199	1549	Α	2315	1	373	DULANT ANTOTACIGIVAVVRGSLFFFFLFLI
	- {			{		LKBI AECHSNVI SHSYCVHQDVMKLATADIA
	1	į .	1	1		DARROYCE TAILLYMGXDRMFISLSYFLIL
	1	1			409	DDVDDOORKMSFFFKTELGEKLVIKFLFEID
200	1550	A	2334	2	409	COUDING DEDUCT KKKAPFINKKLKAHQIYV
	1	- {			l	THE VOLVEIO ASMOVOAYNGGNANPRPANN
٠ ،	1	1				EEEDEEDEYDYDYESLSDDNILEDRPENKSC
}		- 1	- 1			DQLQFEYKEEM
1	l l		ł			ISWEAQIAEIIQWVSDEKDARGYLQALASKM
201	1551	A	2350	3	512	TEELEALRSSSLGSRTLDPLWKVRRSQKLDM
201	1,331	1	1	}	}	SARLELQSALEAEIRAKQLVQEELRKVKDAN
1	l l	ł				SARLELQSALEAEIRARQLVQEELARVINDA
l	l	- }	1		i	LTLESKLKDSEAKNRELLEEMEILKKKMEER
1		}		1		FRADTGKLMLCDSALFEYKYFSNECFYFLFI
1 .		1		1		LIVTLEAPTEFQIQY
				- 	1003	DESVSSOEL SPGEPLTSPPWAPLGAPERPEHL
202	1552	A	2351	1	1003	ADVITED AGGATRDSAASDILLUUIVLIHSL
		l		1 '		I DTEKET OF LHOYFVRAGGMEGPEGLGRKY
1	}	1	1	1	1	CLAMITUTE DTYOGLIOEEGAGIUNDED
1	1			1		I IMPOESI VOGI REDTIRLHOLVETVELKIR
Į.	1.	- 1		1		ENQPPSKQVKPLFRHFRRIDSCLQTRVAFRO
		1	1	- (1	DEIFCRVYMPDHSYVTIRSRLSASVQDILGS
		- {	- 1	1		TEKLQYSEEPAGREDSLILVAVSSSGEKVLL
1	1	- [1	1		PTEDCVFTALGINSHLFACTRDSYEALVPLP
ı		l		1		PIEDCALI APGINOUPLACIANO I PURA LA CAMBILIA
1	1	l	l			EIQVSPGDTEIHRVEPEDVANHLTAFHWELI
1.		- 1			1	CVHELEFVDYVFHGE
		-+-	2361	1 2	403	NNLNCAEPLFEQNNSLNVNFNTQKKTVWL
203	1553	A	2301	1 "	1	CADDACCIDI MI ONEARILLNEEDWINATA AT
1		- 1	1	1		SUCD CATTERVAR AVKNTRK VAVSLSVHIKE
1	1	ì	- 1	l	1	LKHGASLDNFHFIGGSLGAHISGFVGKIFHG
1	j		j	1		I CRITCL DP
1	1	1				SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSP
204	1554	A	2390	280	476	AGSRLGAMRRCAREMDATPMPPAPSCPSE
204	1334	1				
1	ł	- {		(T CONTROL OF VACCES GPWTV
		 	2400	543	745	AAVALRDISWQQPYPMDFYAGSSLGPWTV
	1555	- A	. 2700	1 - 15		HGQDRRPHAPGRPARGKVQEGSARPPSAV
205	1 .555	ı	1		1	11005:02:

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	I D-A mortic Acid F=Glutamic Acid
NO: of	NO: of	hod	ID NO:	beginning	location	E=Phenylalanine G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine K=Lysine L=Leucine,
eotide	seq-]	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid	of peptide	T-Threonine V=Valine, W=Tryptophan,
				residue of	sequence	V=Tyrosine X=I Inknown, *=Stop codon,
					Scquence	/=possible nucleotide deletion, \=possible
	1		}	peptide sequence	1	nucleotide insertion
			2106	122	485	DI SPOSPEDHPOGHRRLLPKRPVRGSLMPGH
206	1556	Α	2406	122	100	TULIDCDV9CTTNDTPDOTWVSVGSLRMG1GG
	1	ļ	}		1.	MGANASTSPRCWDLSSGNKKWIIQVPILASIV
	1	ļ	İ	1	1	REPORT I ATGVGGMCACVPRNOPLTGT
			0.400	289	418	LWILYRHKQQVQHNHSNRLSCRPSQEDRAT
207	1557	Ā	2409	207	1 110	LITINAT DEENTLS
		<u> </u>	0412	64	492	VQGTGXXFIAFTEAMTHFPASPVWAGMFFL
208	1558	A	2413	04	1752	I M DIT OF COMPORTMACHT PHILITER VPKEMEL I
	1	l		ì	1	GCCCVFAFLVGLLFVORSGNYFVTMFDDYSA
		1	1	1		TLPLTLIVILENIAVAWIYGTKKFMQELTEML
l		1	Į.	l .		GFRPYRFYFYMWKFVSP
	1	 	2417	3	877	EKERLLDEWFTLDEVPKGKLHLRLEWLTLMP
209	1559	Α	2417			NASNLDKVLTDIKADKDQANDGLSSALLILY
]	ļ	1	1	1	ł	LDSARNLPIRYKTNEPVWEENFTFFIHNPKRQ
	1	1	1			DLEVEVRDEQHQCPLGNLKVPLSQLLTSEDM
1	1			i		TVSQRFQLGNSGPNSTIKMKIALRVLHLEKRE
	ļ	1		l	i	RPPDHQHSAQVKRPSVSKEGRKTSIKSHMSG
1		l	1	!		SPGPGGSNTAPSTPVIGGSDKPGMEEKAQPPE
1		1.	1			AGPQGLHDLGRSSSSLLASPGHISVKEPTPSIA
-	1.					SDISLPIATQELRQRLRQLENGTTLGQSPLGQI
1		1.	1		•	QLTIP
	1500	HA-	2422	35	456	REFAASDLEPFTPTDQPISPEAITQPSCIKRQRA
210	1560	I A	2422	1 3 3		AGNPGSLAATIDHKPCSAPLEPKIQASRNQRW
1.	1	1	1	{	1	GAVRAAESLTDIAEPASPQVHETPIDASQTQK
1		1	1	ļ		VEPASKSRFTPELQAKVSHSRERALSTMDATP
		ŀ				HHAQPQRGEG
	1561	A	2431	1	764	RRYSQKLIQHTACQLLRTYPAATRIDSSNPNP
211	1201	^	2431	1		LMFWLHGIQLVALNYQTDDLPLHLNAAMFE
)	ļ	}		{	ANGGCGYVLKPPVLWDKNCPMYQKFSPLER
		1	1			DLDSMDPAVYSLTIVSGQNVCPSNSMGSPCIE DLDSMDPAVYSLTIVSGQNVCPSNSMGSPCIE
1		1				VDVLGMPLDSCHFRTKPIHRNTLNPMWNEQF
	i	- }	-	1		LFHVHFEDLVFLRFAVVENNSSAVTAQRIIPL
	1 .	- {		ł	}	KALKRGYRHLQLRNLHNEVLEISSLFINSRRM KALKRGYRHLQLRNLHNEVLEISSLFINSRRM
1		1		l l	i	EENSSGNTMSASSMFNTEERKCLQTHRVTVH
1	1	1		}		GRGTTGHLGCPINDDPSLTLTVSWVMEDKPI
212	1562	A	2436	1	411	GIRGTTGHLGCPINDDPSLTLTVSWVNLLDIAT YIGNGTKKEDDSLTIFAVAKRDHVSDTCGAC
212	1302	1 "	1	1	1	YIGNGTKKEDDSLTIFAVAKRDHVSDTCSMC TDLDHNLDKGYLTVLGEQATPTNRLGALPKG
1	1	ļ	1	1	1	RANRTRDLELTYLAERIVRLTWIPGDANNRPI
1	1			1	1	RANKTRDLELI YLAEKIVKLI WIFGDAINIGI
		1		}		TDYDCQIEEHQ
213	1563	A	2445	1	1294	MSSIGCLWVSRSSQIDGLTAEKSGPEKPHGT WLMPELHPKEQILELLVLEQFLSILPEELQIWV
213	1,000	'`	15	1	1	QQHNPESGEESVTLLEDLEREFDDPGQQVPAS
	1	1	1	1		PQGPAVPWKDLTCLRASQESTDIHLQPLKTQ
1	1	1				PQGPAVPWKDL1CLKASQESTDIREQPERIOR
	1			Į.		LKSWKPCLSPKSDCENSETATKEGISEEKSQG LKSWKPCLSPKSDCENSETATKEGISEEKSQG
İ	1	1	1	l		LPQEPSFRGISEHESNLVWKQGSATGEKLRSP LPQEPSFRGISEHESNLVWKQGSATGEKLRSP
1		1		ĺ		SQGGSFSQVIFTNKSLGKRDLYDEAERCLILT SQGGSFSQVIFTNKSLGKRDLYDEAERCLILT
i	1	- 1		1	1	TDSIMCQKVPPEERPYRCDVCGHSFKQHSSLT
		ì		1		QHQRIHTGEKPYKCNQCGKAFSLRSYLIIHQR IHSGEKAYECSECGKAFNQSSALIRHRKIHTG
		j	l	1		EKACKCNECGKAFSQSSYLIHQRIHTGEKPY
1	{	1	ı		1	EKACKUNECGKAF3Q531LIIIQKIIII GERTVECNE
1	1	1	- 1	l l		ECNECGKTFSQSSKLIRHQRIHTGERPYECNE ECNECGKTFSQSSKLIRHQRIHTGERPYECNE
-	- 1	1	1	1	1	CGKAFRQSSELITHQRIHSGEKPYECSECGKA
		- 1		i		FSLSSNLIRHQRIHSG
<u></u>			2461	1	615	GIPGSTISSSRNIFLEDDLAWQSLIHPDSSNTPL
214	1564	A	2401	1.		STDI VSVOEDAGKSPARNRSASITNUSLUKSU
		1	}	1		CDLAUPGVETSVSPOANRTYVRIETIEDBRKIL
ł		1		1	1	LDSVQLKDLWKKICHHSSGMEFQDHRYWLR
}	1	- 1	1	1		THPNCIVGKELVNWLIRNGHIATRAQAIAIGQ
ı		- 1 -				

000 V	SEQ ID	Met	TSEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of nucl-	peptide	nou .	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
eq-	uence	ì	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
201100	l	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	İ		residue of	sequence	/=possible nucleotide deletion, \=possible
	1		1	peptide		nucleotide insertion
		l	1	sequence		AMVDGRWLDCVSHHDQLFRDEYALYRPLQV
				1		I ESVYCOLECSKLIL
			<u> </u>	<u> </u>	0022	GPGVRSSQDGMADVFVHLRTAWPRCSFISGQ
215	1565	Α	2464	3	2932	UCPGRHGRRVCSSODSMADVFVHLRTAWPT
	1		1			CSLISGOHGPGESVSYEDDDIPAPASLLHVNA
	1		1	ĺ	1	A ADAI TNDTAPVI CTAPNNTAOKEK VPSGMK
						OPPAGURISSRTPDLTCAVSTHSTVPGVRISSC
	1	1	1	1	}	TPDI TCAVSIHSTVPSVCISSCIPDLICAVSIH
	1	i	1	1		STYPGYRISSCTPDLTCAYSTHSTYPGYKISSK
	1	į.	ł	ì		TPDLTCAVSIHATVPGVRISSCTPDLTCAVSIH
	ł	1	1			ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
	Į.	1	.			TPDLTCAVSIHSTVPGVRISSCTPDLTCAVSIH
		1		L		ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
	ļ	-	1	1		TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
	1	1		1	1	ATVPGVRISSCTPDLTCAVSIHATVPGVRISSC TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
			1	1	}	ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
	}	1	1	1	1	TPDLTCAVSIHATVPGVRISSCTPDLTCAVSTI
	1	1	l			STVPGVRISSRTPDLTCAVSIHATVPGVHISSC
	1	1	i i	1	1	TPDLTCAVSTHSTVPGVRISSRTPDLTCAVSIE
	1	1	- (1	1 ***	STYPGYCISSRTPDLTCAVSIHSTVPSVHISSCI
		1		1	İ	DDI TCAVSIHSTVPGVRISSRTPDLICAVSINS
	1	1		ļ		TVPGVHISSCTTDLTCAVSIHATVPGVHISSCT
		1		1		PDI TCAVSTHTTVPGVRISSRTPDLTCAVSIH
Į.			1			TVPGVRISSCTPDLTCAVSTHSTVPGVRISSRI
l]	1	ł		. }	PDI TCAVSTHLTVPGVRISSRTPDLTCAVSIH
	1 .	Į.	1	İ		TVPGVHISSCTPDLTCAVSIHATVPGVRISSKI
1		1		ı		PDITCAVSIHATVPGVHISSCTPDLTCAVSTH
		- 1		1	. (TVPGVRISSRTPDLTCAVSIHSTVPGVHISSCI
l		ì		•		PDLTCAVSTHSTVPGVHISSCTPDLTCAVSTH
ì		.				STVPGVHISSRTPDLTCAVSIHATVPSVHISSC
1	1	1	1			TPDLTCAVSIHSTVPGLLTSVSQTSTG
216	1566	A	2477	1	414	FRTKSYRKGSYRCIVSEWIAEQGNWQEIQEK
210	1500	1.]		AVEVATVVIQPTVLRAAVPKNVSVAEGKELI LTCNITTDRADDVRPEVTWSFSRMPDSTLPG
ł	1	- [-		1	RVLARLDRDFLVHSSPHVALSHVDARSYHLI
	1	ı	1	}		RVLARLDRDFLVHSSFHVALSHVDFBGTT
				l		VRDVSKENSGYYY CRTLCEGPQRFEEYEYLGYKAGLYEAIADHY
217	1567	A	2480	2	460	MQVLVCQHECVRELATRPGRLSPIENFLPLH
1						DYLQFAYYRVGEYVKALECAKAYLLCHPDI
1		- 1			į .	EDVLDNVDYYESLLDDSIDPASIEAREDLTM
1		1		1		VEDLIKI ESELIKSAAEGLGXSYTEPNYW
					202	AESSPHESPAPOFPECGFYGLYDKILLFKHDP
218	1568	A	2483	140	383	SANLLQLVRSSGDIQEGDLVEVVLSASATFE
		- [I OTRPHALTVHSYRAP
					120	CCDIVILAGAAALASGSOGDREPVYRDCVL
219	1569	A	2489	3	428	CEEONCSGGALNHFRSRQPIYMSLAGWICK
		1		1	1	DOWNECHWATTAGLYLOEGHKYPOFHGKW.
	.	-	1	1	1	FSRFLFFOEPASAVASFLNGLASLVMLCRYR
1	- 1	- (LYDAGGPMYHTCVAFAWVS
			1		1297	MOGEAVRECTONOCVSLHPOEVDSVAMAP
220	1570	A	2498	1	1431	A DK IDRI VOATPAFMAVTLVFSLVTLFV VDF
	1	ſ	- 1			LITUTECO FAEMRELIOTEKGHMENSSAWVVEI
1	1		1			LAT K CRYDNYNSOLOVLGDHLGNINADIQM
1	- 1	1)	l	POVI KDATTI SLOTOMLRSSLEGTNAEIQKI
1	- 1		1			PEDITERADAL TEOTI NELKSSLENI SIELHV
1				1	\	CDCI ENANSEIOMLNASLETANTQAQLANS
	1		1	1	ł	I KNANAFIYVI RGHLDSVNDLKI UNQVLKI
	l l	- 1	- 1		1	LEGANAEIQGLKENLQNTNALNSQTQAFIKS
i	- 1	- 1	1	l l	- 1	LEGANALIQUERENLON INALITOOT GIT III

			1000	D . 15	Deading 1 2	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	İ	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ł	914	correspondi ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		ļ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	•		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	Sequence	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		ļ	 	sequence		FDNTSAEIQFLRGHLERAGDEIHVLKRDLKM
						VTAQTQKANGRLDQTDTQIQVFKSEMENVN
		ļ				TLNAOIOVLNGHMKNASREIQTLKQGMKNA
		1 .	1			SALTSOTOMILDSNLQKASAEIQRLRGDLENT
						KALTMEIQQEQSRLKTLHVVITSQEQLQRTQ
221	1571	A	2501	3	500	RVRLNNDGLSPLMMAAKTGKIGIFQHIIRREV
221	13/1	^	2501	1 -	500	TDEDTRHLSRKFKDWAYGPVYSSLYDLSSLD
	1	ļ		1		TCGEEASVLEILVYNSKIENRHEMLAVEPINE
	· ·	1		•		LLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
	•	1		1		AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFT
						GVLFFFTN
222	1572	A	2508	3	395	DAHCQRKLAMQEFMEINERLTELHTQKQKL
	1.					ARHVRDKEEEVDLVMQKVESLRQELRRTER
1	<u> </u>	}	1			AKKELEVHTEALAAEASKDRKLREQSEHYSK
		Ì		1	1	QLENELEGLKQKQISYSPGVCSIEHQQEITKL
						KTDLEKKS
223	1573	A	2544	2	412	NDPAIISNFSAAVVHTIVNETLESMTSLEVTK
		1	1	j		MVDERTDYLTKSLKEKTPPFSHCDQAVLQCS
1		1		}	ł	EASSNKDMFADRLSKSIIKHSIDKSKSVIPNID
	1.91			· ·		KNAVYKESLPVSGEESQLTPEKSPKFPDSQNQ
		L		l		LTHCSLSAA
224	1574	A	2552	401	1	GASLCFISTAFTVLTFLIDSCRFSYPERPHFLSM
				Ì	Į.	CYNIYSIAYIVRLTVGRERISCDFEEAAEPVLI
	Ì	1	ì			QEGLKNTGCAIIFLLMYFFGMASSIWWVILTL TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA
	1	1	ł	1 .		VK
		ــــــــــــــــــــــــــــــــــــــ	-	504	1	MSARKERREKGEEEGEGEKDGDEDEKEEEKE
225	1575	Ā	2563	724	11	GLGEEEKEAGKKKKQEEKEKEKGAVYSR
l	1	1		ł	•	VARICKNDMGGSQRVLEKHWTSFLKARLNC
		1	-	1		SVPGDSFFYFDVLQSITDIIQINGIPTVVGVFTT
i		ĺ	1	1		QLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTP
]				1	1	DSVWTAVPEDKVPKPRPGCCAKHGLAEAYK
1		1		1		TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFT
1	1	1				KTRVRYRLTAISVDHSAGPYH
226	1576	A	2571	449	3	EGVLFVYGNYVGDVMNFEMAAEMAQEVAIP
220	1370	1	1 2011	1	-	TRTVLTTDDISSSPIEDRDGRRGVAGNFFIFKV
1	1	1	1			AGAACDRGMSLEACEAVTRKANRRTYTMG
	İ	Ţ			1	VALEPCSLPQTRRHNFEIGAEEMEIGMGIHGE
		İ	j			RGVIREKMMPADAIVDHIMDRIFS
227	1577	A	2575	3	.1197	VLSDLCLFYYRDEKEEGILGSILLPSFQIALLTS
l	1	1				EDHINRKYAFKAAHPNMRTYYFCTDTGKEM
1		1		l		ELWMKAMLDAALVQTEPVKRVDKITSENAP
1	1				1	TKETNNIPNHRVLIKPEIQNNQKNKEMSKIEE
1	i			ł		KKALEAEKYGFQKDGQDRPLTKINSVKLNSL
l				1	1	PSEYESGSACPAQTVHYRPINLSSSENKIVNVS
	1	1				LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ
	j		j	1		LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS
	1		1	1		HRAQIMARYPEGYRTLPRNSKTRPESICSVTP
	1.					STHDKTLGPGAEEKRRSMRDDTMWQLYEW
	1		}	1		QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT
1	1	1	1	ĺ		MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI
1	1	1			<u></u>	QRGDVTIDRRHRAHHPKVK
				3	330	LPFLGLGSVLPQGMVMASPEMNPTICSVFEA
228	1578	A	2583	1 2		
228	1578	A	2583			HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE
228	1578	A	2583			KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
228	1578	A	2583			KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD PTMGIKPHLWWVAA
228	1578	A	2583	1	448	KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD PTMGIKPHLWWVAA DDKNAOGIKRHVKPTSGNAFTICKYPCGKSR
					448	KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD PTMGIKPHLWWVAA

			-	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met ·	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
(O: of	NO: of	hod	1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in USSN	location	corresponding	I=Isolencine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence			ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			İ	residue of	sequence	V=Turnsine X=Unknown, *=Stop codon,
			l		Scquence	/=possible nucleotide deletion, \=possible
			1	peptide	ļ	nucleotide insertion
			<u> </u>	sequence		GGTCLAGNLCTCPYGFVGPRCETMVCNRHC
			j			ENGGQCLTPDICQCKPGWYGPTCSTA
			<u> </u>		100	AVTFSVVFAYVADITQEHERSMAYGLVCMFI
230	1580	Ā	2593	2	138	LYLLYLLRNAFFLR
						SGPYTDFTPWPTEEQKLLEQALKTYPVNPPER
231	1581	A	2595	185	2	WEKIAEAVPGRTKKACIKRYKVADLRISK
		1	, ·	Í		STVTGQPRRLLDTAGHQQPFLELKIRANEPGA
232	1582	A	2596	1	391	GRARRATPTCEPATPLCCRRDHYVNFQELGV
		1	1	1		GRARRIPICEPATPLCCRRDHI VII QLEGV
	l	1	 	Į.	1	RDWILLPEGYQLNYCSGQCPTHLAGSPGIAA
	1	}	1			FHSAVFSLLKANNPWPGRTSWCVPTARRPLS
		1				LLYL
	1602	A	2601	184	403	LLFSDEIIMAAPLRIADVTSGLIGGEDGRVYV
233	1583	Α.	2001	101		YNGKETTLGDMTGKCKSWITPCPEEKVNVL
	1	1	1	l	ì	NSIPYWERIT
			- 2014	178	335	PLTLCLPENNKPPQADAVPDKELTLPVDSTT
234	1584	A	2614	1/0	333	DGSKSSDDOKIISYLWEKTQ
				 	896	DVI FVYGTGVASTRHEMGTLDKHKELEDL\
235	1585	A	2616	2	870	AKFLNVEAAMVFGMGFATNSMNIPALVGKO
		1				CLILRDEVNHTSLYLGARLLGATIGIFKHNYA
		1		1		QSLEKLLRDAVIYGQPRTRRAWKKILILVEG
		1	1.	1	1	YSMEGSIVHLPQIIALKKKYKAYLYIDEAHSI
	1	1	j		Į	GAVGPTGRGVTEFFGLDPHEVDVLMGTFTK
	1	1	1			FGASGGYIAGRKARILSPPACLVPNTGSHSLI
	1	1		-		FGASGGYIAGKRAKILSFFACEVITTOOTISE
	1	1	-			RLTRDLQMNEAMVALVTDRLQGWNSGEGN
		i				WDRADKFGDLVDYLRVHSHSAVYASSMSPI
		1		· ·		AEQIIRSLKLIMGLDGTTQ
236	1586	A	2621	1	392	NTSSFPAQPSSPARPSLPHLSQHPSNPLLPLAS
230	1380	1				ADHPQCGRFLPLHEPEPLCPSPSLSYPTLVSS
		1	ļ	1	}	WSSPFSSHHGCPPGLYPFPTSPKTIQPPGLAQ
	1	ĺ	1	1	ì	KMLCIPPGRQQLRGAQSMPGHGALSPLLLPF
	1				1	A
	1		2628	398	1 .	DLVCKISGFGRGPRDRSEAVYTTMSGRSPAL
237	1587	Α	2020	350	1.	WAAPETLQFGHFSSASDVWSFGIIMWEVMA
		ł	1		ĺ	GERPYWDMSGODVIKAVEDGFRLPPPRNCP
	1	1 .	1	i		LMHRLMLDCWQKDPGERPRFSQIHSILSKM
		1	1	1	l	OUDEDDWA
	1				1104	WSPCSI TCGVGLOTRDVFCSHLLSREMNET
238	1588	A	2631	1	1104	ILADELCROPKPSTVQACNRFNCPPAWYPA
	1	1	1	ì		WQPCSRTCGGGVQKREVLCKQRMADGSFL
	1	l	1	1		MÓLCZKICOGOAĆWEATCWÓWITHOODE
		1	1	1	1	LPETFCSASKPACQQACKKDDCPSEWLLSD
	1	1		1	- [TECSTSCGEGTQTRSAICRKMLKTGLSTVV
	1		1		1	TLCPPLPFSSSIRPCMLATCARPGRPSTKHSP
	1	į	- 1	ł	- 1	AAARKVYIQTRRQRKLHFVGGGFAYLLPKT
		1				VVLRCPARRVRKPLITWEKDGQHLISSTHV
		1)	}	VAPFGYLKIHRLKPSDAGVYTCSAGPAREH
Ì	•	- (. [1		VIKLIGGNRKLVARPLSPRSEEEVLAGRKGC
1		ļ	1	1	1	KEALOTHKHQNGIFSNGSKAEKRGLAANPO
Ì	1	1	1		1	RVDDLVSRLLEOGAPCSSSKKKN
L					678	MK PONTI I DEHGHVHITDFNIAAMLPREI'Q
239	1589	A	2636	. 1	0/6	TMAGTKPVMAPEMFSSRKGAGYSFAVDW
		1		- [,	SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFE
ĺ	ĺ	-		1		TVVTYPSAWSQEMVSLLKKLLEPNPDQRPS
	1	l		J		LSDVQNFPYMNDINWDAVFQKRLIPGFIPNI
1	1	{		[TSDAGULL IMINDIAM DVALGER CILILIA
1		1	1	- (l	GRLNCDPTFELEEMILESKPLHKKKKRLAKI
	ł	1		i	1	EKDMRKCDSSQTCLLQEHLDSVQKEFIINR
ł		- 1			1	KVNRDCI
	1			1		TOUR TOUR PROPERTY OF THE PROP
2.2	1.000	-+-	2620	380	3	ELLDPI IPMKIKCIELLI AALI 333 IDQI KA
240	1590	A	2639	389	3	ELLDPTTPMRTKCIELLYAALTSSSTDQPKA LWQNFAREIEEHVFTLYSKNIKKYKTCIRSK ANLKNPRNSHLQQNLLSGTTSPREFAEMTV

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide .	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uciicc	ŀ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T-Threonine, V=Valine, W-Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	l		peptide	Dodgoone	/=possible nucleotide deletion, \=possible
	{	ł		sequence		nucleotide insertion
	<u> </u>	├	 	scquence		EMANKELKQLRASYTESCIQEHYLPQVIDGTL
		l				Y
		<u> </u>	1		3	IRLTILRCVFMRLATICVLVFTLGSKITSCDDD
241	1591	A	2640	392	3	TCDLCGYNQKLYPCWETQVGQEMYKLMIFD
	1			ĺ		FIILAVILFVDFPRKLLVTYCSSCKLIQCWGQ
		i	[QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM
	Ì	1	i	ļ		Y
		L			ļ <u>. </u>	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR
242	1592	Α	2642	405	1	MVLMAGAKPGMLLLCFMCCTTLLSMWLSNT
		ì			1	STIAMVMPIVEAVLQELVSAEDEQLVAGNSN
	1	\				TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK
	(1				
	}	Į	i			SPLMISQACI
243	1593	A	2646	-412	2	CLAMIKGIQSSGKIIYFSSLFPYVVLICFLIRAF LLNGSIDGIRHMFTPKLEIMLEPKVWREAATQ
			1			LENGSIDGIRHMF1PKLEIMLEFKVWREAKIQ
			1		1	VFFALGLGFGGVIAFSSYNKRDNNCHFDAVL
		ł	1		1	VSFINFFTSVLATLVVFAVLGFKANVINEKCIT
	1					QNSETV
244	1594	A	2650	1	1271	MTTTLIGLLKTARLLRLVRVARKLDRYSEYG
			T .			AAVLMLLMCIFALIAHWLACIWYAIGNVERP
4 .		1		1	1	YLTDKIGWLDSLGQQIGKRYNDSDSSSGPSIK
-				1		DKYVTALYFTFSSLTSVGFGNVSPNTNSEKIF
		1				SICVMLIGSLMYASIFGNVSAIIQRLYSGTARY
	1	([HMQMLRVKEFIRFHQIPNPLRQRLEEYFQHA
	1	1	1	1	i	WTYTNGIDMNMVTNGTCSSCTSDDGHFILVS
	ì	1	Ì	1 .		NHHQGGLIYSWNDAASMQRPFNHIKSSLLGS
	ł	1	ĺ	1		TSDSNLNKYSTINKIPQLTLNPSEVKTEKKNSS
	1	1	Ì		l	PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA
		1	1	1		DVLPEYKLQAPRINKFTILHYSPFKAVWDWLI
	i	i	1	í		LLLVIYTAIFTPYSAAFLLNDREEQKRRECGY
		1		ļ	ļ	SCSPLNVVDLIVDIMFIIDILINFRTTYVNQNEE
	1					VVSDPASV
046	1595	A	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFFLDNVIMW
245	1393	\ ^	2030		-	WESLLLLTAYFCYVVFMKFNVQVEKWVKQ
i					Ì	MINRNKVVKVTAPEAOAKPSAARDKDEPTLP
1	1	ı		1	[AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD
						PHV
			000	200	506	VI.VI.OMNYYOMLIIYYVLFFKVNEFLAFEGPI
246	1596	Α	2660	200	1 200	I I DMRTKHLIKTNOLSOATALAKLCSDHPEIG
	\			1	1	IKGSFKQTYLVCLCTSSPNGKLIEEVSMFSFIS
l		1	1.	1	1	NYFLS
L		4		 	+262	DAWVKNDIIFNQTERKQKISENLKHLASVRV
247	1597	Α	2678	3	267	VQKNLVFVVGLSQRLADPEVSPLVFFVILIFF
						VSLSYLEIIFDPAQLCDSSEHIIS
L	_L				1	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF
248	1598	A	2687	1	404	GAAIKSVKNPDKKSIENQVLDSLVPLLLYSQD
						GAAIKSVKNPDKKSIENQVLDSLVFLLL ISQD ENDAVAEESRQVLTICAQFLKWKLPREVYSK
1	1	1	1	1		ENDAVAEESKŲ VLIICAŲ LIKWALIKEVISK
1	-			ì	1	DPWHIKPTEAGTICRFFEKKCKGKINILEQTL
1	1	1		I		MYSKNPKL
249	1599	A	2692	1	440	FRRRRRERDCAAQGARRHCRHLAECKLV
~ " /	1	1 -		ı		SFPIGIYKVLRNVSGQIHLITLANNELKSLTSK
1			1	1		FMTTFSQLRELHLEGNFLHRLPSEVSALQHLK
Į.	1	l	1	1	Į.	AIDLSRNOFQDFPEQLTALPALETINLEENEIV
1	1			1		DVPVEKLAAMPALRSINL
	+		2602	450	21	I.L.PGSLGVPILHSOPWDPSPQCPHRAPSTPRRL
250	1600	Α	2693	459	41	PPLGALSQALTFLSRAAKNHSQDPGKGTKPFP
						AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF
1		1	1	1	}	NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG
1		1		1		ISSCPDLKLTKSSTP
1			1	1	1	1990LDFVF1V9911
	1601		2694	2	404	FVFDLKLRVPGFAALLIHGASSVPGPETVRLR

SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		l	1	amino acid	of peptide sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Ì	ì		residue of	sequence	/=possible nucleotide deletion, \=possible
	}	1	l l	peptide sequence		nucleotide insertion
				Sequence	 	OVPKKKAPDHSSGRKEELVTTHTVDKLETKK
		ì			1	DVGDVI CGLSGELLHSLLLPRRKTEKRALGSH
]	}		l	1	RKAGFPEHPVAPEPLSNSCQISKEGREQVLSEI
		ļ				GAGDCL
	1602	A	2697	421	1	POKSHSGAYQCFATRKAQTAQDFAIIALEDG
252	1602	l A	2057	1		TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPT
	1	1	}]		VTWALDDEPIVRDGSHRTNQYTMSDGTTISH
	1	1	}	l l		MNVTGPQIRDGGVYRCTARNLVGSAEYQARI
		}			1	NVRGPPSIRAMRNIT
253	1603	A	2698	65	401	ACCQWRRTLIPAKSTTVSCTISTPHHPFRGSYS FDDHITDSEALSRSSHVFTSHPRMLKRQPAIEL
233	1005	1	}	1		PLGGEYSSDVPRPLSTQLSSSLLGYFSTLMTG
		1		1.		AAFTNNIASSTIIL
	•	1		<u> </u>		GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ
254	1604	A	2699	438	301	RVRGPWEAGPGVGY
				<u> </u>		LQNREDSSEGIRKKLVEAEELEEKHREAQVS
255	1605	A	2700	1	842	A OUR EXPLIENCE PROPERTY FERTING THE PROPERTY OF THE PROPERTY
		1	i	1		DVPTI ENMMORHEEEAHEKGKILSEQKAMII
		1	Ì	1		AMOSKIRSI FORIVEL SEANKLAANSSLEI QK
		Ì		ł	į.	I NEW TODERNICH BUOKEAL ELONGER FROM THE PROPERTY OF THE PROPE
	1	1	1			DVI EEGI EKISHODHSDKNRLLELEIKLKEV
	1.			1		LEBEROKI FI KROLTELOLSLOEKESQLIALA
	1 .	1	1		1	A A D A AT ESOL ROAKTELEETT A EA E BEIQAL.
		1	1	į		VGLGSNIFRLLKASARMSVELALSILAHP
056	1606	A	2701	2	405	FVGGPGADPPVAVMWDPRAARMDLTAYAE
256	1000	1^	2701	-		LLKESGNQVLKNGNFSLAIRKYDEAIQILLQL
	1	ļ		1		YQWGVPPRDLAVLLCNKSNAFFSLGKWNEA
ļ			1	-	1	FVAAKECLQWDPTYVKGYYRAGYSLLRLHO
					<u> </u>	PYEAARMFFEGLR FVESASSRPPGCFSGDGRFWLVSEGSRRGWI
257	1607	A	2702	2	399	FVESASSRPOCESODOR WEVE SERVER FNPSFSFLDPRYSVGGDENIGTVTTLANILRE
	1 200.				j	NPSLKGFSVGTGKETSPNAFLNQAVAGGRA
		- 1	1			DLPVQARRLVDLMKNDTRIHFQEDWKIITLF
	l	1	- 1	ł		CCNIDI
					1097	CVGAROGEARDRIRRFFPKGDLEVLQAQVE
258	1608	A	2709	T 1	1097	ATDEFT I TVYSSEDGSEEFETIVLKALVKAC
		1			1	CODACAVI DEI RI AVAWNRVDIAOSELIKOI
1		١.	.			OWDSEHI FASLMDALLNDRPEFVKLLISHGE
1	1	1		1	1	I GUELTEMBLAGI YSAAPSNSLIKNLLDQAS
	-	- }	ł		ľ	CACTY ADAI KGGA AFLRPPDVGHVLRMLLU
1	l l	- 1	l			KMCAPRYPSGGAWDPHPGQGFGESMYLLS
1)	1		VATSPI SI DAGI GOAPWSDLLLWALLLINGA
1	1	-		1		OMANYEWEMGSNAVSSALGACLLLRVMA
1])		}	}	I EDDAFRA ARRKDLAFKFEGMGVDLFGECY
1	- 1	- 1		1	1	SSEVRAARLLLRRCPLWGDATCLQLAMQAI
1	1			}	1	ARAFFAQDGVQSLPTQKWWGDMARR
250	1609		2721	1	403	VYLGAGPGLFFSNEGAKEGEKANIPKLMLP
259	1009	1	1	}		GGFSQREMVTGERSPSPEEEEEEEEGFGER
1				1		SCRRGLFRVRLTRVGLAAPSKASRGQEGDA PKSPVREKSPKFRFPRVSLSPKARSGSGDQE
1	1		1		1	PKSPVKEKSPKFKFPK VSLSPAARSUSUDQE
		1				GGLRVRLP
260	1610	A	2728	1	477	LLGGDLRYHLQQNVHFTEGTVKLYICELAL
200	1010	'	1 -, -0			LEYLORYHIIHRDIKPDNILLDEHGHVHITDI
			-	1		IATVVKGAERASSMAGTKPYMAPEVFQVY
-	1	- 1	1	1	1	DRGPGYSYPVDWWSLGITAYELLRGWRPY
			1	{	1	HSVTPIDEILNMFKVERVHYSSTWCKGMVA
1.	- 1		1			LTITDFILVLYRYYRSPLVQIYEIEQHKIETW
261	1611	A	2730	3	547	EIYLQGCFKPLVSISPNDSLFEAVYTLIKNRI

						Amino acid sequence (A=Alanine O=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		١.	1	residue of	sequence	Y=1yrosine, X=Unknown,Stop codon,
		l	1	peptide		/=possible nucleotide deletion, \=possible
]	1		sequence		nucleotide insertion
						RLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLP
1	1	1		}	1	RPSFLYRTIQDLGIGTFRDLAVVLETAPILTAL
}						DIFVDRRVSALAVVNECGTHPQDERLGLGW
	i	l				GLGEPGSEERLFPAAITSR
0.00	1612	Ā	2733	3	431	GPEFPGSAKLVFLDLSYNNLTQLGAGAFRSA
262	1012	^	2/33	-		GRLVKLSLANNNLVGVHEDAFETLESLQVLE
	į .	1		ľ		LNDNNLRSLSVAALAALPALRSLRLDGNPWL
	Ì	1		j.		CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM
1	1	1	1	1		PSRRIST RACRRPASRV
		1	0736	2	343	PARISGUDPPVRKATKGGENCSFEDNKNWQF
263	1613	Α	2736	2	343	I WGLNGNFNFFKEPWGGRNNHAKGFRTTW
	1	l	1	1	Í	ARSSSQNNRTFQNNRNFLRLQRDSQKKGQFA.
l .	1			İ	1	RLISPLVNLPQSPGGLEFQYQAT
				<u> </u>	1015	RAMLKCLREGOPPPSYNWTRLDGPLPSGVRV
264	1614	Α	2738	2	245	DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH
1	1	1		1	1	DTVDVLDPPEDSGKQVDL
	1					AAGDAPLRSLEQANRTRFPFFSDVKGDHRLV
265	1615	A	2752	2	388	LAAVETTVLVLIFAVSLLGNVCALVLVARRR
		1		1		RRGATACLVLNLFCADLLFISAIPLVLAVRWT
1 .		1				EAWLLGPVACHLLFYVMTLSGSVTILTLAAV
1	1	1		1	1	
	1	1	ì			SLER
266	1616	A	2755	192	1,	AFREVGGYWGLLCEHLYAIPSKTSEGNWTAK
200	1010	1 **			1	LQGYLPLQDAFHIFQDPLTGDLPWPELILGLP
İ	1	1	l l	1		V
000	1617	A	2760	434	714	ASRLEKQNSTPESDYDNTPNDMEPDGMG:YM
267	1017	1	2,00	1		HRTSVPGEGLPRARDLAGLGQQKQFTTHTPF
				1		LYFQTHKGLKDSSIRSEVTCLGISQCWRKGFF
	1,510	A	2762	1	405	IACTFCGQDEWSPERSTRCFRRSRFLAWGEP
268	1618	Α.	2/02	1.		AVLLLLLLSLALGLVLAALGLFVHHRDSPL
	İ		1	1		VOASCOPI ACEGI VCI GLVCLSVLLFPGQPSP
	ì		1	ł	{	ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE
		1	i	1	ļ	I DI SWAE
		 -	2772	13	243	TRPAEKIQYLVLFFVMSHPSQAYDKLSLSDHL
269	1619	A	2/12	3	243	LIAVLNLLRREVSEHGRHLQQYFNLFVMYAN
	1	- 1		1	j	1 CENT SESEECEDVSY
L					486	FI OSOOACTHTKETEOLRSOLOTLKQQHQQA
270	1620	A	2789	1	400	VEOLAR A FETHSSL SOELOARLOTVIKEKEEL
		ì		1	ĺ	I OT STEP CKYL ONKOAETCOLEEKLEIANEDR
1		1	1	1		KHALERFEQEAVAVDSNLRVRELQRKVDGIQ
		ì		1		KAYDELRLQSEAFKKHSLDLLSKERELNGKL
	1	-		1		RHLSP
					1.0	KEKRVTVQLPTESIQKNQEDKLKMVPRKQRE
271	1621	A	2795	1	568	FSGSDRGKLPGSEEKNQGPSMIGRKEERLITE
1	1	1	1	1		RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN
1	1	- 1		·		FQQTQIQTAESKAEHKKLPQPYNSLQEEKCLE
	}	- 1	}	1		FUUTUUTAESKAETIKKLI UT I HOLUDEKUDE
1	1	- {	1	1		VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE
	1]	- 1			SQRDDGKGALNIVEFLRKREELHQILSTVKQP
272	1622	- A	2797	8	523	KCMQGKYAGAMESEPCVCTEADFDCDYGYE
212	1022	^	1			RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST
	1	1	1	ı	1	GYRKVVSNNCTDGVREQYTAKPQKCPGKAP
1		1	1	1	1	P.G. RIVTADGKI TAEOGHNVTLMVQLEEGD
1	1	1			1	VORTLIOVDFGDGIAVSYVNLSSMEDGIXHV
- 1		1		1	1	YONXGIXRXTVOVDNSLGS
				- 72	395	HPSRSNVGPROLTVWNTSNLSHDNRRKYIFS
273	1623	A	2801	72	333	DEEGONOLGIRIHODIPLPPRRRELPALRTING
		Ì	1	ŀ	1	KADSLNVSRNSVMQELSELEKQIQVIRQELQL
			} .	1		AVSRKTELEEYH
	1					
					220	II WI VEETGTWVYPVFAKISLLGLAALFSLRE
274	1624	- A	2805	168	320	ILWLYFETGTWYYPVFAKLSLLGLAALFSLRE IFIARNGVVGETLTHCKRV

	1		1 000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	1)	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	-	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ	ł		peptide		/=possible nucleotide deletion, \=possible
		ļ	,	sequence	}	nucleotide insertion
275	1625	A	2812	208	321	GSLATCQLSEPLLWFILRVLDTSDALKAFHD
2						MGKIIFQ
276	1626	A	2813	41 .	266	AGRSLHGAGDRAWVGISPTDWSPKVVELCK
2.0		l	1			KYQQQTVVAIDLAGDETIPGSSLLPGHVQAY
						QVGPVRRNGEAGPG
277	1627	A	2817	3	410	VLQERLDNFQRKCIQLASSTEGKVDKLLMRN
		ļ		1		LFISYLHTPKHKQHEVLQAMGSILGITGEEME PLFQEEHGTATRWMTGWLEGGSKSVPKTPL
•		}			I	GLNQQPALNGSFSELFVKFLKTESLSSTLPTX
			Ì			LPPHNSPGKIK
					1.5	GLSGPSCSCPHSPLPTIISRAQLETALKWRNYE
278	1628	A	2821	238	457	VKLRLLLHLEELQMEHDIRHYDLESVPMTWD
		1	į	1	1	PVDQNPRLV
		ــــــــــــــــــــــــــــــــــــــ		240	1	PLIPANLPAHSNPLQPLPSLPHPFLPATHKFPT
279	1629	A	2822	342	1	TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS
			İ	ì		CRLPSRPSVSRELPPQSGPASSVPLAPTPLPDS
	}	İ			į	VPSORHPTXPPPAS
000	1630	HA-	2825	307	77	PSMVWSYHWGVKOKRLALCVFSFEEGGRRK
280	1030	A	2023	1 307	ļ ''	CGQYWPLEKDSRIRFGFLTVTNLTGAVGEPG
	1		l .			VAFOCDGORRREPTC
281	1631	A	2827	81	381	KMGTAVWVPKEKEKRDKASQEGGDVLGAR
201	1031	1"				QDCTPSLKSLVATGNLLDLEETAKAPLSTVSA
			1		1	NTTNMDEVPRPQALSGSSVVWVSGCVASRS
						VILSLTSG
282	1632	A	2830	471	160	KLPXDKYELEPSPLTQYILERKSPHTCWQVFV
						TSSGKYNELGYPFGYLKASTTLTCVNLFVMP YNYPVLLPLLDDLFKVHKLKPNLKWRQAFDS
			1	1		YLKTLPPYYL
				<u></u>	140	VSPALSLTPTIFSYSPSPGLSPFTSSSCFSFNPEE
283	1633	A	2835	462	148	MKHYLHSQACSVFNYHLSPRTFPRYPGLMVP
		i	1			PLQCQMHPEESTQFSIKLQPPPVGRKNRERVE
•			1.	1		SSEESAP
-001	1:00	 _	2836	12	384	KTLPRTLLDILADGTILKVGVGCSEDASKLLQ
284	1634	A	2030	2	50.	DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL
		1		1		KSLAETVLNFPLDKSLLLRCSNWDAETLTED
		1	1			QVTYAARDAQISVALFLHLLGYPFSRNSPGEK
		1		1		KR
285	1635	A	2843	20	271	PIRPYYSYSGLDRDCSWLPLAKAWLPDVMIL
203	1000			j		VCDRVSEDGINRQQAQEWCIKHGFELVELSP
	1	Į.				EELPEEDGKCLCVRRKYGTYI
286	1636	A	2845	197	278	TAEDVLTVAYEHGVNLFDTAEVYAAGK
287	1637	A	2851	2	427	FVAEVREWAKYMEVHEKASFTNSELHRAM
				Ī		NLHVGNLRLLSGPLDQVRAALPTPALSPKDK AVLQNLKRILAKVQEMRDQRVSLEQQLRELI
l		1		1	1	QKDDITGSLVTTDHSQMKKLFEEQLKKYDQL
ļ		1		1		QKDDITGSLVTTDHSQMRKLFEEQLKKTDQE KVYLEQNLAAQDRVLCALT
		<u></u>		1	1.00	FVNLGILTCIECSGIHREMGAHISRIQSLELDK
288	1638	Α	2859	2	469	LGTSELLPAKNYGNNSFNDIMEANLPSPSPKP
		1		1	1	TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA
İ	ľ	1				KLNELLEAIKSRDLLALIQVYAEGVELMEPLL
	1	1	1	i	1	EPGQELAETALHLAVRTADQTSLHLVE
		1	1	 	454	FVASGPATARMSDSQFFCVAEERSGHCAVV
289	1639	A	2861	2	454	DGNFLYVWGGYVSIEDNEVYLPNDEIWTYDI
	1 .	1	1	1	1	DSGLWRMHLMEGELPASMSGSCGACINGKL
	1	1		}	1	YIFGGYDDKGYSNRLYFVNLRTRDETYIWEK
	1			1	1	11100100101010101000
Ĺ		ĺ	i		1	ITDFEGOPPTPRDKLSCWVYKDKLIYFG
000	1,545	ļ.	2060	 	378	ITDFEGQPPTPRDKLSCWVYKDRLIYFG FROGOLYKVFLHGSQGQVYHSQQVGPPGSAI
290	1640	A	2868	1	378	TTDFEGQPPTPRDKLSCWVYKDRLIYFG FRQGQLYKVFLHGSQGQVYHSQQVGPPGSAI SPDLLLDSSGSHLYVLTAHQVDRIPVAACPQF PDCASCLQAQDPLCGWCVLQGRCTRKGQCG

EQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
O: of	NO: of	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ıcl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
q	uence	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			' ''	amino acid	of peptide	T-Threonine, V-Valine, W-Tryptophan,
	1	}]	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	-	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	 					RAGQLNQWLWSYEEDSHCLHIQSLLPGHHPR
	J	<u> </u>			385	QE FRYMPNNRQQLLRKRHIGNDIVTIVFQEPGAL
91	1641	A	2870	1	363	PETPKSTRSHFOHVFVTVKVHNPCTENVCYSV
•		1		į	-	GVSRSKDVPPFGPPIPKGVTFPKSAVFRDFLL
	1	1			ľ	AKVINAENAAHKSEKFRAMATRTRQEYLKD
	ł			1		TΔ
	1640	<u> </u>	2877	3	188	RPTRPPPATTOSPESTMDTSLKKEKSAILDLYI
.92	1642	Α	2077	"		PPPPAVPYSPRYVAVHCHGMLVSCWCHL
	1643	A	2878	ī	427	REKEEEVEEEDKVVKETEKEAEQEKEEDSL
293	1043	1^	20,0	1		GAGTHPDAAIPSGERTCGSEGSRSVLDLVNYF
		1	1	1		LSPEKLTAENRYYCESCASLQDAEKVVELSQ
	ł	1		1		GPCYLILTLLRFSFDLRTMRRRKILDDVSIPLL
	.					LRLPLAGGRGQAYDL
294	1644	A	2879	109	245	QLCCFCFRQTTLIVYILSFIGMVIFTFTLDLRY
274	1044	1 **				IIVFVTGGVLG
295	1645	A	2880	3	320	LASSQHGILNNLSLLFSICKTCIRTMDHHCPR
493	1045	1 **				NNCVGEQNHRFFCALHCKSKHFCIEFTLNTN
			1			FNCFLPGAEKSTIDAPFSLQPFLQDSKYNTAL
		1	j	l	l	LSESISQ SQYSHSLDYHLLQVTKNPFTLGDSSNPGQTE
296	1646	A	2892	209	363	RLQEFSQKMDQVRGHWPVST
						SPXTLXLDTFILLGIQDNILVLILATPPFMAGG
297	1647	A	2893	8	424	KLYSTMGRFLRDRKNPACREMAVVLLANLA
						QGDSLAARAIAVQKGSIGHLLGFLEDSLAAT
		1			1	QIQQSQASLLHMHNPPFEPTSVDMMRRACRA
	1		\	1		LLALAKVDDNHSEF
					445	FWIYFPSFFMTGYLPLGFEFAVEITYPESEGTS
298	1648	A	2894	310	443	SCI I NASAOVNI.
					492	KIKAKNI TNYDLCSIFLGTSTLLVWVGVIRYI
299	1649	A	2898	1	432	GVFOAVNVLILTMOASLPKVLRFCACAGMI
		l	- }	1	l l	I CYTECGWIVI GPYHDKFENLNIVAECLI'SL
		ţ	}	1	1 .	VNGDDMFATFAOIOOKSILVWLFSRLYLYSF
	ĺ	1	}	1		SLFIYMILSLFIALITDSYDTIKKFQQNGFPETI
		1	-			I ORR
200	1650	-	2901	 	445	PVWWNSLNGASEVIFSVHVKDGGSFPKTDS
300	1030	^	2,01	1:		TVTVRFVNKADFPKVRAKEQTFMFPENQPV
	1	1	Ì			SLVTTITGSSLRGEPMSYYIASGNLGNTFQID
		.				LTGQVSISQPLDFEKIQKYVVWIEARDGGVP
						FSSYEKLDITVLDVNDNAPIF
201	1651	A	2902	162	433	THFICLPLGYCFPLLDKDLQLPSGFNCNFDFL
301	1031	1^	2,02			EPCGWMYDHAKWLRTTWASSSSPNDRTFPC
		1		1		KPAVSEDMKELRPACSTYFNPRFPYKL
302	1652	-	2909	2	412	GPQMLCKKIYFIWVTRSQCQFEWLADIMQE
302	1032	^	1 -707	-		EENDHQDLVSVHIYVTQLAEKFDLRTTMLY
	1	1		}		CERHFOKVLNRSLFTGLRSITHFGRPPFEPFF
		ı		1		SLQEVHPQVRKIGVFSCGPPGMTKNVEKAC
l		j				LVNRQDRAHFM
303	1653	-IA	2914	291	453	KLNRWLCFFYSWSFGILLYEMVTLGAPPYPE
303	1055	(**				VPPTSILEHLQRRKIMKRPSSCS
304	1654		2926	179	354	PGVPSQALRKAESLKKCLSVMEAKVKAQTA
304	1054	-]			NKDVQREIADLGEVGAASLPPSSGPGA
305	1655	A	2938	135	438	GMGYLHAKGILHKDLKSKNVFYDNGKVVII
1 303	1,000	1"		1		DFOLFSISGVLQAGRREDKLRIQNGWLCHLA
		1		1		PEIIRQLSPDTEEDKLPFSKHSDVFALGTIWY
						LHAREWP
306	1656		2944	2	329	VRWNSCVNCSCAFGNGASLSTSLGESSGCL
1 300	1000	1		1		EIGKWLSCSLLSFPSPLAVLITFCIVTVLGRE LTKGALWAVFLLAGSALLCAEVTGVIWRQF

WO 01/57188

			T 070	S (2.4.1)	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide		/=possible nucleotide deletion, \=possible
	1	I		sequence		nucleotide insertion
			 			SKTKLSFKVSSSA
307	1657	A	2950	2	411	NYLCIAKNSAGSAMGKTRLVVQVPPVIENGL
307	1057	1		-		PDLSTTEGSHAFLPCKARGSPEPNITWDKDGQ
	1	1	}	l		PVSGAEGKFTIQPSGELLVKNLEGQDAGTYT
	1	1		İ		CTAENAVGRARRRVHLTILVLPVFTTLPGDRS
	1	1.	1		·	LRLGDRLWLR
308	1658	A	2951	1	407	PTRPPRVRFDNEFDAESQRKRTTSVSKMERM
500	1.000					DSSLPEEEEDEDKEAINGSGNAENRERHSESS
		1		į	1	DWMKTVPSYNQTNSSMDFRNYMMRDETLEP
		1		}		LPKNWEMAYTDTGMIYFIDHNTKTTTWLDP
		Ì		İ	<u> </u>	RLCKKAKAPEDC
309	1659	A	2954	2	179	QDFLTLTLTEPTGLLYVGAREALFAFSMEALE LQGAVRGGAVGGSRACQRARPRGAVLG
	'.		l			QDMMERAIIDTFVGHDVVEPGSYVQMFPYPC
310	1660	A	2959	1	419	YTRDDFLFVIEHMMPLCMVISWVYSVAMTIQ
		1	1	1	1	HIVAEKEHRLKEVMKTMGLNNAVHWVAWFI
		1				TGFVQLSISVTALTAILKYGQVLMHSHVVIIW
	1	1	}		1	LFLAVYAVATIMFCF
			10000	 	465	MKPQMPGLGAPNGYGPGRGRAGVPGGPERR
311	1661	A	2963	3	403	PWVPHLLPFSSPGYLGVMKAQKPGAGEGMK
		1	147	ì		POKPGLRGTLKPOKSGHGHENGPWPGPCNA
			}			RVAPMILPRLPTPGVPSDKEGGWGLKSQPPS
	4	1	1	1		AVQNGKLPGHQPPNGYGPGAEPGFNGGLEPQ
	}	1	1	Į		l KI
312	1662	A	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM
312	1002	1"	1-75			HTGGCSPKTKPHIKEECIVPTPCYKPKEKLPV
ļ	1	1	1	1	ì	EAKLPWFKQAQELEEGAAVSEEPSFIPEAWS
Ì	1	1			1	ACTVTCGVGTQVRIVRCQVLLSFSQSVADLPI
İ				1		DECEGPKPA
313	1663	A	2969	2	430	VVADNCRQGYLDALRFLERRGLTKEPVLWT LVSKEPPAPADGNWDAGCDQRRKGGLSLNW
				1		KVPHVQVKDVPNFEQLSPELEAALKKACTRD
1					}	PSRWARFWHSGPGQVLTYLLLPCTLPFEYIYF
	1	1	İ	1	[.	RSRRLVVWLPDVPADLWWMQ
	نـــــــــــــــــــــــــــــــــــ				33	LDXSHNALQRLRPGWLAPLFQLRALHLDHNE
314	1664	Α	2971	422	33	LDALGRGVFVNASGLRLLDLSSNTLRALGRH
ĺ	'		1			DLDGLGALEKLLLFNNRLVHLDEHAFHGLRA
	-	ŀ	ł	1		LSHLYLGCNELASFSFDHLHGLSATHLLTLDL
		1		l	}	SSNRM
 115 -	1665	A	2973	1	525	ITVSTHASGSPFGLEPQSGWLWVRAALDREA
315	1002	^	27/3	1	1	OFLYTIKVMAVSGSKAELGOOTGTATVRVSI
1	İ	1	1	1		LNONEHSPRLSEDPTFLAVAENQPPGTSVGRV
	1	- [ì	FATDRDSGPNGRLTYSLOOLSEDSKAFRIHPQ
	1	1		1		TGEVTTLQTLDREQQSSYQLLVQVQDGGSPP
		1				RSTTGTVHVAVLDLNDNT
316	1666	- A	2978	2	400	ELVVELVSAGKSGPERNTYEVQVVTGNVPKA
1 210 .	1000	1,,		1-		GTDANVYLTIYGEEYGDTGERPLKKSDKSNK
	1 .	- 1		1		FEQGQTDTFTIYAIDLGALTKIRIHDNTGNR
1	1	1		1		AGWFLDRIDITDMNNEITYYFPCQRWLAVEE
1						DDGQLSRE
317	1667	A	2981	3	440	VLNCQGRPTRPVRINGDGQEVLYLAESDNVR
1		-		J	J	LGCPYVLDPDDYGPNGLDIEWMQVNSNPAH
1	[1		1	1	HRENVFLSYQDKRINHGSLPHLQHRVRFAAS
1	1		-	1		DPSQYDASINLMNLQVSDTATYECRVKKTTM
				1		ATRKVIVTVQARPAVPMCWTEGQ LPEKEFPIIRKSSSLKVTKCLFTEQPKPIIILRFA
318	1668	A	2995	119	414	LPEKEFPIIRKSSSLKVIKCLFIEQFRFIILKFA ENYDARLLRIDIANTLREQVQELFNKTYGKQ
				1 .		RRTPGEGHVAAVDREVAGFPVPAEGISGETIH
ı					332	GFFAYTYGRLVVVEDLHSGAQQHWSGHSAEI
1 .	1669	A	2999	2		

EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence			ng to first	acid residue	Contamine R=Arginine S=Serine,
ience		ļ	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ì	į	(amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
,]		1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1		}	peptide	ł	
	l .		ì	sequence		nucleotide insertion
			 			STLALSHSAQVLASASGRSSTTAHCQIRVWD
	l	i	i	{	1	VSGGLCQHLIFPHSTTVLALAFSPDDRLLVTL
	1		1	}	\	GDHDGRTLALWGTGHL
	<u> </u>	<u> </u>	-	(02	322	IDESTGLUTVNYLDYETKTSYMMNVSATDQA
320	1670	Α	3000	693	322	PRINCIPLE STATE OF THE PRINCIPLE OF THE P
	1	l	1			ILENLALGTEIVRVQAYSIDNLNQITYRFDAY
	l	1	ł	1	1	TSTQAKALFKIDAITVRGWGQGAPFFPI
	1	1		Ì	i	ISTUARALINDATI VRO WOODI EDEA CODI PROPI
201	1671	A	3001	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPQPC
321	1071	1.	1 2001			GWGQSSDLLSRIDLDELMKKDEPPLDFPDTLE
	Į.	1	1	1		GFEYAFNEKGQLRHIKTGEPFVFNYREHLHR
	1	1	1	1		WNQKRYEALGEIITKYVYELLEKDCNSKKVS
				100	447	EDUDNSI FPGRGDSOCACCPSSPVWVFLETGI
322	1672	A	3007	192	447	LFPWLFLQVEVIKKAYMQGEVEFEDGENGK
	ł		1		1	DGAASPRNVGHNIYILAHQLARH
	1	1			J	KELLFYHLIVNNINFFNTRYAKIHIPIIASVSEH
323	1673	A	3019	18	245	KELLFYHLIVNINGFN IK TAKITII IIAO VOOL
323	1075	1 **	1		į .	QPTTWVSFFFDLHILVCTFPAGLWFCIKNIND
	1.	1	l l	ł		ERVFGKRGF
			3020	523	797	LCYFSARYHQRKIFGILYIFTLSAINRKEPNLFI
324	1674	A	3020	323	1	YI FIFFEMESHSYTHAGVQRHNLNSLQPLPPG
	1	1		1	ļ	FK PESCL CFL SSWNYRGAPPGPANF
		1 _				NDFLPLYFGWVLTKKSSETLRKAGQVFLEEL
325	1675	A	3022	2	156	GNHKAFKKELRQCRWQVGAL
	T	į		·		KMVRGSKKLISFFPGGPYGILAGRDPSKGLAT
326	1676	A	3023	38	172	KMVKGSKKLISFFFGGF I GILAGIGEI SINGELI
320	10,0	1	1			FCLNKEALKDEFE
	1677	HA-	3027	1	385	LTLEFLLLPAASELAHGKRLACCIVDHKLPEC
327	10//	^	1 302,	1.		GFYGLYDKILLFKHDPTSANLLQLVRSSGDIQ
	1	- 1	1.	-	Į.	EGDLVEVVLSASATFEDFQIRPHALTVHSYR
	ł)	- 1 '	1	l l	PAFCDHCGEMLFGLVRQGLKCDGCGLNYHK
	ł	1	i i	1	1	l PC
	1					ITRPTISCQRPGPGLAAGMLPYTVNFKVSART
328	1678	A	3030	13	569	LTGALNAHNKAAVDWGWQGLIAYGCHSLV
		- 1	1		Į.	VVIDSITAQTLQVLEKHKADVVKVKWAREN
1	1	- 1	t	Ì	Ĭ	YHHNIGSPYCLRLASADVNGKIIVWDVAAGV
1	1	-	i	1	ì	YHHNIGSPYCLKLASADVNGKIV WDVARIO
	.]	-	1	1		AQCEIQEHAKPIQDVQWLWNQDASRDLLLA
1	1		1	ļ		HPPNYIVLWNADTGTKLWKKSYADNILSFSF
ļ	1	l l	ì	1		D
L				100	744	SVNI PPSI WPWEEAMDSTKSEPLKGSPEAED
329	1679	A	3038	90	1 /	CNIEVKKLVNPSOYRFEHLVTOMKWRLQEG
1					Į.	RGEAVYQIGVEDNGLLVGLAEEEMRASLKT
1	-	1			Į.	HRMAEKVGADITVLREREVDYDSDMPRKIT
1	1	-				VLVRKVPDNQQFLDLRVAVLGNVDSGKSTL
1	1	1	1	1		VLVKKVYDNQQFLDLKVAVLUNVDSGKSTL
1		l.	- [.	LGVLTQGELDNGRGRARLNLFRHLHEIQSGF
1	i	- 1	1	1		TSSISFEILGFNSKGEVHGINGTQWGQTLRMC
1		Ì	1	1	1	w
1					397	LCSTILLLTIPSWVLSOITLKESGPTLMKPTE
330	1680	A	3040	3	27/	I TI TOTESGESI NTSGVGVAWIROPPGKALE
1		1		I		WLALIYWDDDKRYSPSLNDRLTIAKDTSRN
1		l	1 .	1	1	VVLTMTNMGPVDTATYYCAQFARGARGSN
1	- 1	-	1	I	1	VVLIMININGPVDIALLICAQUARGARGSI
1	1	- 1	1	1		WFDPWGQ
		-+-	3043	3	1509	AGIRHEAPPTTSNRHRROIDRGVTHLNISGLE
331	1681	_ A	3043	1,		LADD CIAIDWVAGNVYWTDSGRDVLEVAQM
1	l	1	1	- 1		GENEKTLISGMIDEPHAIVVDPLRGTMY WSI
1	1	j	1	- 1		WGNHPKIETAAMDGTLRETLVQDNIQWPTO
1	1		1	1		LAVDYHNERLYWADAKLSVIGSIRLNGTDP
)	}	ı	- 1	1		LAVDYHNEKLY WADAKLSVIOSIKLIGIDI
1	ł	- 1		- 1		VAADSKRGLSHPFSIDVFEDYIYGVTYINNR
1	1	1	1	1		PKIHKFGHSPLVNLTGGLSHASDVVLYHQH
l .		- 1	1	- 1	1	ODEVINDCORKKCEWLCLLSPSGPVCTCPN
1		L L	1			
				İ		REI DNGTCVPVPSPTPPPDAPRPGTCNLQCF
						KRLDNGTCVPVPSPTPPPDAPRPGTCNLQCF GGSCFLNARRQPKCRCQPRYTGDKCELDQC

				·		Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoloucine, K=Lysine, L=Leucine,
eotide	seq- uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	acuce		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uchc				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
•	Ì	ŀ		peptide	1	nucleotide insertion
		<u> </u>		sequence		WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC
			}			TOOUCAGYCANNSTCTVNOGNOPQCRCLPG
	Ì		Ì	ļ.		DI CORCOVROCSGYCENFGTCOMAADGSKQ
	1	ł	1	{	1	CRCTAYFEGSRCEVNKCSRCLEGACYVNKQS
		ł				GDVTCNCTDGRVAPSCLTCVGHCSNGGSCT
		1	1	1		MNSKMMPECQCPPHMTGPRCEEHVFSQQQP
	1	l				GHIASILIP TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG
332	1682	A	3045	3	952	AVDEEVGDYFPEFLDMLEESPFLKMTLPWGT
	1		į			T SSURLOCKSOSDDGPIMWVRPGEQMIPTAD
	1	1	1	i		MPKSPFKRRRSMNEIKNLOYLPRTSEPREVLF
	}	1		Ì	.	EDRTRAHADHVGOGFDWOSTAAVGVLKAV
	l	į .		Ì		OFGEWSDOPRITKDVICFHAEDFTDVVQKLQ
		1		1		LDLHEPPVSQCVQWVDEAKLNQMRREGIRY
		1	1	i	ĺ	ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW HIRLKQYHPVVEATQNTESNSNMDCGLTGKR
	1 .	1		1		ELEVDSQCVRIKTESEEACTEIQLLTTASSSFP
	1	1	· I			DASE
			1 2016	497	167	CACSTODEL PGRATRSLTRPANOKGCDGDRL
333	1683	A	3046	497	107	VVDGCAMIAMNGSVFAOGSOFSLDDVEVLI
	1		·	1		ATLDLEDVRSYRAEISSRNLAVSAPVDICVG
		1		1		CSSKTWKVAPFVRAWWRP
334	1684	A	3053	37	276	VITDLEEQLNQLTEDNAELNNQNFYLSKQLD EASGANDEIVQLRSEVDHLRREITEREMQLTS
334	100	1		į.		QKQVRRVNKVVRSLEDF
1		l			046	T WDAWGDWSDCSRTCGGGASYSLRRCLTGR
335	1685	Α	3054	2	846	L NICECONTRYKTCSNHDCPPDAEDFKAQQU3A
		1	1] .	L VNIDVOVOGHYYEWLPRYNDPAAPCALKCH
(1	-		1	A OCONI VVELAPKVLDGTRCNI DSLDMCISU
ļ		1	1	1	ì	ICQAVGCDRQLGSNAKEDNCGVCAGDGSTC
ļ				1		RLVRGQSKSHVSPEKREENVIAVPLGSRSVRI TVKGPAHLFIESKTLQGSKGEHSFNSPGVFVV
{		1		ŀ		ENTTVEFQRGSERQTFKIPGPLMADPIFKTRY
Į.	1	i i		*I	1	TAAKDSVVQFFFYQPISHQWRQTDFFPCTVT
1	ŀ	Ì	ļ		į.	l. CGGG
		4	3058	54	347	VVGKOFAGAHSDSCCLLHTPPRLTPAHSRKA
336	1686	A	3038	"	1	I DNISDIVSOKDOVHVČIMCLRAIMNYQVŠKO
Į		1				AWDWRLGSPACPHWGLHKLPRLWDPLSLYF
					<u> </u>	VLCWGT TABLES AT VRDCWVEVOOR
337	1687	TA	3059	2	709	ILTSLVELTRFETLTPRFSATVPPCWVEVQQE QQQRRHPQHLHQQHHGDAAQHTRTWKLQT
]. "					1	DSNSWDEHVFELVLPKACMVGHVDFKFVLN
ľ		1	İ		1	SNITNIPOIOVTILKNKAPGLGKVNGLRLCPF
		1				I EDHKEDIL CGPVWLASGLDLSGHAGMLILI
1		1				SPKI VKGMAGGKYRSFLIHVKAVNERGTEEI
1			1			CNGGMRPVVRLPSLKHQSNKGYSLASLLAK
			-	1		VAAGKEKSSNVKNENTSGTRK
338	1688	-	3060	85	384	KAFYNYHVLELLQMLVTGGVSSQLEQHLDK
338	1000	^	3000			DKVYGVADSCTSLLSGRNRCKLGLLSLHETII SDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDI
-						
	.	1				EELNP CFLCLSGDFMVMTIFFNVSRRFGYVAFQNYV
339	1689,	A	3063	236	362	PSSVTIMLSWV
1					1240	DI WOFTPI HEAASKNRVEVCSLLLSYGADP
340	1690	A	3065	3	1249	I I NCUNIC CAIDI APTPOLKERLAYEFKGHSL
						OAADEADVTRIKKHI.SLEMVNFKHPQTHEIA
1		- I -	İ			T LICA A ASPYPK RKOICELLL RKGANINEK TK
		- }	1	1		FLTPLHVASEKAHNDVVEVVVKHEAKVNAL DNLGQTSLHRAAYCGHLQTCRLLLSYGCDPI

606 15	OPA YA	1/-4	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in	location	corresponding	t=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ì	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		l	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
	}	i		peptide	ì	nucleotide insertion
		l	1	sequence		IISLQGFTALQMGNENVQQLLQEGISLGNSEA
					l	DROLLEAAKAGDVETVKKLCTVQSVNCRDIE
	·			Į		GRQSTPLHFAAGYNRVSVVEYLLQHGADVH
	İ	ĺ	1	1		GROSIPLHFAAGINKVSVVBILLQIIGADVII
	1	1		1		AKDKGGLVPLHNACSYGHYEVAELLVKHGA
	1	1	İ			VVNVADLWKFTPLHEAAAKGKYEICKLLLQ
	1	Į.	1	J		HGADPTKKNRDGNTPLDLVKDGDTDIQDLLR
	İ		1	1		GDAALLDAAKKGCLARVKKLSSPDNVNCRD
		i		ļ	1	TQGRHSTPLHLAGK
241	1691	A	3070	1	547	GVLIPSFQNQLFADILAGIESVTSEHNYQTLIA
341	1091	^	3070	1.	1	NYNYDRDSEEESVINLLSYNIDGIILSEKYHTI
	ł	Į.		1	İ	RTVKFLRSATIPVVELMDVQGERLDMEVGFD
	1	1	1			NROAAFDMVCTMLEKRVRHKILYLGSKDDT
	ì	1	1	1	l	RDEORYOGYCDAMMLHNLSPLRMNPRAISSI
	1	l	ł	Ì	Í	HIRMOLMRDALSANPDLDGVFCTN
			 	1462	3	RINECRKPSDADILVPGDTISLIGTTSLRIDYNE
342	1692	A	3073	463	13	IDDNRVTAEEVDILLREGEKLAPVMAKTRILR
		1			}	AYSGVRPLVASDDDPSGRNVSRGIVLLDHAE
1				l		RDGLDGFITITGGKLMTYRLMAEWATDAVC
Ì	}	Į.	1	ł		RKLGNTRPCTTADLALPGSQEPAKVP
						LLIYLAIFAPVAMSALAGVKSVQQVRIRAAQS
343	1693	A	3075	250	1	LGASRAQVLWFVILPGALPEILTGLRIGLGVG
				+		WSTLVAAELIAATRGLGFM
		1	· ·			LYFDAYLQSLQVAAISTFCCLLIGYPLAWAV
344	1694	A	3076	2	138	LYFDAYLOSDQVAAISTFCCEERGTTEAT
1		1				AHSKPSTRNILLLL LKIRGQRIELGEIDRVMQALPDVEQAVTHAC
345	1695	A	3078	469	3	LKIRGQRIELGEIDRYMQALFDYEQAY111AC
313		-			1	VINQAAATGGDARQLVGYLVSQSGLPLDTSA
}		ľ			1	LQAQLRETLPPHMVPVVLLQLPQLPLIANGKL
	1	1		i		DRKALPLPELKAQAPGRAPKAGSETIIAAAFS
	-		1			SLLGCDVQDADADFFALGGHSLLAMKLAT
346	1696	A	3082	404	2	QNITSKDLDVRLDPQTVPIELEQLVLSFNHMI
340	1070	1.	000-			ERIEDVFTRQSNFSADIAHEIRTPITNLITQTEI
	1			1		ALSQSRSQKELEDVLYSNLEELTRMAKMVSD
1	-		l	1		MLFLAQADNNQLIPEKKMLNLAHEVGKVFD
Į.		1		1		QFEALPE
240	1697	A	3084	3	340	NELTFKEAEISKLYTKVHPAYRTLLEKRQALE
347	1097	Α.	3004	1-		DEKAKLNGRVTAMPKTQQEIVRLTRDVESGQ
		1		ł		OVYMQLLNKEQELKITEASTVGDVRIVDPAIT
	1]				OPGVI KPKKGLIILGAI
-	1200		3086	723	10	TOAMVWQQKACAEDDPQLSGRHWLHAATL
348	1698	Α	3080	1 /2	1	VNIA A VPHI KGDDLAEOAOALSNRA YEEAA
1		-	1	1	1	ORLPGTMROMEFTVPGGAPITGFLHMPKGDG
1		1		1	1	PEPTVI MCGGLDAMOTDYYSLYERYFAPKGI
1	1	1		1	1	AMI_TIDMPSVGFSSKWKLTQDSSLLHQHVLK
	1		1	1		AL PNVPWVDHTRVAAFGFRFGANVAVRLAY
]			- 1	1	1	1.FSPRI.KAVACLGPVVHTLLSGLKCQQQVPE
		1	1	1	i	MYLDVLASRLGMHDASTKSSTRENH
					1240	RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV
349	1699	A	3087	2	249	GFGVAMSQALGPFSLRAGVASSTLGIAQVCG
1	}	- }	l	ł	{	SSLWIWLAAVVGIGAWNM
1			_L			EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR
350	1700	A	3099	3	424	ANTPDSDITEKTEDSSVPETPDNERKASISYFK
				1		ANTIPODITENTED SOFETI DIE DISTINA
	1				1	NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN
1		1		1		KDTVIIVSEPSEDEESQGLPTMARRNDDISELE
	i			1_	1	DLSGMEDLK
					404	IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG
251	1701	- \	3108	1 2	ייטד ן	
351	1701	A	3108	12	107	MEGIVVMVIETELSWGAYYKAPLYSLALKCL
351	1701	A	3108	2	107	MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLETIILLGLTIVYHAREIOLFMANYGADDWR
351	1701	A	3108	2	107	MEGIVVMVIETELSWGAYYKAPLYSLALKCL
351	1701	A	3108		101	MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLETIILLGLTIVYHAREIOLFMANYGADDWR

						Amino acid sequence (A=Alanine C=Cysteine,
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nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	· '	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
-	1			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	ì	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide		/=possible nucleotide deterion, /-possible
				sequence	l	nucleotide insertion
352	1702	Ā	3110	341	2	AQLAEVCPPQTLLTTNTSSISITAIAAEIKNPER
352			1			VAGLHFFNPAPVMKLVEVVSGLATAAEVVE
	1	Į	1	,		QLCELTLSWGKQPVRCHSTPGFIVNRVARPY
		(Ì	İ	YSEAWRALEEQVAAPEVI
353	1703	A	3111	3	188	HFSLFRIAFAVFLTYMTVGLPLPVIPLFVHHEL
333	1,705	1	1	1		GYGNTMVGIAVGIQFLATVLTRGYAGRLA
354	1704	A	3116	367	225	WQLFHLNGTFLNIGETDTESCVNGWVYDRSS
354	1704	1^	3110	} "		FPFSNMTEVRGLVFLS
	1000	 	3117	101	53	VINLVYLISSPRPELKPVDKESEVVMKFPDGF
355	1705	A	3117	107	1	EKFSPPILQLDEVDFYYDPKHVIFSRLSVSADL
1		1	1	ì		ESRICVVGENGAGKSTMLKLLLGDL\APVRGI
1	Ì	ì	1	i		RHAHRNI.KIGYFSOHHVGAAGT*TFSACGNL
	ì	1				LGTOVFLGRPEEEY\RHOLGFGMGISGELGHA
	1	}	1	1	1	SSLPACLGGOKEAEVAFCSDGLLPCPNFL\IL\
1	}	1		1	1	DEPTNIHLGHGRAIEALGPCLQTISGVGVILVS
1		ļ	1			HE*SALSRLVCRE\LWVC*GRSTSPF
		+		137	466	DCCDDWCFHNORLEEHOARAWOGAMDAG
356	1706	A	3121	137	1 400	AASREHARWOGTGLAPGTRVAVAPTCVQGL
	1	1	1	1		PQERSVCRPFFSSRWREGPVWALGAGAHGKP
1	1	1	1	(1	RWSGGVRCVVRGGRWFTPAPH
		<u> </u>	1	1240	229	MI FAPGPSDGCELSNPSASRVSCAGQMLEVQ
357	1707	A	3124	1249	229	PGL VFGGAAAVAEPDHLREAGITAVLTVDSE
}		1				EPSEK AGPGVEDLWRLFVPALDKPETDLLSH
1	İ]		1		LDRCVAFIGQARAEGRAVLVHCHAGVSRSV
İ						AUTAFI MKTDOLPFEKAYEKLOILKPEAKMN
1		}		1		EGFEWQLKLYQAMGYEVDTSSAIYKQYRLQ
1		1				KVTEKYPELQNLPQELFAVDPTTVSQGLKDE
1	1	1	1	l l		VLYKCRKCRRSLFRSSSILDHREGSGPIAFAH
1	1	j	1	}	.	KRMTPSSMLTTGROAOCTSYFIEPVQWMESA
{	ł	١.	1		İ	LLGVMDGQLLCPKCSAKLGSFNWYGEQCSC
1	1.	1			1	GRWITPAFQIHKNRVDEMKILPVLGSQTGKI
					120	EVETLGPRTPGP/EAQSPTPGSCPGWQEPSPGP
358	1708	. A	3127	816	139	TPPP*LSGPGPQGAPVLGKLLPDPEETPAGKTP
	1			3	ŀ	LGKHFWWGL\PVTSANFSPGAAA*FGGALSPP
		1.			ì	GGDL/GHMLLQGPPSPFRLQQQ*QTPPGSHSP
		1	-		l	PTANREINPGPAAAADTRSCWGHKRSWRGW
	j	- }	-	į.		RGLAPWRLGFGSPGIP*PAPAGIP/GRPTWEGG
		- 1	į.	i		KGAGGKPSETLTRSPPVWRGKRGSANGFLSW
1		1	1	į	1	
						VQILQ HEHLLLLLCVFLVKSQGVNDNEEGFFSARG
359	1709	A	3132	3	191	HRPLDKKREDAPNLRPALADUTVCDYRAQIA
		- 1		1	1	*AASTPKRAASIAHNAVSCR*AQIA
	-		<u>'</u>			REPPRPALLFF*DRVSLCCPGWNAVVQSQLT
360	1710	A	3134	1	286	AAPTSQVQ/SDSPTFPSSWDYRHVPEYPANFL
1	1	j	1	1		*RQGFPMLPRLVSNSWAQTVHPPRPPKVLDL
						1
		1				QA PCD PDI PCVP CPP HS/WA
361	1711	A	3135	56	1449	PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA
301	1 -/	1	1			AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR
1	1		İ			VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N
	Ì	-	1	1	ı	GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA
İ		- 1		[GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD
1		1			1	PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ
1		1	1		1	APGLPHRTSIRPGWRRLTEPEAWARRHRRPW
	1.	1		Ì		GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT
	1	1	}	1	1	DDI TVMSRCLAPDLKAPASGPRGWRRGMPQ
		1	- (-	1	SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA
1	İ		1.	1	i	GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT
				1	1	The same of the sa
1	1		1	l.		F/LIPSPT*MSPALVIQPPVPPTQMGLRISGLPK
				Ì		F/LIPSPT*MSPALVIQPPVPPTQMGLRISGLPR QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RNQSPLGNDTLSSGLPMGPRRQVWPLARVG GHSSPREPQVLKKPLWGQTDIAGVGSASLYP DNL RVGMVLGTREVGDSTPPPSPPLYPFTGNEFVQ HNTWQLSRVYPSDLRTDSSNYNPQELWNAG CQM/V*GGSRDWEEGVEEQQVGNKFSSDGR VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS LKEGLEGLHGESCSSFLLGPSVAMNMQTAGL EMDICDGHFRQNGGCGYVLKPDFLRDIQSSF HPEKPISPFKAQTLLNQVISVQQLPKVDKTKE
						GSIVDPLVKVQIFGVRLDTARQETNYVENNG FNPYWGQTLCFRVLGPDFPMLRFGKMDYDW KSRNDLLGKTPCPGTCMQQGYRHIHLLSKDG ISLRPASIFVYICIQEGLEGDES MFAGSYGKSMFSFSKKVLNCLPKWRYHFVIA
363	1713	C	3139	60	248	PAMNESPI APHLHOHLVFSVFQVLTILIGV**
364	1714	A	3140	57	418	SAFKTLQLPAFSLYFDLGSLKLLILRIHTSIVK NHKVESPRTMSPG*DPQSFLQIPQPRPPQLRV GLTSGLIQHFHSPSSCQFPLLRGPPFPRQPPLGI SGASLCPVLSPPR*PLQPSSL
365	1715	A	3145	122	413	LLPYPSLFVFLRQCHFVTRLECNGVVSAHCN LHLPGSSDSPASAS*VAGTTGVCHHTRLIF\VF LV*TGFHYVAQAGLELLTA*S\PPQLPKVVGL QA
366	1716	A	3150	247	2	VGEKLHDIRFGNDFDMTPKAQATKEKIDKLN FIKIKKLCIEGYY/NREPQNGRKIFANYVS\DK GLMATIYEELLKLSNKLIQ GLMATIYEELLKLSNKLIQ
367	1717	A	3152	3	2350	QKLKONOPKRAHVEDGGSRSKQGNEQSKKT PIEKSDFAAATHPRAFYLSKPDETPNAWMSD SGTGLTYWKLEEKDMHHSLPETLEKTFISLSS TDVSPNQVLTLDPTLHMKPKQQISGIQPHGLP NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN VTSQLPGFPKYPSHTKASPVDSWKNQTFQNE SRTSSTFPSVYTITSNDISVNTVDEENTVMVAS ASVSQSQLPGTANSVPECISLTSLEDPVILSKIR QNLKEKHARHIADLRAYYESEINSLKQKLEA KEISGVEDWKITNQILVDRCGQLDSALHEATS RVRTLENKNNLLEIEVNDLRERFSAASSASKI LQERIEEMRTSSKEKDNTIIRLKSRLQDLEEAF ENAYKLSDDKEAQLKQENKMFQDLLGEYES LGKEHRRVKDALNTTENKLLDAYTQISDLKR MISKLEAQVKQVEHENMLSLRHNSRIHVRPS RANTLATSDVSRRKWLIPGAEYSIFTGQPLDT QDSNVDNQLEETCSLGHRSPLEKDSSP/GSSST SLLIKKQRETSDTPIMRALKELDEGKIFKNWG TQTEKEDTSNSLL*/INPRQTETSVNASRSPEK CAQQRQKRLNSASQRSSSLPPSNRKSSTPTKR EIMLTPVTVAYSPKRSPKENLSPGFSHLLSKN ESSPIREKTYSEKATDNHVNHSSCPEPVPNGV KKVSVRTAWEKNKSVSYEQCKPVSVTPQGN DFEYTAKIRTLAETERFFDELTKEKDQIEAAL SRMPSPGGRITLQTRLNQVKCLSLNLL
368	1718	A	3163	2	2550	EKASOGGAGUAGE RVPGSPAPSSLPLHSPGACGTEVDMDPQRSPL LEVKGNIELKRPLIKAPSQLPLSGSRLKRRPDQ MEDGLEPEKKRTRGLGATTKITTSHPRVPSLT TVPQTQGQTTAQKVSKKTGPRCSTAIATGLK NQKPVPAVPVQKSGTSGVPPMAGGKKPSKRP AWDLKGQLCDLNAELKRCRERTQTLDQENQ

			000	Danding d	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	İ]		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	Į.	1	Ì	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide		
		1		sequence		nucleotide insertion
						QLQDQLRDAQQQVKALGTERTTLEGHLAKV
		İ	ŀ	1		QAQAEQGQQELKNLRACVLELEERLSTQEGL
	1	1	ļ		ł	VQELQKKQVELQEERRGLMSQLEEKERRLQT
	1		ł	1	1	SEAALSSSQAEVASLRQETVAQAALLTEREER
	1	l)		1	LHGLEMERRRLHNQLQELKGNIRVFCRVRPV
	i	Ì		1	}	LPGEPTPPPGLLLFPSGPGGPSDPPTRLSLSRSD
	1	l .		ļ	1	ERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDE
i	1	1	1	j	l	VFEEIAMI,VOSALDGYPVCIFAYGQTGSGKTF
	Į.	1	i	ì		TMEGGPGGDPOLEGLIPRALRHLFSVAQELSG
		i		1	ŀ	OGWTYSFVASYVEIYNETVRDLLATGTRKGQ
	1	1	}	1	ł	GGECEIRRAGPGSEELTVTNARYVPVSCEKEV
ĺ	1	ļ	1	1	•	DALI HI ARONRAVARTAONERSSRSHSVFQL
				İ		OISCEHSSRGLOCGAPLSLVDLAGSERLDPGL
	1 .	.		}	1	ALGPGERERLRETQAINSSLSTLGLVIMALSN
	1 .	1	1	1	1	KESHVPYRNSKLTYLLQNSLGGSAKMLMFV
1	1	1	ļ .	I		NISPLEENVSESLNSLRFASKVEPSVLFGTAQS
1	1	1	1)	ļ	NRKWKTDPDLCVCVCVCVCVCVCVCVCVP
{	-	1	1	Į.	i	MSMYRVRGGRVAGGCFIGWRAPCPRAIK
		1		<u></u>	<u> </u>	GYTSQGRWIDIERGPLTANTESLHENNFNALP
369	1719	A	3165	365	12	GYTSQGRWIDLERGFLTANTESLIEMWING GYTRKIE*I*IYKKN*INFGGVGLLNIVKISILS/K
***	1		1			IYRFDAIPVKILTRFFINLDKLILKFVLKTKIAK
	•	- 0		1	· ·	IYRFDAIPVKILIKFINEDKLICKF VEKTKEEK
		1	ì			NRIKTFYIMRRKKLGDSS GASISPSAVIDGVEGLKPMQEQEAQEAGPCLD
370	1720	A.	3170	393	42	GASISPSAVIDGVEGLKPMQEQEAQEAGICLD
5,0	17-1	1				*HMAPEQWVAPR\RLLFRLIFSVLHALIIAAAA
	1	l l		1	}	QSSAEEDEDPRN*GQSSEDQAPNQNGLIVIVH
	1			1	1	RVHVPLGAAATVPVHRSHFPR
371	1721	A	3173	770	510	GNGGCGLSQIPPSHLGAFSRGSLLSRG\DPRGP
1,371	1,21	''		İ	1	PPHPVIFFVFVVE\QGFTVLARMVSIS*PCDPP
1		ı	1	1	İ	ALASQSAGITGVSHLARPQNLYF
372	1722	A	3180	381	76	RVLHHDNVPAHSSPQKREISQEFQLEIRHLP*S
312	1/22	1"	3100	}		PDLAPSGCFLFLNLKNIFK\GTHFSLVDNVKK
1	1	1				TVSTWLH/SQNAQFYKDRLNGWYHCLQKCL
	1					OHY*AYVEK
002	1723	A	3181	410	14101	RREVAGPEGKGLLLASAHTMLTPPLLLLLPLL
373	1/23	^	3101	110		SALVAAAIDAPKTCSPKQFACRDQITCISKGW
	1		1			RCDGERDCPDGSDEAPEICPQSKAQRCQPNE
1	ŀ)	HNCLGTELCVPMSRLCNGVQDCMDGSDEGP
	1	1	1			HCRELOGNCSRLGCOHHCVPTLDGPTCYCNS
	-	i		1		SECT CADGETCE OF DECS VYGTCS QLCTNTD
	}	1	1		}	GSFICGCVEGYLLOPDNRSCKAKNEPVDRPP
1	1	1	1	1		VLLIANSQNILATYLSGAQVSTITPTSTRQTTA
1	1	1		1		MDFSYANETVCWVHVGDSAAQTQLKCARM
1	1	1	1			PGLKGFVDEHTINISLSLHHVEQMAIDWLTGN
}	1	ł	ì			FYFVDDIDDRIFVCNRNGDTCVTLLDLELYNP
1	1	1				KGIALDPAMGKVFFTDYGQIPKVERCDMDG
ı	1	1				KGIALDPAMOKVFF IDTOQUE VERCENDO
1	1	1	1	1		ONRTKLVDSKIVFPHGITLDLVSRLVYWADA
1		1		1		YLDYIEVVDYEGKGRQTIIQGILIEHLYGLTVF
1		1			1	ENYLYATISDNANAQQKTSVIRVNRFNSTEY
	1	1		}		QVVTRVDKGGALHIYHQRRQPRVRSHACEN
		ì				DOYGKPGGCSDICLLANSHKARTCRCRSGFS
1		1		1	1	LGSDGKSCKKPEHELFLVYGKGRPGIIRGMD
	1	1	}	ŀ	1	MGAKVPDEHMIPIENLMNPRALDFHAETGFI
			1	1	1	YFADTTSYLIGRQKIDGTERETILKDGIHNVE
I	1	i i		1		
		1				GVAVDWMGDNLYWTDDGPKKTISVARLEK
1						AAOTRKTLIEGKMTHPRAIVVDPLNGWMYW
				•		AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW TDWEEDPKDSRRGRLERAWMDGSHRDIFVT
						AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW TDWEEDPKDSRRGRLERAWMDGSHRDIFVT SKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI
						AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW TDWEEDPKDSRRGRLERAWMDGSHRDIFVT SKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI LLNGTDRKIVYEGPELNHAFGLCHHGNYLFW
				·		AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW TDWEEDPKDSRRGRLERAWMDGSHRDIFVT

					_	
SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	peptide	"""	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-		[[USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	i i	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	{	l i	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i		1		peptide	Joqueilee	/=possible nucleotide deletion, \=possible
	1			sequence	1	nucleotide insertion
				sequence	 	FEIR\MYDAQHQQVGSNKCRVNNAGCSSLCL
		1		ì		ATPGSRQCACAEDQVLDADGVTCLANPSYVP
1	1	1		Į		PPQCQPGEFACANSRCIQERWKCDGDNDCLD
1	1		١	l .		NSDEAPALCHQHTCPSDRFKCENNRCIPNRW
	1	1	ļ		i	LCDGDNDCGNSEDESNATCSARTCPPNQFSC
	1	1	İ	1	1	ASGRCIPISWTCDLDDDCGDRSDESASCAYPT
İ	1	1	Į.	ļ		CFPLTQFTCNNGRCININWRCDNDNDCGDNS
		١	l	ļ)	DEAGCSHSCSSTQFKCNSGRCIPEHWTCDGD
	1	1		i		NDCGDYSDETHANCTNQATRPPGGCHTDEF
				ŀ	Į.	QCRLDGLCIPLRWRCDGDTDCMDSSDEKSCE
1		1	1	ł	. ·	GVTHVCDPSVKFGCKDSARCISKAWVCDGD
1		ĺ	l			NDCEDNSDEENCESLACRPPSHPCANNTSVC
		1		1	1	LPPDKLCDGNDDCGDGSDEGELCDQCSLNN
[1])	}	GGCSHNCSVAPGEGIVCSCPLGMELGPDNHT
1	{	1	}	1		COIOSYCAKHLKCSOKCDONKFSVKCSCYEG
1	1	1		1	1	WVI.EPDGESCRSLDPFKPFIIFSNRHEIRRIDLH
1]	j	1	1	KGDYSVLVPGLRNTIALDFHLSQSALYWTDV
		1	1		1	VEDKIYRGKLLDNGALTSFEVVIQYGLATPEG
	}	1.		1		LAVDWIAGNIYWVESNLDQIEVAKLDGTLRT
}		1	1	1	1	TLLAGDIEHPRAIALDPRDGILFWTDWDASLP
1		1	1			RIEAASMSGAGRRTVHRETGSGGWPNGLTV
1 '	1	1	1	1		DYLEKRILWIDARSDATYSARYDGSGHMEVL
1	1	1	1	1	{	RGHEFLSHPFAVTLYGGEVYWTDWRTNTLA
1	\	1		1	1	KANKWTGHNVTVVQRTNTQPFDLQVYHPSR
ļ		1			ì	OPMAPNPCEANGGQGPCSHLCLINYNRTVSC
)	1	}	l	1	1	ACPHLMKLHKDNTTCYEFKKFLLYARQMEIR
1			ì		1	GVDLDAPYYNYIISFTVPDIDNVTVLDYDARE
1		}		l	1	ORVYWSDVRTOAIKRAFINGTGVETVVSADL
-	1	ì		ì		PNAHGLAVDWVSRNLFWTSYDTNKKQINVA
		1	1	1		RLDGSFKNAVVQGLEQPHGLVVHPLRGKLY
İ		1			l	WTDGDNISMANMDGSNRTLLFSGQKGPVGL
1	Ì	1	1		1	AIDFPESKLYWISSGNHTINRCNLDGSGLEVID
	1	Ì		1	1	AMRSQLGKATALAIMGDKLWWADQVSEKM
		1	İ	1	1	GTCSKADGSGSVVLRNSTTLVMHMKVYDESI
		I	1			QLDHKGTNPCSVNNGDCSQLCLPTSETTRSC
	1	1	-	1.		MCTAGYSLRSGQQACEGVGSFLLYSVHEGIR
Ī			}	1	1	GIPLDPNDKSDALVPVSGTSLAVGIDFHAEND
	i				1	TIYWVDMGLSTISRAKRDQTWREDVVTNGIG
1		1	1	ı		RVEGIAVDWIAGNIYWTDQGFDVIEVARLNG
1				}		SFRYVVISQGLDKPRAITVHPEKGYLFWTEW
1				1		GQYPRIERSRLDGTERVVLVNVSISWPNGISV
ļ				1		DYQDGKLYWCDARTDKIERIDLETGENREVV
	1	}		1		LSSNNMDMFSVSVFEDFIYWSDRTHANGSIK
		-		1	1.	RGSKDNATDSVPLRTGIGVQLKDIKVFNRDR
	1	-		1	1	QKGTNYCAYANGGCQQLCLYRGRGQRACA
]	}.	1	1	}	CAHGMLAEDGASCREYAGYLLYSERTILKSI
-	1	1	1	1	1	HLSDERNLNAPVQPFEDPEHMKNVIALAFDY
l			1			RAGTSPGTPNRIFFSDIHFGNIQQINDDGSRRIT
	1			1	1	IVENVGSVEGLAYHRGWDTLYWTSYTTSTIT
		1		1		RHTVDQTRPGAFERETVITMSGDDHPRAFVL
-			1		1	DECONLMFWTNWNEQHPSIMRAALSGANVL
	}	- 1		1	1	TLIEKDIRTPNGLAIDHRAEKLYFSDATLDKIE
				1		RCEYDGSHRYVILKSEPVHPFGLAVYGEHIF
	- 1	1	1	1		WTDWVRRAVQRANKHVGSNMKLLRVDIPQ
	}	- 1		1		QPMGIIAVANDTNSCELSPCRINNGGCQDLCL
		Ì	1	l		LTHQGHVNCSCRGGRILQDDLTCRAVNSSCR
- 1 '	1	 .		1		AQDEFECANGECINFSLTCDGVPHCKDKSDE
1	1	- 1	1	1		KPSYCNSRRCKKTFRQCSNGRCVSNMLWCN
- [1		1		GADDCGDGSDEIPCNKTACGVGEFRCRDGTC
				1		IGNSSRCNQFVDCEDASDEMNCSATDCSSYF
L						

						· · · · · · · · · · · · · · · · · · ·
000 70	epo m	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	denoc	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uaia	l	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
)	1	peptide		nucleotide insertion
		1	l	sequence		RLGVKGVLFQPCERTSLCYAPSWVCDGAND
		1			, .	CGDYSDERDCPGVKRPRCPLNYFACPSGRCIP
	1	1	1			MSWTCDKEDDCEHGEDETHCNKFCSEAQFE
	1	ì	i	l .		CONHRCISKQWLCDGSDDCGDGSDEAAHCE
	ł	1		į		GKTCGPSSFSCPGTHVCVPERWLCDGDKDCA
		l		1	1	DGADESIAAGCLYNSTCDDREFMCQNRQCIP
		Į		}		KHEVCDHDRDCADGSDESPECEYPTCGPSEF
	1	1	1	1	1	PCANGROLSSROWECDGENDCHDQSDEAPK
			ì		-	NPHCTSPEHKCNASSOFLCSSGRCVAEALLCN
	1	1	1	1	1	I CODDCGDSSDERGCHINECLSRKLSGCSQDC
}	1	1	Ì	1		EDI KIGFKCRCRPGFRLKDDGRTCADVDECS
!	1	1		1	1	TTFPCSORCINTHGSYKCLCVEGYAPKGGDP
1	1					HSCKAVTDEEPFLIFANRYYLRKLNLDGSNY
1		1	}	1 .		TLLKOGLNNAVALDFDYREQMIYWTDVTTQ
(1	-	1	1	,	GSMTRRMHLNGSNVOVLHRTGLSNPDGLAV
· ·		1		1		DWVGGNLYWCDKGRDTIEVSKLNGAYRTVL
ł	1	1	1		Í	VSSGLREPRALVVDVQNGYLYWTDWGDHSL
	1		1	1	1	IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTE
1				1		RIYWADAREDYIEFASLDGSNRHVVLSQDIPH IFALTLFEDYVYWTDWETKSINRAHKTTGTN
	1	- [i		KTLLISTLHRPMDLHVFHALRQPDVPNHPCK
Ì		1	-	[1	VNNGGCSNLCLLSPGGGHKCACPTNFYLGSD
1	1	ł	i	ì		GRTCVSNCTASQFVCKNDKCIPFWWKCDTE
Ì		1	1		Ì	DDCGDHSDEPPDCPEFKCRPGQFQCSTGICTN
	1			l		PAFICDGDNDCODNSDEANCDIHVCLPSQFK
		1	1	-		CTNTNRCIPGIFRCNGQDNCGDGEDERDCPE
{				1		VTCAPNOFOCSITKRCIPRVWVCDRDNDCVD
	1	ì		l		GSDEPANCTOMTCGVDEFRCKDSGRCLPARW
		1	1	1		KCDGEDDCGDGSDEPKEECDERTCEPYQFRC
			Ì]		KNNRCVPGRWQCDYDNDCGDNSDEESCTPR
1			l	ł	}	PCSESEFSCANGRCIAGRWKCDGDHDCADGS
		j		1.		DEKDCTPRCDMDQFQCKSGHCIPLRWRCDA
	1 .	1	.1	1		DADCMDGSDEEACGTGVRTCPLDEFQCNNT
ĺ		1		1.		LCKPLAWKCDGEDDCGDNSDENPEECARFV CPPNRPFRCKNDRVCLWIGRQCDGTDNCGD
	- [-	1			GTDEEDCEPPTAHTTHCKDKKEFLCRNQRCL
1	1	1		İ		SSSLRCNMFDDCGDGSDEEDCSIDPKLTSCAT
1		1	1	1		NASICGDEARCVRTEKAAYCACRSGFHTVPG
1		- 1	1			OPCCODINECT REGTCSOLCNNTKGGHLCSC
		1				APNEMKTHNTCKAEGSEYOVLYIADDNEIKS
		- I			1	I EDGLIPHS A VEO A FOODES VRIDAM DVH V KA
		- 1			·	CONVINTAIWHTGTISYRSLPPAAPPITISNKAK
1	1	i	1	[ļ	POIDEGVTHI NISGI KMPRGIAIDWVAGNVY
	-	1	1	l	1	WTDSGRDVIEVAOMKGENRKTLISGMIDEPH
1	1					AIVVDPLRGTMYWSDWGNHPKIETAAMDG
1				- 1	1	LRETLYQDNIQWPTGLAVDYHNERLYWADA
1]	1	1		KLSVIGSIRLNGTDPIVAADSKRGLSHPFSIDV
1		1	1	1	- [FEDYTYGVTYINNRVFKIHKFGHSPLVNLTGC
		-				LSHASDVVLYHQHKQPEVTNPCDRKKCEWL
		- 1				CLLSPSGPVCTCPNGKRLDNGTCVPVPSPTPF PDAPRPGTCNLQCFNGGSCFLNARRQPKCRC
		1				QPRYTGDKCELDQCWEHCRNGGTCAASPSG
		- 1				MPTCRCPTGFTGPKCTQQVCAGYCANNSTC
1		1	ì			VNQGNQPQCRCLPGFLGDRCQYRQCSGYCE
1	- 1	į		}	ł	NFGTCQMAADGSRQCRCTAYFEGSRCEVNK
1	1	- 1		ı		CSRCLEGACVVNKQSGDVTCNCTDGRVAPS
		ļ		1		CLTCVGHCSNGGSCTMNSKMMPECQCPPHN
l l	- 1					TGPRCEEHVFSQQQPGHIASILIPLLLLLLLVL
- 1						
		l	1			LVACVVEWYKRRVOGAKGFOHORMINUAM
						VAGVVFWYKRRVQGAKGFQHQRMTNGAM NVEIGNPTYKMYEGGEPDDVGGLLDADFAL

NO: of NO: of hod ID NO: beginning nucleotide D=Aspartic Acid, E=((A=Alanine C=Cysteine, Glutamic Acid,
NO: 01 NO: 01 not 15 NO: 05 NO: 01 NO	
	Glycine, H=Histidine,
nucl- peptide in indeceded to the peptide V-I amin	ne. L=Leucine.
entide Seg- OSSIV Ideation The Advantage No. 10	sparagine P=Proline.
sen- uence Usings Contespond Contespon	vinine S=Serine
1914 ng to first acid residue Columnia, x	ine W=Tryntonhan
1 1 1 Minio 40-0 1 == 1 1 1 = 1 4 4 7 1 1	noum *=Ston codon
1 conduct control of the control of	deletion \=nossible
peptide /=possible nucleotide	defendit, —possible
sequence nucleotide insertion	ATLYMGGHGSRHSLASTD
DPDKPINFINPVY	AILIMOONOSCIBLASID
EKRELLGRGPEDE	IGDPLA
374 1724 A 3187 191 1815 CLELASAGKIPEES	KALSLLAPAPTMTSLMPG
AGIL PIPTPNPLTT	LGVSLSSLGAIPAAALDPNI
ATLGEIPQPPLMGI	NVDPSKIDEIRRTVYVGNL
NSQTTTADQLLEF	FKQVGEVKFVRMAGDET
QPTRFAFVEFADQ	NSVPRALAFNGVMFGDRP
I I I I I I I I I I I I I I I I I I I	PEMTPOAAAKELEEVMKR
VREAOSFISAAIEP	GWLHSTSLCNDFLGCF*RR
	TFHLCLINWDL*LF*AYTA
K*FFPPRVWKEO*	KKRR\RSRSHTRSKSRSSSK
	RSRSHNRSRSROKDRRRSK
SPHKKRSKSRERR	KSRSRSHSRDKRKDTREKI
KEKERVKEKDREI	KEREREKEREKERGKN
	KDKEKDREREREKEHEKD
PDKFKEKFODKE	KEREKDRSKEIDEKRKKUK
VSRTPPRSVNASR	RSRSSSRERRRRRSRSSSRS
PRTSKTIKRKSSRS	SPSPRSRNKKDKKREKERD
HIGEPPERENTS	MRKSSNDRDGKEKLEKNST
S HISERCERCIOS.	
TARGOLOGICA AT OF	FQWDIIRHPPL\SPNLALSG
375 1725 A 3192 415 101 AHSSHQTRAILQE	HFSSVKK\TTLTWLNSQDP
W. W	PSSFRNGLNDWYHHSQKC
	1 331 KHODHO / 11215 (
PDLDGAYVKK	PPPGFKQFCLGRSSSWDYR
376 1726 A 3199 931 418 GV*WCDLGSPQP	ETGFLHAGQAGL\GDPPAS
	TWPKNHLIFYACLVIRSKRI
	WPKINIER TACEVICORE
K K	POSSIDSELSTSELEDDSISM
377 1727 A 3201 274 1285 KTGYTSRGSPLSP	OSSIDSELST SELECTED SISM
1377 [313] 1 [[GVKLODLIDVON	MARLQEESLRQDYASTSAS
VSRHSSSVSLSSG	KKGTCSDQEYDQYSLEDEE
EFDHLPPPQPRLP	RCSPFQRGIPHSQTFSSIREC
RRSPSSQYFPSNN	TYQQQQYYSPQAQTPDQQP
NRTNGDK/PPKK	YA*PSPDAKYNCH**QH\SSP
VTVRNSQSFDSSI	LHGAGNGISRIQSCIPSPGQL
QHRVHSVGHFPV	/SIRQPLKATAYVSPTVQGSS
NMPLSNGLQLYS	ENTGIPTPNKAAASGIMGRS
ALPRPSLAINGSN	ILPRSKIAQPVRSFLQPPKPL
SSI STI.RDGNWR	DGCY
378 1728 A 3202 112 1789 VPGVTESRPSVLI	RGDHLFALLSSETHQEDPIT
378 1728 A 3202 112 VKGEVHKVELD	RVKLSFSMSLLSRFVGWG*
PEKVNEY/TENRO)PLRV\OHRALELTGRWLLW
DATED VAPROVI	PLLPSDVKLKLYDRSLESNP
	TTRPAPYIIFGPPGTGKTVT
I VEATKOVVKHL	PKAHILACAPSNSGADLLC
OPI PVHI PSSIVE	RIJAPSRDIRMVPEDIKPCCN
N/DAKKGEVVFP	AKKKLOEYRVLITTLITAGK
I VSAOFPIDHFTI	HIFIDEAGHCMEPESLVALAG
I MEVKETGDPGC	GOT.VLAGDPROLGPVLKSPL
TOKHGLGYSLLE	ERLLTYNSLYKKGPDGYDPQ
TOKNOLO I SEDIL	PTILDIPNQLYYEGELQACA
PATABEBECOM	AGILPROGFPIIFHGVMGKD
DVVDRERICKW	EEAATVTSYLKLLLAPSSKK
EREGNSPSFFNF	/ISPYRKQVEKIRYCITKLDR
GKARLSPRSVGV	AND TANKA BUTE TO VILLED IN
ELRGLDDIKDLK	VTCCSTVTPCLPCAPTCPLP
ETSSSFHSSPRPR	PTPAALNRARALPEPLTPGD
SNLRVWDGIRKI	PACTINIOCUS
370 1729 A 3206 432 130 PKAAPSVXLWFI	PPFL*GSFKPTKGHTXCVXIK GRQIAXXRQGGKVETTTAL
379 1729 A 3206 432 130 FRAM SYNCHIA	CODIAXXXXIXXXXXXXXXIIIAL

				3 10 1 1	Deadigted and	Amino acid sequence (A=Alanine O=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	}	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
1	Į.		l i	residue of	sequence	/=possible nucleotide deletion, \=possible
	Į.		1	peptide		
		l l		sequence		nucleotide insertion
	 	 	 			XKQSNNKGTRASSYXEPDAXEQWKFPHKKL
1	1	1	1	ľ		QLPGXTHE
	1020	A	3207	187	507	GGTGHPHPARPPLSGVGGCQCSHSKPWTAGS
380	1730	l A	3201	107	1	PEQRDHPAPHKQIEAGQGLPGPQAWGG*KGP
	1	1		j	1	AXLLPGPGGGPGPVASLEARAQASSGVTPNG
İ	1	1				GGRTYPYPTFSSGE
			1	ļ	840	GTRPGHT.PAPSDGFCV/HL*SIPSWGSF*GESL/
381	1731	A	3225	1	040	EMQLITSLGLQEFDIARNVLELIYAQTLVWIGI
ł		1		l	1	FFCPLLPFIQMIMLFIMFYSKNISLMMNFQPPS
1		1	1			KAWRASQMMTFFIFLLFFPSFTGVLCTLAITI
1	ì		1			WRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRP
	1	1	, .	1		GYLWYVWIYRNLIGSVHFFFILTLIVLIITYLY
1	1	1	l l		1	WQITEGRKIMIRLLHEQIINEGKDKMFLIEKLI
	1 '	1	1	1		WOLLEGKKIMIKETHEOIINEOKEKALPHICE
1	.]	ŀ	1	1		KLQDMEKKANPSSLVLERREVEQQGFLHLGE
		·]	ļ		HDGSLDLRSRRSVQEGNPRA
382	1732	A	3238	256	38	LLMIKVSSTCFSCHLHHHHHHHHHHHHQGHNS
302	1752	1	1			LFFSLKSSSNSSTLPVYLSYNIILVFSKCLVFDF
1	1	1	}			LFSNACL
- 000	1733	A	3241	1542	343	KGAPSFVRLYQYPNFAGPHAALANKSFFKAD
383	1/33	A	3241	15.2		KVTMLWNKKATAVLVIASTDVDKTGASYYG
	1	1	1			FOTT HYIATNGESAVVOLPKNGPIYDVVWNS
	}	1	1	ł	1	SSTEECAVYGEMPAKATIFNLKCDPVFDFGTG
	i		1			PRNAAYYSPHGHILVLAGFGNLILQI*AD/IMK
1	ŀ		l	1	Ì	VWNVKNYKLISKPVASDSTYFAWCPDGEHIL
	1		į.	1	Į.	TATCAPRIEVNNGYKIWHYTGSILHKYDVPS
	}	}	1	ł	ł	NAFI WOVSWOPFLDGIFPAKTITYQAVPSEVP
1	1	1	1	1	1	NEEDKVATAYRPPALRNKPITNSKLHEEEPPQ
Ì	ļ	1	Į.	İ	1	NMKPOSGNDKPLSKTALKNORKHEAKKAAK
1	1	- 1	l.			QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP
ŀ	1	ŀ	1			EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK
	ļ	1				NQLEKIQKETALLQELEDLELGI
					1	IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP
384	1734	A	3242	3	678	RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP
		- 1		l .		LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS
	1	1	ł		1	ASLVRATVRAVSKRKLQPTRAALTLTPSAVN
ı	1	1	- 1	l	J	ASLVRATVRAVSKRALQFIRAALILITORVI
1	1	ı	- [{		KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL
1		1	1			EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL
ļ	l l		1	ł		GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES
						FNI
205	1725	A	3243	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL
385	1735	^	3273	1		KEERIL PEPGSETPTVASEALAELLHGALLKK
		-		1	1	GPEMGYLPGPPLGPEGGEEETTTTIITTTTVTT
				1		TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL
1		-1		1	1	GLI DCTYSIHVYPGYGIEIOVOTLNLSQEEELL
	1	1		1	}	VI AGGGSPGLAPRILANSSMLGEGOVLRSPI
	1	l	1	1		NIRT I I HEOSPR VPRGGGFRIHYOAYLLSCGFP
	-					PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG
	- [1	FETLICLNGTRPSWNGETPSCMASCGGTHNA
			- 1			TIGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL
1	1	1	i	1	1.	HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS
1	1	- {	i	1		DMDDVPERGLISDAQSLYVELLSETPANPLLL
				-{	1	SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG
	1	ļ		1		ALATFSCLPGYALEPPGPPNAIECVDPTEPHW
			1			ALATIBULITUT ALEFTUTTINATEUV DI TETTI
	ł	l	1	1		NDTEPACKAMCGGELSEPAGVVLSPDWPQS
1	1			1		YSPGQDCVWGVHVQEEKRILLQVEILNVREG
	ļ	1		1	1	DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS
	1			1		GPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPR
	-		.			MOTOPEL PPPEWGWRTASHGDLIKG I VL I I Q
	1			1		CEPGYELLGSDILTCQWDLSWSAAPPACQKI
L						

					W 19 4 4 4 4 4	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, c-Clusing H-Vistiding
nuci-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	Į .	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
401.00				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
· ·	1	ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	ĺ	ļ	1	peptide		/=possible nucleotide deletion, \=possible
١.			1	sequence		nucleotide insertion
				sequence		MTCADPGEIANGHRTASDAGFPVGSHVQYRC
1	1	1	ł	1	[LPGYSLEGAAMLTCYSRDTGTPKWSDRVPKC
ì	Ì		ŀ	ţ	1	ALKYEPCLNPGVPENGYQTLYKHHYQAGESL
ŀ	Į.	l	1	1	ł	RFFCYEGFELIGEVTITCVPGHPSQWTSQPPLC
1	1	ľ	ł	ì	İ	KIPC I EGYELIGEVIII CVFOIL SQW I SQITEC
ŀ	l	1				KVTQTTDPSRQLEGGNLALAILLPLGLVIVLG
}	1	Į.		ļ		SGVYIYYTKLQGKSLFGFSGSHSYSPITVESDF
	j					SNPLYEAGDTREYEVSI
386	1736	A	3250	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDT
300	1,,50	1	3			RKLLMTWALEVAVVMKKSETYAPLFCLPSF
1	1	1		1	ļ.	HKFCKGLLADTLVEDVNICLQACSSLHALSSS
1	1	1		ł	l	LPDDLLORCVDVCRVQLVHRGTCIRQAFGKL
} ']	1	1	1	1	LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP
j .		1		1	i	SNTFHPQDFSD/VISFILYGNSHRTGKDNWLE
		1	1	l	1	RLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
1	1	1	1	J		AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIR
1	1	1	1	1		SLAGHTLNPDQDVSQWTTADNDEGHGNNQL
	1	ì	ì	1	1	RLVLLLQYLENLEKLMYNAYEGCANALTSPP
	ì				1	KVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLA
1	1	1	1		1	KVIKITLY INKQICQDWLIKIKLSIMIK VODEN
	 .			1	•	GOPAVTVRHGFDLLTEMKTTSLSQGNELEVSI
1	1	1			ł	MMVVEALCELHCPEAIQGIAVWSSSIVGKHL
1	1	1	1		{	LWINSVAQQAEGRFEKASVEYQEHLCAMTG
		1				VDCCISSFDKSVLTLASAGCKSASLKHCLNGE
1	1				i	SRKSVLSKPTDSSPEVINYLGNKACECYISTA
į.	1	j				DWAAVQEWQNAIHDLKKSTSSTSLNLKADF
1	1	1.		}	ł	NYIKSLSSFESGKFVECTEQLELLPGENINLLA
		1	1		ì	GGSKEKIDMKKLLRNM
202	1737	A	3255	380	76	MDIFLYNCKYQVQTEI*NSIQHIMA\SKKLSRF
387	1/3/	^	3233	300	1 "	LKYVHNL*AENYKTLMK*INEDLNKQRDVPY
1				Į.		S*TARLNKMSIPTKTIFRFKAIYIKIPATYFIET
1	1	1	1]	NMO
L					400	PQWLGLQVYALPPANFVFFVEMRSTILAQTG
388	1738	A	3260	685	428	FELLDSSDLPASASKSAGITCMSHHARTLSLK
	-		İ			PELLUSSULFASASKSAGIICMSIIITAKI LODIK
1						*WPFCLSATQEKFC*PASEGVAW
389	1739	A	3269	1	332	LDGYHTPIYMLNRIIRLPAAL*IISDQTGHALTI
1	i	1	i	ı		LTRLETQMINADYQNKLTLDYLLTTDREVYE
	ŀ	1			1.	PFNLTNYCLHIHNQRLGAYDLG*V*Q/KLAHV
	1				1	PVQV*HGFDPEAMFR
390	1740	A	3270	2	372	GRCHDQNKGKS\DGPDAQAEACGGESTYQEL
3,70	1,70	1.,	1 "	\		LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH
1	1	1		1	1	SPRGVKKVHKFVNKGEKGIMVLAGDTLGIGV
1		1		1	1	YCLLPCMC*DRKLTYAHIPSTTDLGAGAGY
-	- 1541	+	2002	1	187	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ
391	1741	Α	3273	1.	107	HVETFFQ\EELTRSQEGMKLGENFLMFAMPP
]	J	1	1	1	DDSKESKGK*FFQEMLDIMKAISDMMGKCTY
1	1	1			1	PVLKEDAPRQHVETFFQVGINQKSRGHEVRR
1	1	1	1		1	
١ .	1	1.	L	1		KFPDVCHAPR
392	1742	A	3281	901	521	FFFGDGVSPCRQAGV*WHDLDSLQNLPPGFK
			1		1	RFSYLSLPSSW\DYRHVLPRQANFCIF/M*RRG
1		1	1		1	FTMLARMVSIS*PRDLPALASQSAGITGVSHH
1	1	1	1	1	Í	APPOMDFTFALLCFALKGCLPRQKEGGTLNLI
393	1743	1 _A -	3283	385	3	RNRSVVPEFVLLGLSAGPQTQTLLFVLFVVIC
373	1 1 1 4 3	1^	1 3203	1 303	1	LLTVMGNLLLLVVINADSCLHTPMYFFLGQL
1	1		1	}	1	SFLDLCHSSVTAPKLLENLLSEKKTISVEGCM
1	1		1			A*VFFVFATGGTESSLLAVMAYDRYVAIRTR
1			1	1		
					<u> </u>	G
394	1744	A	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYLHLGKC
		1				LDNCPEGLEANNHTMECVSIVHCEVSEWNP
1	1	1		1		WSPCTKKGKTCGFKRGTETRVREIIQHPSAKG
1	1		i		1	NLCPPTNETRKCTVQRKKCQKGERGKKGRE

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteme, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	
eotide	seq-	l	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1	l		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	i	1	residue of	sequence	/-possible nucleotide deletion, \-possible
1		l	ì	peptide		nucleotide insertion
				sequence	 	RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN
		1	1	,		KQQQ
	<u> </u>	<u> </u>		<u> </u>	340	RVLYVPSMGFCILVAHGWQKISTKSVFKKLS
395	1745	A	3286	1	340	WICLSMVILTHSLKTFHRNWDWESEYTLFMS
		ì		1	1	ALKVNKNNAKLWNNVGHALENEKNFERAL
	1					KYFLOATHVOPDDIGAHMNVGR
	I	ļ	2002	1	172	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL
396	1746	A	3293	1	11/2	IAFMKORRMGLNDFIQKIANNSYACKQ
		 	2005	12	401	AFPACGASSCTPPSLRSSSSOSVGPLRPGRPL
397	1747	A	3295	1 12	1401	WSEACAFL*AAAPOGPASPCCGLPSGFPRVW
	1		1	ł	1	AOCCPPGGALRFPEGLGSVLSPRRCPQVSRGS
		1		1		GLSAVPQEVPSGFLGPGLRACPQEAPSRFLRA
	1		1			GLT
	1	+	3300	1912	2768	KORRWONIORKGPKRYTVIAGNSQSHQPMIFS
398	1748	A	3300	1912	1,00	MIRKLPKVTCRDVLPEIRAICIEEIGCWMQSY
1	1	1	1	1		STSFLTDSYLKYIGWTLHDKHREVRVKCVKA
İ	ļ	1	ļ	i	1	LKGLYGNRDLTARLELFTGRFKDWMVSMIV
1	1		1	1		DREYSVAVEAVRLLILILKNMEGVLMDVDCE
	1	ŀ			.]	SVYPIV*ASN*GLASAVGEFLYWKLFYPECEI
	1	1	1	!		RTMGGREQRQSPGAQRTFFQLLLSFFVESKSH
1		l		ì	1	SVTOAGVOWOFSAHRDLCLPGSSNSHVSASK
}		1		1	l	VAGIAGAHRHTWLIYVFFSWRQGFAVLAGL
		1	1			VSNS
200	1749	A	3301	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSE
399	1/49	1 ^	3301	1 550		SPPPITDSWAPFISLTHHVLSQSQSPLSSNCWI
	1	1	1	1		CLSTHTQ*FTALPADLLTWTQSNVSLHISYLAI
}	ł	1	ľ	į		PFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
1	1	İ				GRAVALLHLIASGLTSIQTNTASSKPPIWGYL
	}	ŀ			1	STQTSFISPPPLCLSRTYPNPAHATMVGQVPQ
		i				SLCGLIFTL/RTPCRPSILHPNYKIISTSAWQKV
	1			ļ	· ·	LCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAAN
		- 1		j		SALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGS
İ			1	ì	1	N/RLTVDKDNFFLSPKPNSLHQLPSQ\TPYQAL
1		Ì		1		TGAALAGSYPIWENENTLSWLPTFTYNFCLST
			ì		Ì	PSLFFLCDTN*YLCLPANWSGTCTLVFQAPTI
]	ļ	ļ	Ì	ł	l .	NILPPNQTILISVEASISSSPIRNKWALHLITLLT
	1	1				GLGITAALGTGIAGITTSITSYQTLFTTLSNTVE
		i			Ì	DMHTSITSLQRQLDFLVGVILQNWRVLDLLT
		- {	1			TEKGGTCIYLQEECCFCVNESGIVHIAVRRLH
1	Ì		İ			DRAAEL*HQVADSWWQGSSLLRWIPWVAPF
1	1	- 1		1	1	LGPLIFLFLLLMIGPCIFNLVSRFISQRLNCFIQ
		1	İ	1		ASMQKHIDNIFHLCHV*YQSLRGNHSEAPEPR
	1	İ	1			P THWRHSSGVPGSTTARRRRELEIATSDNQE
400	1750	A	3303	2	453	THWRHSSGVPGSTTAKKRRRELEIATSDAGE YYNRLCQEVTNRERNDQKMLADLDDLNRTK
		1				YYNRLCQEVINKERNDQRMLADDDDLAKKI KYLEERLIELLRDKDALWQKSDALEFQQKLS
}						AEERWLGDTEANHCLDCKREFSWMVRRHHC
1	1 .	- 1		1		RICGRIFCYYCCNNYVLSKHGGKKERCC
1	}	}	L			MAPQHSSLDDKVPQQASTVCFEFQDILQHSQ
401	1751	A	3304	1	626	CTEHKDSLWGPGARSQPFGAHNTRLSPDSCP
						EKIVLRALKDSRAGMPEQDKDPGVQENPDD
		i	1	-		QRRVPQGTGDAPSAFRPLWDNGGLSPFVSRP
{	i	- 1	{			GPLERDLHAQRSEVTYNQRSQSSWMSSFPKR
	1	1		1		NAFVSPYSSMGQAQP/GLPKTNPIGESCCWEG
		ļ	1			LSLSTQILG*QKPSKYIPSLCKR
1	1	1	1	L		MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA
402	1752	A	3305	1678	172	WELLARGE THE BLEE CHECKE ASCAL BUSINESS AND LA
1.00						PVGFCLLVLRLFLGIHVFLVSCALPDSVLRRF VVRTMCAVLGLVARQEDSGLRDHSVRVLISN
	1		Ì		1	HVTPFDHNIVNLLTTCSTVSESEAESATGRFP
		l				HVIPPUMNIVNULLICSIVSESEALSAIGRI

					Daniel and and	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spartic Acid. E=Glutamic Acid,
iO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence		١.	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}		i	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Soquonee	/=possible nucleotide deletion, \=possible
. 1		1		sequence		nucleotide insertion
	 	 	 	sequence	ļ	GAOLKAPLSPLAFRMEDTEALPLTPILYPTCQ
	1	ł	İ	٠.		FFFF/IFI NIFI LAFSSPGSOPLLNSPPSFVCWSR
	ļ	i .		ŀ	1	GFMEMNGRGELVESLKRFCASTRLPPTPLLLF
	1			l	1	PREFATNGREGLLRESSWPFSIQDVVQPLTLQ
	ļ	1	Ì	1	1	VQRTLVSVTVSDASWVSELL\WSLFVPFTVY
	1	1	1			QVRWLRPVHRQLGEANEEFALRVQQLVAKE
		1		1		LG\QTGTRLTPA\DKAEHMKRQRHPR\LRPQS
	1	1		t		AQSSFPPSPWVLSS/SDVQTGQTLGFREFKESF
		\				CPHVAIGVFIPERPWPKTGCCKTLTIHLILL+G
		1		1		GPVSFSCPE\DIHPRGT*VPTQQASGLPSFPSYC
	İ		1	İ		PARGGVL*HPSAQQPLTFAKSS\WARAGRAL
	ì		İ	1		QERKQ\ALYEYARRFTERRAPGGLD
403	1753	A	3307	44	447	DPSPSLLAVALGLRAGERTRSGPGSSSPSGGIS
403	1,,55	1	1.			GGASAGLASSPECACGRSHFTCAVSALGECT
		1	}		}	CIPAQWQCDGDNDCGDHSDEDGCILPTCSPL DFHCDNGKCIRRSWVCDSDNDCEDDSDEQD
		1			1	
		1				PRHGWGRRVLGRDRPRLQKVKKSVKAIYIPG
404	1754	A	3311	409	1	QDHVQNEEIYARVLDKFGSNFLSRDNADLGT
	1			1		AFVKFSTLTK*LSALLKNLLQGLSRNVIFTLD
	1	1	1			LLKGDLKGVKGDLKKPFDKAWKDYETKFAI
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	l				150	AAVPVENPWDDPRVRPRVRIFTWEDCIAGQA
405	1755	A	3322	12	458	KVI CNDSYGVTIDWSPKGAFIRLTSQSVGNG
		1		ì		HPASKENDOMVDTIKNTTKVPIIWTYGDMVI
		1		ì	ŀ	PRPOMIRPAVGAKHKELWKILMALKKIKUW
	1	1		ì	\ .	GKYTKPSOYNPNYMLELAHNDSVW
			3324	1	426	I SMI STISTEHRLSVLWPIWYCCHCPTHLSA
406	1756	A	3324	1.	1.20	MCVILWALSLLOSILEWMFCSFLFSDVDSDN
	1	1	\ ·			WCOTLDFI.TAVWLIFLI\LVLCGFTLVLLVKII
						GSQKMPLTRLYVTILLTGLVFLFCSLPLSIQ*
		1	- 1	1		LLYWIEKDLDDL
407	1757	+	3328	213	1841	SGDLSPAELMMLTIGDVIKQLIEAHEQGKDII
407	1,3,	1				LNKVKTKTAAKYGLSAQPRLVDIIAAVPPQY
			1	1		RKVLMPKLKAKPIRTASGIAVVAVMCKPHR
	ł			1		PHISFTGNICVYCPGOPDSDFEYSTQSYTGYE
	İ	1			İ	TSMRAIRARYDPFLQTRHRIEQLKQLGHSVL KVEFIVMGGTFMALPEEYRDYFIRNLHDALS
	1	-	Į	İ		GHTSNNIYEAVKYSERSLTKCIGITIETRPDY
		-		1	}	MKRHLSDMLTYGCTRLEIGVQSVYEDVARL
	1		1		Ì	TNRGHTVKAVCESFHLAKDSGFKVVAHMM
		1	1	ì	1	DLPNVGLERDIEQFTEFFENPAFRPDGLKLY
ĺ		- 1		1	1	TLVIRGTGLYELWKSGRYKSYSPSDLVELVA
	j	-	1	1		RILALVPPWTRVYRVQRDIPMPLVSSGVEHO
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Į	1	ì	1	1	1.	DODII IGI I RI RKCSEETFRFELGGGVSIVKE
	1	- 1		1		HVYGSVVPVSSRDPTKFQHQGFGMLLMEEA
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		- 1		I		OCDAMAKWI'K
		-	ł		1	ALASPRAAGIRHELTSTMAAGKNKRLTKGG
					167	I AIASPRAAGIRHELISIMAAGIAGIAGIA
408	1758	A	3335	3	467	KGAKKKAV/DNIINIGKTLVTRTQRTKIASDQ
408	1758	A	3335	3	467	KGAKKKAV/DNIINIGKTLVTRTQRTKIASD
408	1758	A	3335	3	467	KGAKKKAV/DNIINIGKTLVTRTQRTKIASDO LKGRVFEESLADLQND\TDGYLLRVI*VAFT FRTNOI/REVFNKLIPDSIGKDIEKACQSIYPL
408	1758	A	3335	3	467	KGAKKKAV/DNIINIGKTLVTRTQRTKIASDU LKGRVFEESLADLQND\TDGYLLRVI*VAFT ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPL DDF4RKVKMLKKPKFELRKLMELHGEGSS
408						KGAKKKAV/DNIINIGKTLVTRTQRTKIASDU LKGRVFEESLADLQND\TDGYLLRVI*VAFT ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPL DDFARKVKMLKKPKFELRKLMELHGEGSS
408	1758	A	3335	7	1252	KGAKKKAV/DNIINIGKTLVTRTQRTKIASDO LKGRVFEESLADLQND\TDGYLLRVI*VAFT ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPL DDFARKVKMLKKPKFELRKLMELHGEGSS PRWRNSARDEILLSFPQNYYIQWLNGSLIHG WNI ASLESNI.CLFYLMPFAFFFLESEGFAGL
						KGAKKKAV/DNIINIGKTLVTRTQRTKIASDU LKGRVFEESLADLQND\TDGYLLRVI*VAFT ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPL DDF4RKVKMLKKPKFELRKLMELHGEGSS

			one -	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	1	1		sequence	1	nucleotide insertion
	 			Soquence		LLLCTPVGL\SRMFTVMGQLLVKPTILEDLDE
			ļ			QIYIITLEEEALQRPTKWAVFIRW/KYNIMELE
		1		[Į.	QELENVKTLKTKLERRKKASAWERNLVYPA
	1					VMVLLLIETSISVLLVACNILCLLVDETAMPK
1	ļ.	ł	'			GTRGPGIGNASLSTFGFVGAALEIILIFYLMVS
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1		l	1		ŀ	ILVLSSALPVMSRTLGITRFDLLGDFGRFNWL
		1				GNFYIVLSYNLLFAIVTTLCLVRKFTSAVREE
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410	1760	A	3339	127	1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLL
""	1					WLALACSPVHTTLSKSDAKKAASKTLLEKSQ
1	'	1		1	1	FSDKPVQDRGLVVTDLKAESVVLEHRSYCSA KARDRHFAGDVLGYVTPWNSHGYDVTKVFG
		l .	1	1		SKFTQISPVWLQLKRRGREMFEVTGLHDVDQ
	1	1	1	İ	İ	GWMRAVRKHAKGL\P*CLGSCLRTGLTMISG/
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		1		1	ľ	ALLVIPPAITPGTDQLGMFTHKEFEQLAPVLD
		1		Į.		GFSLMTYDYSTAHQPGPNAPLSWVRACVQV
Ì	,		1	1	1	LDPKSKWRSKILLGLNFYGMDYATSKDAREP.
1		1		ļ		VVGARYIQTLKDHRPRMVWDSQVSEHFFEY
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		l	1 2240	74	2701	PWSE VATRKLAKGFTOFAKMTEGTKKTSKKFKFFK
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATODDMYTVPKSPPAYARSSDMYSHMGTM
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAONSOAAROAOEAGPKPNLVPGGV
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMYTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE FLKLSSTDLRSHAWYHGRIPREVSETLVQRN
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIOYLFEQESFDHVPALVRY
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDVVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HYGSRKAYSEOSGAIIYCPVNRTFPLRYLEAS
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGOGSSKPASPVSPSGPKGSHMKRRSVTM
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDOIPDLHSPMSPISESPSSPAYSTVTRVHA
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCFVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA ADAAPSATALPASPVARRSSEPOLCPGSAPKT
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCFVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGFKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPPDSIRSCA LSMDQIPDLHSPMSPISESPSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCOLOPPVRGSREWAATETSSOQARSYGE
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCFVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSTHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE PLKELSFNGAPEGDWGKTFTVPIVEVTSSFNP
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HOESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATEOSI LIPRDNRPLEVGLLRKVKELLAEVDA
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCOLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMEILTTPHGRKKLRLDLLERFHTMSIML
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAITYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR OPHTEGAILYFKKLKFFLKSLNEGKEGPPLSN
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCFVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCFVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV
411	1761	A	3342	74	2701	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HOESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FOARPELLEVFSTEFOMRLLWGSQGASSSQA
411	1761	A				PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHG\RKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA PRYPKEDKYLTALSHKLEFAVRSSEL
411	1761	A	3342	74	898	PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGFKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCOLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL
						PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYBKFDKVLTALSHKLEPAVRSSEL IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI I PDTI HI I PDRDNDKSLROFFYTFOACL*ELL
						PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYBKFDKVLTALSHKLEPAVRSSEL IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI I PDTI HI I PDRDNDKSLROFFYTFOACL*ELL
						PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAITYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL
						PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAITYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAVWGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL KRLCNRTALMFVAVAGLTFFALSFGFYYEYG WFFLEHTYFYHLTRRDIRHNFSPYFYMLYLT
						PWSE VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAITYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL

SEQ ID NO: of nucl- eotide. seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide insertion VMPLVRMPWKRAVVLLMLWFIGQAMWLAP AYVLEFQGKNTFLFIWLAGLFFLLINCSILIQII SHYKEEPLTERIKYD PIPVRWNSLEGRLLRGYEQHANDGKDYISRN *DLRSWTAADMAAQITKRKWEAEEFAEQIKA
	,					YLEGTCVER/LRTHLENGKETLQLTEQSSQPTI PIVGIVAGLVLLGAVVTGAVVSAVMCRKKNS GHFLPTDRVSYSEAASSDHAQGSDVSLTACK V
414	1764	A	3363	1488	453	HQILELKKKILKTYNPDYDEDLVQEASSEDVL GVHMVDKDTERDIEMKRQLRRLRELHLYST WKKYQEAMKTSLGVPQRERDEGSLGKPLCP PEILSETLPGSVKKRVCFPSEDHLEEFIAEHLP EASNQSLLTVAHADAGTQTNGDLEDLEEHGP GQTVSEEATEVHMMEGDPDTLAELLIRDVLQ ELSSYNGEEE\DPEEVKTSLGVPQRGDLEDLE EHVPGQTVSEEATGVHMMQVDPATLAKSDL EDLEEHVPEQTVSEEATGVHMMQVDPATLA KQLEDSTITGSHQQMSASPSSAPAEEATEKTK VEEEVKTRKPKKKTRKPSKKSRWNVLKCWD IFNIF
415	1765	A	3369	431	315	IPWSWVGRLSVRKMSILF*LTYNYNAILNKTP PSFSPSL
416	1766	A	3373	42	651	RQEKMGLGEIGASGVLRSMLKERKKQNMKG NGNVTLTPLLPAVQCGCHLQPAGRSPLPSSHS APGLCSPLHPLQPQQEASTCPSGTLQGREKAA PGQGRPLCSLWAGGAGAIPGERGAEGRGPSD QAPDPKSGPWLFPPGLGAPAEVRLHNVPHNL RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH
417	1767	A	3382	2	2061	EAQDPRACGPDAGGRFAARDAPGNSLRPPPS SPP/GWPGQLRLLPRVPGSELRCGKPERGRLP ASPPGKIRGWPPGISKRPGLGGRSFPPGFAPRT WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP KNAGRCGGA\RGPRLSLGPPPGPPPAPALPAR ASAGAGAAAAALAVGGVRGAGGARGTGGY GHCSGR/PTGRTGPGPQGPGPPMPARPR*AS\S TRGSRRGPGSRPARAAAAPRAGDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP R\GPGWDCALLPSPGPRSPRAVGCAEPEIWDP SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY PLKGPGLPPPWGPRTQTGHVIITVQPSGSCIEH SKSLD/RGPWGAPPWGPSSSGLCSPKLATAGP PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD HSSCEGHPDLHAGREMPAAPGLSELERVRFT VGCGGLASGISSASVSGLSPNRAGGPGQGDW EMYPVSWQTQESGGQG/SPKTGR*VGMLQA GAGSLQGGTGDGVWGLWEDGP/RG*DSPLPS GTGTEP*TPTTSIPFFPQPSGVYPSRATLLPMPS Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA KGIGQLSEIPLLNVETAFWSMWVTYFRK
418	1768	A	3398	304	2121	EEEEEEEDEDDDDNNEEEEFECYPPGMKVQV RYGRGKNQKMYEASIKDSDVEGGEVLYLVH YCGWNVRYDEWIKADKIVRPADKNVPKIKH RKKIKNKLDKEKDKDEKYSPKNCKPPALGPN PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI EITSILNGLQASESSAEDSEQEDERGAQDMDN NGKEESKIDHLTNNRNDLISKEEQNSSSLLEE

						/A Algeiga Co-Cycleine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Arnino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	Ì	,	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Scquonee	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
		<u> </u>		sequence		NKVHADLVISKPVSKSPERLRKDIEVLSEDTD
	1	İ			ļ	VEEDEVTKKRKDVKKDTTDKSSKPQIKRGKR
		}	Į	'	1	RYCNTEECLKTGSPGKKEEKAKNKESLCMEN
		l			i	SSNSSSDEDEEETKAKMTPTKKYNGLEEKRK
					1	SLRTTGFYSGFSEVAEKRIKLLNNSDERLQNS
		1		1		RAKDRKDVWSSIQGQWPKKTLKELFSDSDTE
		١.		1		AAASPPHPAPEEGVAEESLQTVAEEESCSPSV
	ì	1				ELEKPPPVNVDSKPIEEKTVEVNDRKAEFPSS
	ì	(1		1	GSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSS
	j		1			VTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGE LQDLQSERE*LASRF*CQCELKQ**SARTRTS*
		1	1	ł	1	KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
		1	ľ	ì	į.	
ļ	1			<u> </u>	<u> </u>	QQKEGK QRECLSIHIGQAGIQIGDACWELYCLEHGIQP
419	1769	A	3399	206	463	NGVVLDTQQDQLENAKMEHTNASFDTFFCE
1	}			1		TRACKHVPRALFVDLEPTVIDGIR
				1010	685	DDI SEFF*IWSSVLVTOARVOWRDLGSPQPLP
420	1770	A	3408	1010	003	PGEK RESCLSLPSSWDYRHPSPRPVNF/HVFLV
		1	1			VMGFHHVGQAGLELLTSGDLPALASQSARIT
		1	1			CVNTHCAOPRGHFH
	<u> </u>	 	3409	355	1326	ADSNLIESCWQELGLGPWGGDWRVEQVGAS
421	1771	Α	3409	333	1020	ASI REPREVESIRELETAVSLLSLELSAFWLGL
	1			1		I VI VODI ENEPKEMLTLSEYHERVKSQGQQL
<u> </u>				1		QQLQAELDKLHKEVSTVRAANSERVAKLVF
		1		1.	j	. QRLNEDFVRKPDYALSSVGASIDLQKTSHDY
1	ì	İ	ľ	{		ADRNTAYFWNRFSFWNYARPPTVILEPHVFP
		1				GNCWAFEGDQGQVVIQLPGRVQLSDITLQHP PPSVEHTGGANSAPRDFAVFFLLSFFTHQGLQ
	İ	1	\	1		VYDETEVSLGKFTFDVEKSEIQTFHLQNDPPA
1	İ	į				AFPKVKIQILSNWGHPRFTCLYRVRAHGVRT
1	Ì	1		į.		SEGAEGSAOGPH
		<u> </u>			421	FFDAOPSIGALVVFKRP*ATTGSDPGPKRGMN
422	1772	Α	3412	2	421	VI_VSCSMRSPESGKGEPGTARDYTPMGRPPP
1	'		Ì	1	1	PVPSVSPGPLPGSLAIAPHSPEPHPWEQQPPRG
	1		1	İ		OARSPPGGWLGSAT/RVRRPHNHP/RGH/HSP
		- 1	Ì	1		VDTAGAPASPGPDVCE
100	1773	A	3420	91	706	DAORATYSSVGPAVSLROROODGAVKESGR
423	1//3	A .	3420	1		RGGVRSESRAAAAMAPIKVGDAIPAVEVFEG
	ľ				ļ	EPGNKVNLAELFKGKKGVLFGVPGAFTPGCS
		1	-	1	1	KTHLPGFVEQAEALKAKGVQVVACLSVNDA
1		1	Į.	1		FVTGEWGRAHKAEGKVRLLADPTGAFGKET DLLLDDSLVSIFGNRRLKRFSMVVQDGIVKA
	i	1				DLLLDDSLYSIFGNRRLRRFSWIV VQBGIVIDI
1	-	1				LNVEPDGTGLTCSLAPNIISQL RQVTRVGTRVLGSTTAAVFLSVEDDNDNAPQ
424	1774	A	3421	4	7688	FSEKRYVVQVREDVTPGAPVLRVTASDRDKG
-				1		SNAVVHYSIMSGNARGQFYLDAQTGALDVV
1	1	- (1	1		SPLDYETTKEYTLRVRAQDGGRPPLSNVSGL
		ľ	1			VYVOVI DINDNAPIFVSTPFOATVLESVPLGY
		- 1	-	1		I VI HVOAIDADAGDNARLEYRLAGVGHDFP
		- 1			1	FTINNGTGWISVAAELDREEVDFYSFGVEAR
		ŀ	1	l	1	DUCTPATTASASVSVTALDVNDNNPTFTQPE
		1	1			VTVDI NEDA AVGTSVVTVSAVDRDAHSVITY
1		ì	İ			OITSGNTRNRFSITSOSGGGLVSLALPLDYKLE
ļ		1			1	POVVI AVTASDOTRODTAOIVVNVIDANIA
		- 1			}	PRIVEOCSHYTVNVNEDRPAGTTVVLISATDE
1					1	DTGENARITYFMEDSIPOFRIDADIGAVIIQA
		1				FLDVEDOVSYTLAITARDNGIPQKSDTTYLEI
		1				I VNIDVNDNAPOFLRDSYOGSVYEDVPPFISV
1	- 1	1	- 1	1	· 1	LQISATDRDSGLNGRVFYTFQGGDDGDGDFI
		L_				

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			000	D	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	r=rnenylalamine, G=Glychic, ri=rnisudnic,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	цепсе		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	1 1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ			peptide	_	/=possible nucleotide deletion, \=possible
		1 1		sequence		nucleotide insertion
				boquesion		VESTSGIVRTLRRLDRENVAQYVLRAYAVDK
		! I				GMPPARTPMEVTVTVLDVNDNPPVFEQDEFD
1	}]		}	1	VFVEENSPIGLAVARVTATDPDEGTNAQIMY
1	Į.	1 1		1	ì	OIVEGNIPEVFQLDIFSGELTALVDLDYEDRPE
				ļ	1	YVLVIQATSAPLVSRATVHVRLLDRNDNPPV
	Į					
1	1	1 1		l	ł	LGNFEILFNNYVTNRSSSFPGGAIGRVPAHDP
1	1				1	DISDSLTYSFERGNELSLVLLNASTGELKLSR
1						ALDNNRPLEAIMSVLVSDGVHSVTAQCALRV
	į			Ì		TITTDEMLTHSITLRLEDMSPERFLSPLLGLFIQ
1	ł			1	(AVAATLATPPDHVVVFNVQRDTDAPGGHILN
				1	1	VSLSVGQPPGPGGGPPFLPSEDLQERLYLNRS
		1			[LLTAISAQRVLPFDDNICLREPCENYMRCVSV
	1	1		1	ļ	LRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGF
1 .	İ	1		1		TGDYCETEVDLCYSRPCGPHGRCRSREGGYT
		1	1	1	1	CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT
İ			1			CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP
	ì		ł	Į.		AHSFITFRGLRQRFHFTLALSFATKERDGLLL
						YNGRFNEKHDFVALEVIQEQVQLTFSAGEST
1			l	İ	1	TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
1	'	1	1			QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS
i		1		{ .		VLGNYSCAA\QGTQGGSKKSLDLTGPLLLGG
1	1"	l		1	1	VPDLPESFPVRMRQFVGCMRNLQVDSRHIDM
ľ	1	Ì	[1 .	j	ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC
1	1	1				VNQWDAFSCECPLGFGGKSCAQEMANPQHF
1						LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD
j	ì		1			GVLLQAITRGRSTITLQLREGHVMLSVEGTGL
					İ	QASSLRLEPGRANDGDWHHAQLALGAIGGP
1	1	i	1	l .		GHAILSFDYGQQRAEGNLGPRLHGLHLSNITV
		1	1			GGIPGPAGGVARGFRGCLQGVRVSDTPEGVN
1	1	1	1	1		SLDPSHGESINVEQGCSLPDPCDSNPCPANSY
	1			1	Ì	CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC
1		1	1	1		EHQSVCTRKPSAPHGYTCECPPNYLGPYCET
1			1			EHOSVCIRKPSAFING I CECFFN I EGI TODI
(1	1	1			RIDOPCPRGWWGHPTCGPCNCDVSKGFDPDC
			· .		1.	NKTSGECHCKENHYRPPGSPTCLLCDCYPTG
		1	1	1.		SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF
	1	1	}	1	1	AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFG
1		1	1	1	'	LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF
1				į		NCTSITFSELKGFAERLQRNESGLDSGRSQQL
	1	1	1	1	}	ALLLRNATQHTAGYFGSDVKVAYQLATRLL
		1	1	1		AHESTQRGFGLSATQDVHFTENLLRVGSALL
1	1	1	1]	1	DTANKRHWELIQQTEGGTAWLLQHYEAYAS
	1	1	1		1	ALAONMRHTYLSPFTIVTPNIVISVVRLDKGN
				1		FAGAKLPRYEALRGEQPPDLETTVILPESVFR
	1	1			1	ETPPVVRPAGPGEAQEPEELARRQRRHPELSQ
	}	1			1	GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK
		1.			1	RPIINTPVVSISVHDDEELLPRALDKPVTVQFR
1	1	1,		1		LLETEERTKPICVFWNHSILVSGTGGWSARGC
1	1	1				EVVFRNESHVSCQCNHMTSFAVLMDVSRRE
J	1		j	}	1	NGEILPLKTLTYVALGVTLAALLLTFFFLTLL
1		1				RILRSNQHGIRRNLTAALGLAQLVFLLGINQA
		1		1		DLPFACTVIAILLHFLYLCTFSWALLEALHLY
		1		1		RALTEVRDVNTGPMRFYYMLGWGVPAFITG
1	1	1	{		1	LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP
	1	1		1		VAFAVSMSVFLYILAARASCAAQRQGFEKKG
1		1	1	l		VALA ASMONIL I ILLA ARASCAA QUE CANODITI I
1	1		1	I	1	PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL
1	1	1	1 .	[1	FHYLFATCNCIQGPFIFLSYVVLSKEVRKALK
1	1		1	1	}	LACSRKPSPDPALTTKSTLTSSYNCPSPYADG
٠.			1	1		RLYQP\YGDSAGSLHSTSRSGKSQPSYIPFLLR
			1	1	1	EESALNPG\QGPPGLGGIPGR/LCFLGRFKDQQ
		-		1		H\DS*TRDFDSDLSLEDDQSGSYASTHSSDSEE
L						

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			COTO	D., 11 4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
donoc		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
İ		l	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	i	l		peptide		/=possible nucleotide deletion, \=possible
t	1	l	1			nucleotide insertion
		l	L	sequence		EEEEEEBAAFPGEQGWDSLLGPGAERLPLHS
			i e			EEEEEEEAAFGEQU WDSLLOI GABADI BIIO
1	i		l			TPKDGGPGPGKAPWPGDFGTTAKESSGNGAP
		Ì	ļ		!	EERLRENGDALSREGSLGPLPGSSAQPHKGIL
		1	l ·	i :		KKKCLPTISEKSSLLRLPLEQCTGSSRGSSASE
		1	1	ł	1	GSRGGPPSRPPPRQSLQEQLNGVMPIAMSIKA
1	l .	1		j	J ·	GTVDEDSSGSEFLFFNFLH
		<u> </u>	-	155	1417	GEPAVQSCDCGCTQRSCPWLLVAPGLLSSSSS
425	1775	Α	3429	155	1417	RAASVREAEDAPLQPASIHPVSQGSRGPEGSL
		ļ		l		COARGI POPPI CARRATE AUSDITECTOR PA
	1	1	1		1	GSAECLPGDPLGARRATRAHSPVPGPPPSLPA
ł	i		1			AGTAVKRGLQPG*GA/GATSTPGTGAATGGL
1	1	Į			l .	CGPAWAAPSAVGPCCCCPSISTTPSQMRSARP
}	1	1	{	l	i	SLGCLPSWAS\PGTEHPPGPQGPGPS*DLCSV*
1	1	1		,	ļ	KREFORGPWAGMVILHRISAADPARAPGPDS
1	1	1		1		NLQSALQQPATGCSEPAAVYSPPIGLWGA**P
l		1	1	i		EYG*PQHSLPG*TAPADR*P\AGIKDRVYSNSI
		1	1	ļ	1	YELLENGQRAGTCVLEYATPLQTLFAMSQYS
	ĺ	١.	1			TELLENGUAGOTO LETATI EQUETATE DE ADADESON
		1				QAGFSREDRLEQAKLFCRTLEDILADAPESQN
ł	1 .	.	1		ł	NCRLIAYQEPADDSSFSLSQEVLRHLRQEEKE
1	1	1		1	1	EVTVGSLKTSAVPSTSTMSQEPELLISGMEKP
ł	1)	1	1	į.	LPLRTDFS
100	1776	A	3431	1662	369	AIWWLSWLQHDLLPTPTQVAIDFTASNGDPR
426	1//6	^	3431	1002	1 ***	SSQSLHCLSPRQPNHYLQALRAVGGICQDYD/
1			i	1		SVGESGAGGNRQGGLAQRIPQLFLLPSDKRFP
	1	1	l	1	1	AFGFGARIPPNFEVG*MRGKEGDGGRVSQAE
1	1	1	1 .			KAGPHCSRLALTG\SHDFAINFDPENPECEGK
	1	-	1	ļ	1	RAGPHCSRLALIGISHDPAINTDIENT DEVICE
1	{	1 .	i			RGDFHLPRLPADTLHTGAQTPLPRAQLPVPST
1 .	1	1	1	1	1	HPRPVFI\EISGVIASYRRCLPQIQLYGPTNVAP
1	ì	1	1.	i	1	INRVAEPAQREQSTGQATKYSVLLVLTDGV
Į	1		1	1	1	VSDMAETRTAIVRASRLPMSIIIVGVGNADFS
1]		l l	ł		DMRLLDGDDGPLRCPRGVPAARDIVQFVPFR
	1		j	1		DFKDVSPPGPFRLKDSSASHPPKSDLRLPPFD
1	i		1	Ì	•	VLLRTREPSWPP*SPTSPSDDPASPTLPLTPNHI
1		1	1			TVPTL\AAPSALAKCVLAEVPRQVVEYYASQ
·	1 '				}	GISPGAPRPCTLATTPSPSP
1	1_	_L			I	
427	1777	A	3446	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW
1				1		GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA
	1					ASRPEASGDCRAGRETAMATLEKLMKAFESL
1			1	1		KSFQQQQQQQQQQQQQQQQQQQQQPPPP
İ				1		PPPPPPPQLPQPPPQAQPLLPQPQPPPPPPPPPPPPPPP
1	1		1	Ī		GPAVAEEPLHRPKKELSATKKDRVNHCLTIC
i				1		FNIVAOSVRNSPEFOKLLGIAMELFLLCSDDA
		1	1	1	1	ESDVRMVADECLNKVIKALMDSNLPRLQLEL
	1	1	1	1	1	YKEIKKNGAPRSLRAALWRFAELAHLVRPQK
		1	1	1	1	INCIANUARROLKAALWAFAELARILARIA
1	-	1	i	[CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP
1		1		1 .	1	KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI
	1	1	1			RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG
		1	1	1	1	LLVPVFDEHSTLLILGVLLTLRYLVPLLQQQV
1	1				1	KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL
1 .		1				TLHHTQHQDHNVVTGALELLQQLFRTPPPEL
'		- 1	1		1	LQTLTAVGGIGQLTAAKEESGGRSRSGSIVELI
	Ì	1		l .	1 .	PATETYANGIOGETAVEESOCIONOSOSTAPRI
		l		1	1	AGGGSSCSPVLSRKQKGKVLLGEEEALEDDS
1	1	1	1	1	1	ESRSDVSSSALTASVKDEISGELAASSGVSTPG
					1	SAGHDITTEQPRSQHTLQADSVDLASCDLTSS
	1	1		[1	ATDGDEEDILSHSSSOVSAVPSDPAMDLNDG
		1		}		TOASSPISDSSOTTTEGPDSAVTPSDSSEIVLD
		l	Į.			GTDNQYLGLQIGQPQDEDEEATGILPDEASEA
1		1	1	1	1	FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF
	1	1		1	1	VLRDEATEPGDQENKPCRIKGDIGQSTDDDS
	ĺ	- 1		1	1	APLVHCVRLLSASFLLTGGKNVLVPDRDVRV
	1	- 1	1	1	1	APLVHCVKLLSASTLLIGGKNVLVPDKDVKV
1	1	- 1		1	1	SVKALALSCVGAAVALHPESFFSKLYKVPLD
L						

070 70	CEO ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide	mou .	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	ucito	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence]		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		i		peptide		/=possible nucleotide deletion, \=possible
ì	ł	1		sequence		nucleotide insertion
	 					TTEYPEEQYVSDILNYIDHGDPQVRGATAILC
ì				,		GTLICSILSRSRFHVGDWMGTIRTLTGNTFSL
l .		1.	1]		ADCIPLLRKTLKDESSVTCKLACTAVRNCVM
			Ì	Ì		SLCSSSYSELGLQLIIDVLTLRNSSYWLVRTEL LETLAEIDFRLVSFLEAKAENLHRGAHHYTGL
	1	1	}		İ	LKLQERVLNNVVIHLLGDEDPRVRHVAAASL
ì	1		Ì	1.	ļ	RLVPKLFYKCDQGQADPVVAVARDQSSVYL
1					}	KLLMHETQPPSHFSVSTITRIYRGYNLLPSITD
1	1	1		Ī		VTMENNLSRVIAAVSHELITSTTRALTFGCCE
}]	1		1		ALCLLSTAFPVCIWSLGWHCGVPPLSASDESR
1	ì	1				KSCTVGMATMILTLLSSAWFPLDLSAHQDAL
1	1	1			1	ILAGNLLAASAPKSLRSSWASEEEANPAATK
}	Ì	1				OFEVWPALGDRALVPMVEQLFSHLLKVINIC
1 .	1	İ	1		1	AHVI DDVAPGPAIKAALPSLTNPPSLSPIRRK
 .		1.				GKEKEPGEOASVPLSPKKGSEASAASRQSDTS
1.		1	1	1		GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA
						NYKYTI DI ONSTEKFGGFLRSALDVLSQILEL
	1	l l				ATT ODIGK CVEETLGYLKSCFSREPMMAT VC
1	}	ì	1	1		VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA
	1					QRLGSSSVRPGLYHYCFMAPYTHFTQALADA
,	<u>. [</u>	1	1	1	1	SLRNMVQAEQENDTSGWFDVLQKVSTQLKT
1					j	NLTSVTKNRADKNAIHNHIRLFEPLVIKALKQ
	1	ı	· [1	ł	YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL
ł		1			i	DSDQVFIGFVLKQFEYIEVGQFRESEAIIPNIFF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR
1.		1	İ			KAVTHAIPALQPIVHDLFVLRGTNKADAGKE
	1		i	Į	1	LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ
ł	1	- [ì	j	CHKENEDKWKRLSRQIADIILPMLAKQQMHI
		1		1		DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF
1		1			Į.	VTPNTMASVSTVQLWISGILAILRVLISQSTED
			1	ĺ		TVI SRIOELSESPYLISCTVINRLEDGDSTSTLE
	1					EHSEGKOIKNLPEETFSRFLLQLVGILLEDIVT
						KOLKVEMSEOOHTFYCQELGTLLMCLIHIFKS
1 .			1	T		GMFRRITAAATRLFRSDGCGGSFYTLDSLNLK
		1	Ì		İ	ARSMITTHPALVILWCOILLLVNHTDYRWW
		- 1			-	ARVOOTPKRHSLSSTKLLSPQMSGEEEDSDLA
	İ	1			,	AKI GMCNREIVRRGALILFCDYVCQNLHUSE
1		1		1	1	HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS
1		1 .	1			AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI
	y . •				1	HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL
					i	ACREVEMLIAANLQSSMAQLPMEELNRIQEY
				1	1	LOSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK
		-		1	}	SQCWTRSDSALLEGAELVNRIPAEDMNAFM
		- (1	SQCWTRSDSALLEGAELVINNI ABDINIVALIN MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA
1		1		1		AREVTLARVSGTVQQLPAVHHVFQPELPAEP
Ì		1	}	1	1	AAYWSKLNDLFGDAALYQSLPTLARALAQY
1			}	1	1	LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL
1		- 1	1	[1	SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL
	1		1	1		WOLKIGOTEFUTHACSLIYCVHFILEAVAVQPG
	1			1		FOLI SPERRTNTPK AISEEEEEVDPNTQNPKYI
		- 1		1]	TAACEMVAEMVESLOSVLALGHKKNSUVPA
				i]	ELTOLI RNITISLARI PLVNSYTRVPPLVWKLG
		1	(WODE DEGET AFPETPVEFLOEKEVEKEFLYK
						INTEGWTSRTOFEETWATLLGVLVTQPLVME
		1			1 '	OFFOPPREDTERTOINVLAVQAITSLVLSAMI
						VOVA CNPA VSCI FOOPRNKPLKALDIKI GKK
1	i	l.			1	I STRUCTUE OF IOAMVSKRENIATHHLY QAWD
1	i	1	1	ĺ		DVDCI CDATTGALISHEKLLLOINPERELUSMS
1	1			1		YKLGQVSIHSVWLGNSITPLREEEWDEEEEEE

	(DEC.	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of,	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	Glutamine, K-Arginine, 3-3crine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ ·			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	1	ŀ	1	peptide		/=possible nucleotide deletion, \=possible
	1	ł		sequence		nucleotide insertion
		 		3043000		ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
1	ì	l	į.	ſ		LELYSRWILPSSSARRTPAILISEVVRSLLVVS
	ì	1	1	1		DLFTERNQFELMYVTLTELRRVHPSEDEILAQ
	\ .	1	ł			YLVPATCKAAAVLGMDKAVAEPVSRLLESTL
	l .	l	1		ł	RSSHLPSRVGALHGILYVLECDLLDDTAKQLI
	1	ì	ľ	1		PVISDYLLSNLKGIAHCVNIHSQQHVLVMCAT
	1	1		1		AFYLIENYPLDVGPEFSASIIQMCGVMLSGSE
\	į.	l l	1	·		AFYLIENYPLDVGPEFSASIIQMCG VMESGDE
ļ		1	1		Í	ESTPSIIYHCALRGLERLLLSEQLSRLDAESLV
1	1	1	1	ŀ		KLSVDRVNVHSPHRAMAALGLMLTCMYTG
1	1	1	ì]		KEKVSPGRTSDPNPAAPDSESVTVAMERVSVL
1	Į.	1	Į.	1	1	FDRIRKGFPCEARVVARILPQFLDDFFPPQDIM
	l	1	1	1		NKVIGEFLSNQQPYPQFMATVVYKVFQTLHS
ì		l	1	l .		TGOSSMVRDWVMLSLSNFTQRAPVAMATWS
1	1	i	1	1		LSCFFVSASTSPWVAAILPHVISRMGKLEQVD
}			1	1		VNLFCLVATDFYRHQIEEELDRRAFQSVLEV
1	1	i	ì			VAAPGSPYHRLLTCLRNVHKVTTC
1	1	1 _				NSRPSPSAALVEVLLRSGSTFPHTVSGGWAA
428	1778	Α	3449	3	430	WGPWSSCSRDCELGFRVRKRTCTNPEPRNGG
			1	1		LPCVGDAAEYQDCNPQACPVRGAWSCWTS
1	1	ì	ł	İ	ĺ	LPCVGDAAEYQDCNPQACFYRGAWGCW16
1	1	1	1	1		WSPCSASCGGGHYQRTRSCTSPAPSPGEDICL
1	i	1	1	**		GLHTEEALCATQACPEGWS
429	1779	A	3464	583	3	DALDRRYLERCHPAAGGWVGEGE*ALCQKT/
429	1//2	1 ^	1 3.0,		j .	RFSGVLEPPLPSLKDGGRFPAWT*RSCSKSLR
1	Ì	1	1	ł	1	AAFTSQFFPSRRSRASPGSAF\GNGQNLTEQHP
	1	1	1	i		CPGSCDPOVLSASWM*VEHRSKFRPPP*NSTI
1		1	ļ	İ		PPES/RS*OGGTVOTGOHSSGREAGSWRARGR
1		1	1	1		NAGRR*KGGGKIGTKQGAVRARKECRGEMA
1			}	J	İ	SGETDSE
	<u> </u>			1	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKA
430	1780	A	3473	2802	270	HLSIQKLLKER\Q\QLPVFKHRDSIVETLKRHR
		Į.			ŀ	VVVVAGET\GSGKSTQVPHFLLEDLLLNEWE
1		1				ASKCNIVCTQPRRISAVSLANRVCDELGCENG
-	1	1		∦.		PGGRNSLCGYQIRMESRACESTRLLYCTTGV
		1	ĺ	İ		LLRKLQEDGLLSNVS/HMFIVDEV\HER\SVQS
	i i	1		1		LLKKLQEDGLLSNVS/HVF1VDEV KIEKUVQU
ì	ļ	Į.	1	1		DFLLIILKEILQKRSDLHLILMSATVDSEKFST
						YFTHCPILRISGRSYPVEVFHLEDIEETGFVLE
	1 .		j			KDSEYCQKFLEEEEEVTINVTSKAGGIKKYQE
1	1	1	1		1 .	YIPVQTGAHADLNPFYQKYSSRTQHAILYMN
	1	1	į .	1	1 .	PHKINI DI ILELI AYLDKSPOFRNIEGAVLIFL
1		1				PGI AHIOOLYDILISNDRRFYSERYKVIALHSI
	Ϊ	1 '	1	1		LSTODOAAAFTLPPPGVRKIVLATNIAETGITI
	1	1			1	PDVVFVIDTGRTKENKYHESSQMSSLVETFVS
Ì		ļ			1	KASALQRQGRAGRVRDGFCFRMYTRERFEG
			1	1	1	FMDYSVPEILRVPLEELCLHIMKCNLGSPEDF
	1	1	1		. [LSKALDPPQLQVISNAMNLLRKIGACELNEPK
1		}		1		LONALDIPOLO VISITATIVI DE LA TECNITA DEL TECNITA DEL TECNITA DE LA TECNITA DE LA TECNITA DE LA TECNITA DEL
-		1		1		LTPLGQHLAALPVNVKIGKMLIFGAIFGCLDP
	1	i		1		VATLAAVMTEKSPFTTPIGRKDEADLAKSAL
		1		1		AMADSDHLTIYNAYLGWKKARQEGGYRSEI
			1	1.		TYCRRNFLNRTSLLTLEDVKQELIKLVKAAGF
1	1	- 1	1	1.	l	SSSTTSTSWEGNRASOTLSFQEIALLKAVLVA
			1	1	. 1	GLYDNYGKIIYTKSVDYTEKLACIVETAQGK
1	1	1	1		ì	AOVHPSSVNRDLOTHGWLLYQEKIRYARVY
	1	- [I	1	LRETTLITPFPVLLFGGDIEVQHRERLLSIDGW
1		- [1	1		IYFQAPVKIAVIFKQLRVLIDSVLRKKLENPK
1	1	- 1			1	TITOME AND A THOUGHT IN THE PROPERTY AND A PROPERTY
			i i	<u> </u>		MSLENDKILQIITELIKTENN
431	1781	A	3474	1	441	FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ
131	1,,01	1.		1		PCPPAPAPSRPRSLGSLGQRVPAALATAAQEL
1	1 .				l l	PATLGGDGGKPALTAGEAALPGLHRSGVPAA
	1	1		{		AARC*PCT/SRPT*STLSPTQAAWWCRPSRRQ
I	1	1	1		1	QRGEASTGGASGRRCGSCFQV

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	F=Pnenylalanine, G=Glycine, H=Fishume,
eotide	seq-	İ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
		ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	[914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l	1	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
1	١.		1	residue of	Sequence	/=possible nucleotide deletion, \=possible
l	1	l	l .	peptide		
1	1	1	1	sequence		nucleotide insertion
400	1782	1A	3478	416	23	QLRRLTLPNFKTY/YSS*IIEIAWH**KNMQID
432	1/02	'A	3470	1		QWFRRESPEIDLCKYS*LSFDKEAKAIK/WKE
ŀ		ĺ			1	CSLFNKWC/YKNWM/LHVQKKRI*VQTLHPS
1		1	l	}	}	QKLK\SKWIKDLNVECRITKLLDQEYPGDLGY
				ì	į.	
	1	l	1			SRALNSGSR
433	1783	A	3504	1876	552	CLAPCSPQPEKNGMQPLLLLLPPLLYQQLLHS
433	1765	1 "	555.			SLGAPGESTLLVRTSKLLVGLGLQLLVWLLL
Į.	1 .	1]	į		OTRSLLALOLHLTSSAPLLAAPTAVCSCSRCS
1	1	1	ł	!	1	APRSRCVARPAARTGLPTPAPASSPAPAASPA
ì		1	1	i		PAASPAPAESTA\PQPLILLPKP/PPAPGAPPPRP
i		1	1	ì		CARREDA A CRORA A CRARRA A CRATTA TA CARREDA
,	İ		1	ì	1	GAPPPRPAASPSPAASPAPPAASPVLTASPPLP
1	1	1		l .	1	AASPSPAASPAPPAASPVLTASPPLPAASPSPA
1		1	1	1	1	ASPAPPAASPVLTASPPLPAASPALAASPVHT
1	1		1	1	1	ASPPVHVASPPVHTASPPVHVASPPVHTASPP
	1	1			1	VHVASPPVHTASPHVHVASPPVHVASPPVHV
1	1		1	1		ASPPVHTASPPVHVASPPVHTASPHVHVASPP
i	j	1	1	}		VHTASPPVHVASPPVHVASPPVHVAYPPVHV
1	i		1			VHIASPPVHVASPPVHVACPDVCCCCDCTCDCFPP
ļ			ľ			ASPPVHVASPPVHVASPPVSCSGDSTSDCFPP
İ	İ	1		ì		QPGAVFPHSLAPSLGGWSHLVAALP
	1.504	+	3516	142	590	GGVNRPRSETEQVKTPVLISSWDYRHPPPRPA
434	1784	Α	3310	142	1 350	SFFVFLV*TGF\TALARMVLISWPCDLPTSASQ
	1			! .	ŀ	SAGITGVRHHA\RLLYFEQESHSVTQAGW\VQ
1	1	1	1	į.		WHNLGSLQPLSLEDRLSPGVLGCSALCRSGV
İ	ł	Į.	1	ì		RTKFGINMVTSRERGTTRLPKEG
	1		ļ.	1		RIKEGINMVISKEROTIKLIKLO
435	1785	A	3529	1	3161	MSLVRAALEALDELDLFGVKGGPQSVIHVLA
433	1703	1	1			DEVQHCQSILNSLLPRASTSKEVDASLLSVVS
1		ł		1		FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF
1	1			ĺ		LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC
1		- 1	1	ì	•	FWPLFWTYFILDGVFSGNAEQVQEYKEALEA
- 1	i i	1	1	į.		VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHT
ŀ		ł	- {	1		VDRVPMGKLPHMWGQSLYILGSLMAEGFLA
4	Į		-	1		PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS
- 1		1	1	ł		PGEIDPLNKKF51 VFKFDV V VQ VI SBITIGOS
- [1	- 1	1	1		SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTIL
1	[- (1	`\	i i	KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF
1	1			i		LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK
	i	i				L YDIRKTIFTFTPOFIDOOOFYLALDNKMIVE
1		- 1	1	1		MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE
-	1	l			1	DGTSLNSSILAALRKMQDGYFGGARVQTGKL
į	1	1	1	1	[DO 12 PURSUITAVE REPORT AS ELECTRICAL AS ELE
1		- (1	1	1	SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN
	ĺ		- 1		1	YDYLESGNWMNDYDSTSHARCGDEVARYL
1 .		1	1		1	DHILLAHTAPHPKLAPTSOKGGLDKFQAAVQI
		1	1		1	TCDLMSLVTKAKELHVQNVHMYLPTKLFQA
						SRPSENTLDSPHPROENOVPSVRVEIHLPRDQ
		l		1	1	SGEVDFKALVLQLKETSSLQEQADILYMLYT
		1		1		MKGPDWNTELYNERSATVRELLTELYGKVG
1			1	1		EIRHWGLIRYISGILRKKVEALDEACTDLLSH
-			-	1		EIRHWOLIK I ISOILKAK VEALDEACT DELSIT
1	ļ	}		1		QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA
1	i i	- 1	1	1 .		SEGDMSISILTQEIMVYLAMYMRTQPGLFAE
1	ì	1		1		MERIRIGLIIOVMATELAHSLRCSAEEATEGL
	1	1	- 1	1		MINI SPSAMKNILHHILSGKEFGVERSVRPID
1	1	i	1	1	1	SNVSPAISIHEIGAVGATKTERTGIMQLKSEIK
1	1	- [.1		1	OSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW
1					Ì	OSLO 19MI LODOLLOVI DÁČONY DRÁGA
	1	1	1	1	1	QRRRRLDGALNRVPVGFYQKVWKVLQKCH
	l				l	GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL
1	1	ŀ		1	1	ND VPOPEYROLL VEAIL VLTMLADIENHSIGS
1		1	1	1	1	TAVEKIVHIANDI.FLOEOKTLGADDIMLAKD
1			1		1	PASGICTLLYDSAPSGRFGTMTYLSKAAATY
1		1	- 1		1	LWOOLCIPPINGW POW CHAIL INCH
1				1		VQEFLPHSICAMQ
436	1786	IA	3546	73	393	CP*LTWELLEVKKAEVLQDSLDGRYSTPSSCL
430	1700	1	55.0			EQPDSCRPYGRSFYALEEKHVIFSLDVGETDN
ı		1				

				= 17. 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A courtic Acid F=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	corresponding	I=Icoleucine K=Lysine L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
netice			}	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
	i			peptide	1	/=possible nucleotide deletion, /-possible
	}	ľ	i	sequence	1 _	nucleotide insertion
			 	Boque		KGKGKTIRGI*TFKGRKGGTYQREHDANPLA
			1	ļ		I DVC A DCCUMPKG
					2939	AVRAEPGLEELSSGLRAHSPSATTVCEPEAQG
437	1787	A	3554	5157	2939	LO A COCOVA AUPHWGI GGAAAAGUS WEFUFF
		1		,		L DDVCGDACDCKPHPPAAPRSPLLPGSKKKPRA
		l .	1			AQPGARARTSPPPASARNMAARPAATLAWSL
	1	1	}	1		LLLSSALLREGCRARFVAERDSEDDGEEPVVF
	1	1	1	Ì	1	PESPLQSPTVLVAVLARNAAHTLPHFLGCLER
	1	1	1		1	PESPLOSPI VLVA V LAKITAATI BITTI BOODES
	1	1]		1	LDYPKSRMAIWAATDHNVDNITEIFREWLK
	1	{	1	1		NVQRLYHYVEWRPMDEPESYPDEIGPKHWP
	1	1	1	1	1	TSRFAHVMKLRQAALRTAREKWSDYILFIDV
	1			1	1	DAIGI TAPOTI MILIAENKTIVAPMLESKUL 15
	1	1	1	1	1.	L NEW CCITER CEVERTEDY VOIREWERIGGE
		1	1		1	I VIDAGUISTEI IDI RKEASDKLITYPPHUD I I W
	}	1			1 .	TEDDITOR A ESSROAGIOMYLCNREHY GILPIP
	ļ.	1	1	}		T VINCOTI OFFITENI IHVOLEAMIUKPYMEPSQ
	i	1	- 1		i .	YVSVVPKYPDKMGFDEIFMINLKRRKGQGGD
	1		1	1	1	RWLRTLYEQEIEVKIVEAVDGKALNTSQLKA
		1	- 1	1	ì	RWLRIL YEQEIEVELYER TEGEIGCEI SHYSV
)	1	ł	1	,	LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV
	1	1	1	1		WKEVIDRELEKTLVIEDDVRFEHQFKKKLMK
	1	- 1	1	i	1	LMDNIDQAQLDWELIYIGRKRMQVKEPEKA
		1	1	1	1	LADATA ANTI VEADYSYWILGY VISLEGAQAL V
	1	i	- 1	}	1	CANDECK MI PVDEFI PVMYNKHPVALIKLI
	i i	-	1 .	\ .	1	A ALCOHOL & ALCAEM LIAMINATION OF A LOUIS
	l l	- 1	1			TSTIWDNETVATDWDRTHAWKSRKQSRIYS
	l l	- 1	1		1	AWNITE AT PPPTSLDTVPSRDEL
1	i	1				TECNOSCI ECRVECLEL RWSFTLVAQARVQ*C
438	1788	A	3563	130	527	NLSSLQPLPPGFK*FSCLSPPRS*DYRRPPPRP
436	1760	1 **		1		NFLYF**RQGFTVLGQAGLELLT/S/GDPPTSA
(1	- 1	1			NFL YF** ROOFT VLOQAGEEDETTO UKTRPSI.
1	}	1	1	1	1	SQSAGITGVSHRAWPVHAISTHISLVKTRPSL
1	l l	1	,	1	}	TLG
			3565	446	1834	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSY
439	1789	Α	3303	440		GQPSLQDELKDNTTVFTRILDRLLDGYDNRL
		1	1	1	• 1	DDGI GERVTEVKTDIFVTSFGPVSDHDME i i
1	1	1	1	į.	1	DVEEROSWKDERLKFKGPMTVLKLNNLMAS
į.	ł	1	i	- [1	VIWTPINTEFHNGKKSVAHNMIMPNKLLKIII
1.		1		l	1	DOTE I VTMRI TVR\AECPMAFGRDFPM\D\AI
1	1	- 1	1	- })	A COL KEGGVAYTRAEVVYEWTREPAKSV V V
1	1	- {		{		AEDGSRLNQYDLLGQTVDSGIVQSSTGEYV
1		.	- 1		- 1	MTTHFHLKRKIGYFVIQTYLPCIMTVILSQVS
1	l l	.	1	1	1	MITHERICATION THE SIGARNS
1		1	1	ľ	1 '	WLNRESVPARTVFGVTTVLTMTTLSISARNS WLNRESVPARTVFGVTTVLTMTTLSISARNS
1	1	- 1			- 1	DUTE A TAMOWETAV CYAP VESALIBEAL VI
1	1	- 1			1	YFTKRGYAWDGKSVVPEKPKKVKDPLIKKN
1		l	ļ.	1	i	LATEVADTATEVTPNI ARGIDPCILATIANSALIE
1	-	1	}	1		LEAK DELK DE PERKETENS VSKIDKT SKLALLE
1		1	1	1		I POPENT VVWATYI NREPOLKAPIPHQ
1		- 1		\		- LOTOCOCEDA A A A AIMREIVHLOAGUCUNUIGA
440	1790		3568	1	350	FWEVISDEHGIDPTGTYHGDSDLQLERINYY
440	1/90	T ^A		1		FWEVIOUEDUILFIGITATIONS DE CHEPPPVPA
1	1	1				NEATGEAPVPSPTALRGPRGPCLG*RPPVPA
1	1	. 1		1	l	GKYVPRAVLVDMEPGTMDSV
					1751	FVAVAGAVSGEPLVHWCTQQLRKTFGLDV
441	1791	A	3569	2	1/31	TERROVAL STRUKERY VIDLLUGNEGANG
				- 1		1 DEED THE WORNINGELISDPLOUGHANDELL
1		1	1			I OVECDIM KROKKCKNKOKALITEDI I
	١	}	Į.	1		LAWTEEN AKAOFNSNSVKKKIKFVNLIIM
1	ı		1	1	1	QDRLAVLLPGRHPCDCLGQKHKLINNCLIC
		1	1	1		QDRLAVLLPGKHPCDCLGQKHCENTT PGD
		1				
			ļ	1	l	RIVCEQEGSGPCLFCGTLVCTHEEQDILRGD
						RIVCEQEGSGPCLFCGTLVCTHEEQDILKOD NKSQKLLKKLMSGVENSGKVDISTKDLLPF QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQ

SEQ ID NO: of nucleotide peptide eotide sequence where the content of the content					5 3	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO. of NO. of USM nucleotide of peptide sequence when the control of the control	SEQ ID	SEQ ID	Met	SEQ	Predicted		D-Accordic Acid E=Glutamic Acid.
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KTAGVKPYECTICGKAFMRISSITIRMON AIRANEKPYKCKEGGRAFSLSQILSKWIER FÜREKPYKCKQCKTFIYHQPFQRIERTHIG PYECKQCGKALSCSSLRVHERIHTGEKPY KQCGKAFSCSSIRVHERIHTGEKPYACK GKAFISTITSVLTHMITHNGDRPYKCKECG FIFPSFLRVHERIHTGEKPYKCKQGGKAFR TSIQHIERIHTGEKPYKCKEGGKAFSISTSTRI HYRVHTGEKPYKCKEGGKAFSRISTRIH HYTGEKPYKCKEGKAFSISTSTRIH HYTGEKPYKCKEGKAFSRISTRIH HYTGEKPYKCKEGKAFSISTRIH HYTGEKPYKCKEGKAFSISTRIH HYTGEKPYECKECAKTFISLENFRHMITHTGEK KCRDGKVFIFPSALRTHERTHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPY FINHVSVSNGPKYELEC*QCGKAFS LKYMRNAGDRKLYKCEK*EKVFNSNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NICHT**NISNI AISTELL**NICHT**NICH	l .	1	1		1	1	QGAKKGLMKQNKAV
KTAGVKPYECTICGKAFMRISSITIRMON AIRANEKPYKCKEGGRAFSLSQILSKWIER FÜREKPYKCKQCKTFIYHQPFQRIERTHIG PYECKQCGKALSCSSLRVHERIHTGEKPY KQCGKAFSCSSIRVHERIHTGEKPYACK GKAFISTITSVLTHMITHNGDRPYKCKECG FIFPSFLRVHERIHTGEKPYKCKQGGKAFR TSIQHIERIHTGEKPYKCKEGGKAFSISTSTRI HYRVHTGEKPYKCKEGGKAFSRISTRIH HYTGEKPYKCKEGKAFSISTSTRIH HYTGEKPYKCKEGKAFSRISTRIH HYTGEKPYKCKEGKAFSISTRIH HYTGEKPYKCKEGKAFSISTRIH HYTGEKPYECKECAKTFISLENFRHMITHTGEK KCRDGKVFIFPSALRTHERTHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPYECKEC GKAFSCSSYRIHKRITHTGEKPY FINHVSVSNGPKYELEC*QCGKAFS LKYMRNAGDRKLYKCEK*EKVFNSNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK*YRKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI QSCENSH*REKSCQCK**RKDIT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NISNI AISTELL**NICHT**NICHT**NISNI AISTELL**NICHT**NICH		1	+	2574	 	2019	MODELITGERI CEGKEGSOCAENESPNLSVIK
AIRANERPYKCKECGRAFSLSQULSKHER. TGEKPYKCKQCGKTIYHOPFQRHERTHIT PYECKQCGKALSCSSSLRVHERIHTGEKPYACK GKAFISYTISVLTHMITHNGBPYKCKECGK GKAFISYTISVLTHMITHNGBPYKCKECGK GKAFISYTISVLTHMITHNGBPYKCKECGK GKAFISYTSVLTHMITHTGEKPYKCKOGKAFR TSIQIHERIHTGEKPYKCKECGKAFSRISYFRHH HTGEKPYECKECAKTFISLENFRRHMITHTGEK KCRDCGKVFIPFSALRTHERTHTIGEKPYECKEC AFTYPTSFQHIMRMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSFQHIMMHTGEKPYECKEC AFTYPTSHAMM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKTHAM TOKT	442	1792	A	33/0	1 *		VTACVEDVECTICGK AFMRLSSLTRHMKSH1
TGERPYKCKQCGKTFIYQFFQHERIHTGEKPY PYECKQCGKAISCSSIRVHERIHTGEKPYACK GKAFISTTSVLTHMTHHNGPRPYKCKECG FIFPSFLRVHERIHTGEKPYKCKQCGKAFS FISIQHERIHTGEKPYKCKQCGKAFS FISIQHERIHTGEKPYKCKECGKSFSARPA HVRVHTGEKPYECKECGKAFSRISYFRIH HTGEKPYECKECGKAFSRISYFRIH HTGEKPYECKECAKTFISLENFRRHMITHTGD KCRDCGKVFIFPSALRTHERTHTGEKPYE CGKAFSCSSYRIHKRTHTGEKPYECKEC AFITYTSFQGHMRMHTGEKPYECKECGK LHSSFRRHTRIHNYEKPLEC*QICGKAFSN LKKPMRNAGSDRKLYKCEK*EKVFNSNIN QSCENSH*REKSCQCK*YRRDTR*FMYS PHNHVSVSNGPYRCCGSPRLYNT*NISNIN VAVVTP*CSTLFKCLWCWCKRAALSVV* DSGRGRWLTPVIPALWEAKAGGSRGQEI ANTVKPHLY DFYERKFGGFEGHKQIVNKWRDLLCSW LSIKKSVLQNNL*FSAASMRFQKVFF HLFFSLFLAAMAMTGSTFCSSMSNHTKE MTKVTLENFYSTLAGHERERMRQKKLE MEEGLKDEEKRLRRSAHARKETEFLRL RIGLEDFESLKVIGRGAFGEVRLVQKKD VYAMKILRADMILEKEQVGHRAERDIL DSLWVVKMFYSFQDKLNLYLIMEFLPG MTLLMKKDTLTEETCFYTAETVLAIDSI GFHRDIKPDNLLDSKGHVKLSDFGLCT KAHRTEFYRNLNHSLPSDFTFQNMNSKR TWKRNRQLAFSTVGTPDYIAPEVFMQT KLCDWSLGVIMYEMLIGYPFFCSETPQ KKVMNWKETLTFPPEVPISEKAKDLILRI WEHRIGAFGVEEKSNSFFECVDWEHIRI AISIEKSIDDTSNFDEFPESDILKPTVATSS TDYKNKDWVFINYTYKRFEGLTARGAII KAAK BERGGLEVBFAVSFLOOLIRYVDEAHOYIL		1		1	1	1	A TO A NEK PVK CKEC\GRAFSLSQILSK\HEKSH
PYECKQCGKAISCSSIRVHERHTIGERYACK KQCKAFSCSSIRVHERHTIGERYACKCGCGKAFR KQCGKAFSCSSSRWHERHTIGERYYCKCECG FIPPSIRVHERHTIGERYYKCKQCGKAFR TSIQHERHTIGERYYKCKECGKAFSRISYFRIH HYRVHTGERYYECKCCGKTRIYTLDLKIHKRNH ERPYECKCCAKTFISLENFRRIMTHTIGENYE CGKAFSCSSYIRIHKRTHTGERYYECKEC AFITYTSFQGHRMITIGERYYECKEC AFITYTSFQGHRMITIGERYYECKEC LHSSFR\HTRIHNYERFLEC*Q\CGKAFSI LKRPMRNAQSDRKLY/KCEK*EKVPINSNI QSCENSH*REKSQCK*YRRDTR*FMYS PHNHVSVSNGPYR/CGSPRLYNT*NISNIF VAVVTP*CSTLFKCLWCWCKRAALSVV* DSGGRWLTPVIPALWEAKAGGSRGQEI ANTVKPHLY DFYERKFEQFIEGHKQIVNKWRDLLCSW LSIKKSVLQNNL*FSAASMRFQKVFF HLFFSLFLAAMAMTGSTFCSSMSNITIKE MTKVTLENFYSNLIAQHEEREMRQKKLE MEEGIKDEEKRLRRSAHARKETEFLRL RLGLEDFESLKVIGRGAFGEVRLVQKKD VYAMKILRKADMLEKEQYGHRABROIL DSLWVVKMTYSFQDKLNLYLIMEFLPGC MTLLMKKDTLTEETCJFYJAETVLAIDSI GFHRDIKNDNLLLDSKGHVKLSDFGLCT KAHRTETYRNLNHSLPSDFTFQNMNSKR TWKRNRQLAFSTVGTPDYJAETVLAIDSI GFHRDIKNDNLLLDSKGHVKLSDFGLCT KAHRTETYRNLNHSLPSDFTFQNMNSKR TWKRNRQLAFSTVGTPDYJAETVLAIDSI GFHRDIKDNLLDSKGHVKLSDFGLCT KAHRTETYRNLNHSLPSDFTFQNMNSKR TWKRNRQLAFSTVGTPDYJAETVLAIDSI GFHRDIKDNLLDSKGHVKLSDFGLCT KAHRTETYRNLSPSDFTFQNMNSKR TWKRNRQLAFSTVGTPDYJAETVLAIDSI GFHRDIKDNSKRSTFEGVDWEHIRI ALSIEKSIDDTSNFDEFPESDLLRFTVATSS TDYKNKDWFINYTYKRFEGLTARGAII KAAK ETERGIEVERAVSFI.OLLRYYDEAHOYIL		1	1	•	1	1	TOPP DVECKOCGKTFIYHOPFORHERIHIGEN
KQCGKAFSCSSSIRVHERTHTIGERPYKCKECG GKAFISTTSVLTHMTHNODRPYKCKECG GFIPPSFLRVHERHITGERPYKCKQCGKAFR TSIQHERHITGERPYKCKECGKSFARPA HVRVHTGEKPYKCKECGKSFARPA HVRVHTGEKPYECKECAKTFISLENFRRHMTHTIGER KCRDCGKVFIPPSALRTHERTHTGERPYE CGKAFSCSSYRIHKRTHTGEKPYECKEC AFIYPTSFQGHMRMHTGERPYECKEC AFIYPTSFQGHMRMHTGERPYKCKECGK LHSSFRRHTRIHNYEKPLEC*QCCKAFSI LKKPMRNAQSDRKLYKCEK*EKVFNSNI QSCENSH*REKSCQCK*YKRDIT*FFMYS PHNHVSVSNGPYR/CGSPBLYNT*NISINI VAVVTP*CSTLFKCLWCWCKRAALSVV* DSGRGRWLTPVIPALWEAKAGGSRGQEL ANTVKPHLY DSGRGRWLTPVIPALWEAKAGGSRGQEL ANTVKPHLY LSIEKKSVLQNNL*FSAASMRFQKVFF LSIEKKSVLQNNL*FSAASMRFQKVFF LSIEKKSVLQNNL*FSAASMRFQKVFF WIKVTLENPYSNLIAQHEEREMRQKKLE MEEGGLKDEEKRLRRSAHARKETEFLRL RLGLEDFSSLKVIGRGAFGEVRLVQKKD VYAMKLIRADMLEKEQVGHRAERDIL DSLWVVKMFYSFQDKLNLYLLMEFLPGG MTLLMKKDTLTEBETQFYIAETVLAIDSI GFIRRDIKPDNILLDSKGHVKLSDFGLCT KAHRTEFYRNLNHSLPSDFTFQNMNSKR TWKRNRRQLAFSTVGTPDYIAPEVFMOY KLCDWWSLGVIMYEMLIGYPPFCSETTQ KKVMNWKETLTFPPEVPISEKAKDLILRI WEHRIGAPGVEELKSNSFFEGOVWEHIRI AISIEKSIDDTSNTDEFFESDILKPTVATS TDYKNKDWVFNYTYKRFEGLTARGAII KAAK		1 .	1	1	1	1	DVECKOCGK ALSCSSSLRVHERIHTGERFTEC
GKAFISYTSVLTHMTHNGDRYKCRUCGKAFR FIFPSFLRVHERHTGEKPYKCKQCGKAFR TSIGHERHITGEKPYKCKECGKAFRAPAI HVRVHTGEKPYKCKECGKAFSRISYFRIH HTGEKPYECKKCGKTFNYPLDLKHIKRNIH EKPYECKECAKTFISLENFRRHMITHTGERPYE- CGKAFSCSSYTRIHKRTHTGEKPYECKEC AFIPYTSFQGHMRMHTGEKPYKCKECGK LHSSFRRHTRIHNYEKPLEC*Q\CGKAFS\ LKRMRNAQSDRLYJKCEK*EKVFINSNI QSCENSH*REKSCQCK*YRKRDIT*FMYS PHNHVSVSNGPYR/CGSPIRLYNT*NISINI VAVVTP*CSTLFKCLWCWCKRAALSVV* DSGRGRWLTPVIPALWEAKAGGSRGQEL ANTVKPHLY 443 1793 A 3578 287 114 DFYERKFEQFIEGHKQIVNKWRDLLCSW LSIKKSVLQNNL*FSAASMRFQKVFF LSIKKSVLQNNL*FSAASMRFQKVFF LSIKKSVLQNNL*FSAASMRFQKVFF MTKVTLENFYSNLIAQHEEREMRQKKLE MEEGGLKDEKKRRSAHARKETEFLRL RLGLEDFESKVIGRGAFGEVRLVQKKD VYAMKILRKADMLEKEQVGHRAERDIL DSLWVVKMFYSSPQDKLINLYLIMEFLPGG MTLLMKKDTLTEETQYTAETVLAIDSI GFHRDIKPDNLLLDSKGHVKLSDFGLCT KAHRTEFYRNLNHSLPSDFTFQNMNSKR TWKRNRRQLAFSTVGTPDYJAPEVFMOJ KLCDWWSLGVIMYEMLIGYPPFCSETPQ KKVMNWKETLTFPPEVPISEKAKDLLIR WEHRIGAPGVEEKSNSFFEGVDWEHIRI AISIEKISDIDTSNTDEFFESDILKPTVATS TDYKNKDWVFINYTYKRFEGLTARGAII KAAK		1	1			1	VOCCY AFSCSSSIRVHERTHIUEKPYACKEC
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						Amino acid sequence (A=Alanine C=Cysteine,
QID	SEQ ID	Met	SEQ	Predicted	Predicted end	D_Acceptic Acid F=Glutamic Acid.
); of	NO: of	hod	DNO:	beginning	nucleotide	E-Phenylalanine, G-Glycine, H-Histidine,
cl-	peptide	l	in	nucleotide	location corresponding	1-Inclusing K=1.vsing L=Leucing
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nce		ł	914	ng to first amino acid	of peptide	T=Threonine V=Valine W=Tryptophan,
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1799 A 3598 1202 1070 107	(-		1			corresponding	M-Methionine N=Asparagine, P=Proline,
uence 179			1	09/496	correspondi		Co-Clutomine R=Arginine, S=Serine,
### Propries of Peptide Sequence Peptide Sequence			ł	914	ng to first		Threening V=Valine W=Tryotophan,
Applied	ucilco		1				Y-Tunarine Y=I Inknown *=Stop codon.
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LYSGYPELGPYHKESAVIASBESDYARSINAS FSIPOHLVERLARVMAERTVAMPPRARSIKS FSIPOHLVERLARVMAERTVAMPPRARSIKS FFVTTSVVAFFTDSKTYQRTQDNSCSFGLHAR GVELMRPTTFGFDSFYPAHARCQWALRGD ADSVISLITESEDLASCDERGRILLVTYYNTLL SPMEPHALVQLCGTYPPSVITHESSQNVL LITLITINTERRHFGFEATFFQLPPMSSCGGL RKAQGTFNSPYYROHYPPNDCTWNSCVGRL RKAQGTFNSPYYBOHYPPNDCTWNSCVGRL RKAQGTFNSPYYBOHYPPNDCTWNSCVGRL RKAQGTFNSPYYBOHYPPNDCTWNSCVGRL GELAEVISYDSSPCFGGFTCRGRCTRKELR CDGWADCTDHSDEINCSCDAGHGFTCKNSF CKPLFWVCDSLINDGGDNSDSGGSCPAQFT RCSNGKLSKSQQCNGKDDCGDOSDSASCP KVNVTTCHTYTYRCLNGLCLSKGNPECDGK EDCSDGSDEKDCDCGLRSFTRQRVVGGTD ADBGWPWQVSLHALQGGHIGGASLISFNWL VSAAHCYIDDRGFRYSDFTQWTAFLGLHDQS QRSAPQVGRRLKRLISHPFNDFTDYDTDLL LEKKPAEYSSNVRPICLDDASHYPAGKAIWV TGWGHTQYGGTGALLQKGERVNDTTCEN LLPQOTFRMWCVGFLSGQVDSCQDDSGGL SSVEADGRFQAGVVSWGDGCAQRNKFGVY TRLFLFRDWIKENTGV TRLFLFRDWIKENTGV TRLFLFRDWIKENTGV FYSGSPWRMDGSTERLEARRPAGRLPWSRQ EMTRRPSIMAGRQHGWSAQQSATVANPYG ANPDLIFHLGFEDVYIVKNRPLLVGKAV PATQIFFKCNGEWVRQVDHVIRSTDGSGLP TMEVRNYSRQQVEKVFGLEFWVCCVAWS SGTTKSQKAYRIAAVLRKNFEQEPLAKEVSL EQGIVLPCRPPEGIPPAB MEPSLGQGMDLTCPFGVSPACGAQASSWIFG ADAAEVPGTRGHSQQEAAMPHPEDEEPPGG PAAQSPAGQVEKVFGLEFWVCCVAWS SGTTKSQKAYRIAAVLRKNFEQEPLAKEVSL EQGIVLPCRPPEGIPPAB AS610 A 3620 1 2676 MEPSLGQGMDLTCPFGVSPACGAQASSWIFG ADAAEVPGTRGHSQQEAAMPHPEDEEPPGG PAAQSPAGQAGPTAGVSCSPTPTIVLTGDA TSPEGETDKNLANRVSPHKRLSHBILKVSL ASITSVDRAGHIDLVNDQLPDISISEEDKKKN LALLEEAKLVSERFLTRRGKSRSSPGDSPSAA VSPNLSPASSTSSRSNSLTYPTPFEGDEADVS SPHGGENVPKGLADRKQNDQRKVSQGRLAP PRPVYKSKELBLEQKENFDELYPTPFEGDEADVS SPHGGENVPKGLADRKQNDQRKVSQGRLAP PRPVYKSKELBLEQKENFDELYPTTPFEGDEADVS SPHGGENVPKGLADRKQNDQRKVSQGRLAP PRPVYKSKELBLEQKENFDELYPTTPFEGDEADVS SPHGGENVPKGLADRKQNDQRKVSQGRLAP PRPVYKSKELBLEGKENFDELYPTTSPFLLRGLSWDSOFPE PGPRLQKVLAKLLLAEEKRPAGKAGGALAK APGLDFQGVQVPKMQKLTKLREEHILMNN QNLVGLKLPDLSSAAAQEKGLFSELSPAGELE EKSKGLDWMPRISDVLLRKREIHLANN QNLVGLKLPDLSSAAAQEKGLFSELSPAGELE EKSKGLDWMPRISDVLLRKREIHLANN QNLVGLKLPDLSSAAAQEKGLFSELSPAGELE EKSKGLDWMPRISDVLLRKREIHLANN QNLVGLKLPPLSSAAAGEKGRLFSELSPAGELE EKSKGLDWMPR					1	1	LLLVLLGIGFLVWHLQYRDVRVQRVFNGTM
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GVELMRTITGFPDS TYPAHARCQWALRGD ADSVLSLTFRSFDLASCDERGHL.WITVYNTU. SPMEPHAL VQLCGTYPPSYNLTFHSISQOVL LITILITNTERHPGFEATFPQLFRMSSCGRIL RKAQGTRISPY TGHYPNIDCTWNIEVPRN OHVKVRRKFYLLEFGVPAGTCPKDYVEING EKYGGERSQFVYTSNSKITVERHSDSYTDT GFLAFYLSTOSSDCFQGGFQFCKTGRCIRKELR CDGWADCTDHSDELNCSCDAGHGFTCKNELF CKPLFWVCDSLDNCGDNSDEQGGSCPAQFT RCSNGKCLSKSQQCNGKDDCGDGSDEASCP KYNVVTCIKHTYRCLNGLCLSKGNPECDGK EDCSDGSBECDCCGLRSFTRQARVVGGTD ADEGGWPWQVSLHALGQGHICGASLISPNWL VSRAHCYUDDGGFYSDPTQWTAFLGLHDQS QRSAPGVQERLKRIISHPFPNDTTPDVIALL ELEKPAEYSSWAPPICLPASHNYFAGKAIW TGWGHQYGGTOALILQKGEIRVINQTTCEN LLPQQITPRMMCVGFLSGAVDSCQDSGGPL SSVEADGRIPQAGVVSWADGCAQRNKRPVY TRLFLFRDWIKENTGV FYSGSPPWEMGOSTERLEARRPAGRLPWSSRQ EMTRRSIGHQAGVVSWADGCAQRNKRPVY TRLFLFRDWIKENTGV FYSGSPPWEMGOSTERLEARRPAGRLPWSSRQ EMTRRPSIMAGRGHWSAQQSATVANPVG ANPDLLPHFLGEPEDVYIVKKNEPCLEVWCQVAW SGGTKSKGKAYIRIAYLRKIPEGEPLAKEVSL EQGIVLPCRPPEGIPPAE 450 1800 A 3620 1 2676 MEPSLGQMDLTCPFGVSPACGAQASWSIFG ADAAEVPGTRCHISQQEAAMPHIFEDEEPPGG PQAAQSPAGQGPTAGVSCSPTTIVLTGDA TSPEGETDKILARNYRSPIKRISHEHLKVST ASLTSVDPAGHIIDLVNDQLPDISSISSEDKKN LALLEEAKLVSERFLTRRGKRSRSSGDSFSA VSPNLSPSASPTSSRSNSLTVTPTPEGDEADVS SHPPGEPNVFKGLADRKQDQRAVGGRLAP RPPPVEKSKELAIEQKGNIFFDLQYPETTPKGLA PVTNSSGRMALNSPQFPOVESELKQLLKTQ WEGSSPLRSPTTOPAGAGVGPASQGRCPAGE MGPEAGSKAELPPTVSRPPLLRGLKAQLLKTG WEGSSPLRSPTOPAGAGVGPASQGRCPAGE MGPEAGSKAELPPTVSRPPLLRGLKAQLLKTG WEGSSPLRSPTOPAGAGVGPASQGRCPAGE MGPEAGSKAELPPTVSRPPLRGLKAQKLAK APCLKDFQQVPPNRGKLTKLREHILMRN QNLVGLKLPDLSEAAEGEKGLFSELSPAIEEE ESKSGLDVMPNISDVLLKRLRVHRSLFGSAP LTEKEVENNFVQLSSARRIDSYTLSERNQAE ENDATCHEDTTERFETENKASITSSASLWHHCE	'	i	ļ	1	}	Į.	LYSGVPFLGPYHKESAVIAFSEGSVIAI I WSD
ADSVLSLITESPENANCEGRICHLYLYTYNTL SPMEPHALLVQLCGTYPRSYNLTHISSQNVL LITILITNTERRFDLASCEGRIL RKAQGTPNSPYLTGHYPRIDCTWNIEVPNN QHYKYRKFFYLLEBOYAGTCPKDYYENG EKYGERSQFVYTSNSNKITVRFHSDQSYTDT GFLAFYLSTDSSDPCPGQFTCKTGRCTKELR CDGWADCTDHSDELNGSCDAGHQFTCKNEP CKPLFWYCDSLNDCGDNSDEQGCSPAQTF RCSNGKCLSSQQVOKEDDCGDGSDEASCP KYNVYTCTKHTYRCLNGLCLSKGNPECDGK EDCSDGSDEKDCOGLSFTRQARVYGGTD ADEGGWPWQVSLHALGQGHICGASLISFNWL VSAAHCYDDRGFRYSDPTQWTAFLGHDQS QRSAPGVQERLKRISHFFNDFTFYDYDLALL ELEKPAFYSSMVRPICLPDASHVFPAGKATW TOWGHTQYGGTGALLQKGERVYNQTTCEN LLPQQTPRMMCVGFLSGGVDSCQDSGGL SSVEADGRIFQAGVVSWGDGCAQRNKPGYY TRILFIRDWIKENTGV FVSGSFWRMDGSTERLEARPAGRLPWSSRQ EMTRAPSIMAGRQHGWSAQQSATVANPVG ANPDLLPIFLGBFEDVYIVKNKPVLLVCKAV PATQFFKCRGBWVRQVDHVERSTDGSSGL TMEVRNVSRQQVEKVPGLEFWCQCVAWS SSGTTKSQKAYIRIAYLRKIFEGEPLAKEVSL CGGIVLPCRPPFGIPPAE MEPSLGGGMDLTCFFGVSPACGAQASWSIFG ADAAEVPGTRCHSQGAAAMPHIFEDEEPPGE PQAAQSPAGQQGPTAGVSCSTPITVLTGDA TSPBGCTBUKLANR VISPIKRISHHLKVST ASLTSVDPAGHIDLVNDQLFDISISEEDKKIN LALLEAKLVSERFLRRGKSRSSPGDSSA VSRNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHYDFRSKEKLAIEQKERPPQLYPSTTIKGLA PYTNSSGKMALNSPQPGPVESLEGALLKTQ WEGSPLPRSPTODAGAGVCPPASQGRGPAGE MGPEAGSKAELPPTVSRPPLLRGLSWDSGFPE PGFRUCKVLAKLPLAEEKFPAGKAGGKLAK APGLKPDGQVQPVRMQXLTKLREEHLLMRN QNLVGLKLPDLSEAAEQGKGLFSELSPALEE ESKSGLDVMPNISDVLLKRLRVHRSLPGSAP LTEKEVENNFVQLSSARRIDSYSTLSRNQAE BENSTERTERTEKETERKASITSSASLWHHCE		1	1	1	1		FSIPQHLVEEAERVMAEERVVMLPFRARSERD
ADSVLSLITESPENANCEGRICHLYLYTYNTL SPMEPHALLVQLCGTYPRSYNLTHISSQNVL LITILITNTERRFDLASCEGRIL RKAQGTPNSPYLTGHYPRIDCTWNIEVPNN QHYKYRKFFYLLEBOYAGTCPKDYYENG EKYGERSQFVYTSNSNKITVRFHSDQSYTDT GFLAFYLSTDSSDPCPGQFTCKTGRCTKELR CDGWADCTDHSDELNGSCDAGHQFTCKNEP CKPLFWYCDSLNDCGDNSDEQGCSPAQTF RCSNGKCLSSQQVOKEDDCGDGSDEASCP KYNVYTCTKHTYRCLNGLCLSKGNPECDGK EDCSDGSDEKDCOGLSFTRQARVYGGTD ADEGGWPWQVSLHALGQGHICGASLISFNWL VSAAHCYDDRGFRYSDPTQWTAFLGHDQS QRSAPGVQERLKRISHFFNDFTFYDYDLALL ELEKPAFYSSMVRPICLPDASHVFPAGKATW TOWGHTQYGGTGALLQKGERVYNQTTCEN LLPQQTPRMMCVGFLSGGVDSCQDSGGL SSVEADGRIFQAGVVSWGDGCAQRNKPGYY TRILFIRDWIKENTGV FVSGSFWRMDGSTERLEARPAGRLPWSSRQ EMTRAPSIMAGRQHGWSAQQSATVANPVG ANPDLLPIFLGBFEDVYIVKNKPVLLVCKAV PATQFFKCRGBWVRQVDHVERSTDGSSGL TMEVRNVSRQQVEKVPGLEFWCQCVAWS SSGTTKSQKAYIRIAYLRKIFEGEPLAKEVSL CGGIVLPCRPPFGIPPAE MEPSLGGGMDLTCFFGVSPACGAQASWSIFG ADAAEVPGTRCHSQGAAAMPHIFEDEEPPGE PQAAQSPAGQQGPTAGVSCSTPITVLTGDA TSPBGCTBUKLANR VISPIKRISHHLKVST ASLTSVDPAGHIDLVNDQLFDISISEEDKKIN LALLEAKLVSERFLRRGKSRSSPGDSSA VSRNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHYDFRSKEKLAIEQKERPPQLYPSTTIKGLA PYTNSSGKMALNSPQPGPVESLEGALLKTQ WEGSPLPRSPTODAGAGVCPPASQGRGPAGE MGPEAGSKAELPPTVSRPPLLRGLSWDSGFPE PGFRUCKVLAKLPLAEEKFPAGKAGGKLAK APGLKPDGQVQPVRMQXLTKLREEHLLMRN QNLVGLKLPDLSEAAEQGKGLFSELSPALEE ESKSGLDVMPNISDVLLKRLRVHRSLPGSAP LTEKEVENNFVQLSSARRIDSYSTLSRNQAE BENSTERTERTEKETERKASITSSASLWHHCE			1	1	1		FIRST GIALA FORDSKTVOKTODNSCSTOLIAN
SPMEPHALVOLCGTYPPSYNLIPASSIGNUL LITLITNITERRHOGIE-ATFOLPRMSSCGGRL RKAQGTPNSPYYPOHYPPSYNCTYNEVPNIN OHYVYRFKFYLLEPGYPAGTCPKDYVEING EKYCGERSQPVYTSINSKITVRFHSDQSYTDT GFLAEYLSYDSSDPCFGGFTCRTGCIRKER CDGWADCTDHSDELNOSCDAGHQFTCKNKEP CKPLFWVCDSLNDCGDNSDEGGSCPVAGTT RCSNGKCLSKSQQCNGKDDCGDGSDEASCP KVNVVTCTKHTYRCLNGLCLSKGPECDGK EDCSDGSDEKDCDCGLRSFTRQARVVGGTD ADEGEWPWQVSLHALQGGHICGASLISPNWL VSAAHCYDDDRGFRYSDPTQWTAFLGLHDQS QRSAPJOVGERLKRISHPFFNDFTEPTDYDIALL ELEKPAEYSSMVRPICLPDASHVPFAGKAIWV TOWGHTQYGGTGALLQKGGIRVINOTTCEN LLPQGITPRMMCVOFILSGVDSCQGDSGGFL SSVEADGRIFQAGVVSWGDGCAQRNKPOVY TTLPLFRDWIKENTG EMTRRESIMAGRQHGWSAQQSATVANPVPG EMTRRESIMAGRQHGWSAQQSATVANPVPG EMTRRESIMAGRQHGWSAQQSATVANPVPG ANDELLPHILGEPEDVYTVKNKPVLLVCKAV PATQFFKCNGGWVRQVDHVIERSTDGSSGL TMEVRINSRQQVEKVFGLEFYWCQCVAWS SSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSL EQGIVLPCRPPEGIPPAE 450 1800 A 3620 1 2676 MEPSIGGGMDLTCPFGVSFACGAQASWSIFG ADAAEVFGTRGHSQQEAAMPHTEDEEPTCP PQAAQSFAGQGGPTAGAVGSTPTTPCTGGA ADAEVFGTRGHSQQEAAMPHTEDEEPTCP PQAAQSFAGQGGPTAGAVGSTPTTPCTGGA ASSTSVDPAGHIDLVNQLPDISISEEDKKKN LALEERAKUSSERTLTRRGRKSRSSFGSPSA VSFNLSFSASFTSSRSNSLTVPTTPFEGDEADV SPHLSFGSTDVFKGLROKNDORKVSGGRIAP PVTNSSGKMALNSTQPGPVESLEGKQLLKTG WGSGLFRSTTQDAAGVGPPASQGRPAGEP MGPEAGSKAELPFTVSRPPLLEGLSWDSGFE PGPRLQKVLAKLPLAEEKERFAGKAGGKLAK APGLKDPQQVQPVRMQKLTKLREHILMRN QNLVCLKLPDLSSAARGERGLSELSPAIEE EKSGLDVMPNISDVLRALREVHSSLFGSAPP LTEKEVENVFVQLSSAFRNISSTLESSRIQAE EKSGLDVMPNISDVLRALREVHRSLFGSAPP LTEKEVENVFVQLSSAFRNISSTLESSRIQAE BENLT TERPTIFKER LFPKKASTSSTLESSRIQAE BENLT TERPTIFKER LFPKKASTSSTLESSRIQAE BENLT TERPTIFKER LFPKKASTSTSLESDRQAE BENLT TERPTIFKER LFPKKASTSTSLESDROAP LTEKEVENVFVQLSSAFRNISSTLESSRIQAE	1	l	1		1	1	CARRI ARRITTEGEPHSPY PAHAKCO WALKOD
LITILITNIERRHPGIFEATHFQLPKMSSCOGR. RKAQGTRISPYYPGHIDCTWNIEVPNN QHVKVRFKFYLLEPGVPAGTCFKDYVEING EKYCGERSQFVYTSNSNKITVRFHSDQSYTDT GFLAEYLLSYDSSDPCFQGTCTRCTRCTRKELR CDGWADCTDHSDELNCSCDAGHGFTCKNKE CKPLFWVCDSLNDCGDNSDEGGCSCPAQTF RCSNGKCLSKSQQCNGKDDCGDSDEASCF KVNVVTCTKHTYRCLNOLLSKGPBECDGK EDCSDGSDEKDCDCGLRSFTRQARVVGGTD ADEGEWPWQVSLHALQGGHICGASLISPNU VSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS QRSAFGVQERRLKRIISHPFNDFTDPVDIALL ELEKPAEYSSNVRPICLPDASHVFPAGKAIWV TOWGHTDYGGTGALLQKGERVINQTTCEN LLPQGTPRMMCVGFLSGGVDSCQDISGGFL SSVEADGRIPQAGVVSWGDGCAQRNKPQVY TRIPLFRDWIKENTGV FVSGSPWRNDGSTERLEARRPAGRLPWSSRQ EMTRRSTMAGRQHGWSAQQSATVANFVPG ANPDLLPHFLGEPEDVYTVKNKPLLVCKAV PATQIFFKCNGEWVRQVDHVIERSTDGSSGLP TMEVRINVSRQVEKVFGLEEYWCQCVAWS SSGTTKSQKAYRIAYLRKNFEQEFLAKEVSL EQGVLPCRPFEGIPPA ADAAEVPGTRGHSQCAAAMPHPEDEEPPGE PQAAQSFAQQGGFTAGVSCSPTFTIVLTGDA TSPEGETDKNLANRVHSPHKRLSIRHLKVST ASLTSVDPAGHIDLVHQLPDISISEEDKKKN LALLEEAKLVSERFLTRRGRSSRSGDSPSA VSFNLSPSASSTSSRSNSLTVPTPFBGDEADVS SPHGEPNYPKGLADRKQMDQRKVSQGRLAP RPPVEKSKEIALEQKENFEDPLQYFETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLIKTG WEGSSLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPFTVSRPPLLERGLSWDSGPE PGPRLQKVALKLFLAEEEKRFAGKAGGKLAK APGLKDPQIQVQPVRMQKLTKLREHILLMRN QNLVGLKLPDLSSAAFQBGCPBLSPAREE EKSGLDVMPNISDVLLKLLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKRQAP LTEKEVENVFVQLSSAFRNDSYTLESKRQAP LTEKEVENVFVQLSSAFRNDSYTLESKRQAP LTEKEVENVFVQLSSAFRNDSYTLESKRQAP LTEKEVENVFVQLSSAFRNDSYTLESKRQAP LTEKEVENVFVQLSSAFRNDSYTLESKRQAP	ł	1	1	ŀ	1	1	ADSVLSLTFRSFDLASCDERGRHLVII VINIU
RKAQGTFNSFYYEGHYPRINGLY WILE VAN OHVXVRFFFYLLEPGYPAGTCPKDYVEING EXYCGERSOFVYTSNSNKITVRFBOQSYTOT GFLAFYLSYDSSDPCPGOFTCRTGRCIRKELR CDGWADCTDHSDELNCSCDAGHQFTCKNKEF CKPLFWVCDSLNDCGDNSDEQGSCPAQFT RCSNGKCLSKSQQCNGKDDCGDGSDEASCP KVNVVTCIKHTYRCLNGLCLSKGPECDGK EDCSDGSDEKDCDCGLSFTRQAFVVGGTD ADEGEWPWQVSLHALGQGHICGASLISPNWL VSAAHCYIDDRGFRYSDFTQWTALGLHDQS QRSAFGVQERLLKRISHFFNDFTFDYDIALL ELEKPAFYSSMVRPICLPDASHYPAGKAIWV TOWGHTQYGGTGALLQKGERVNNOTTCEN LLPQQITPRMMCVQFLSGGVDSCQGDSGGEL SSVEADGRIPQAGVVSWGDGCAQRNKPQVY TRLLFFRDWIKENTGO SSVEADGRIPQAGVVSWGDGCAQRNKPQVY TRLLFFRDWIKENTGO EMTRRPSLMAGRQHGWSAQQSATVANPVPQ ANPDLIPHILGEPEDVYIVKNKPVLLVCKAV PATQIFFKCNGGWVRQVDHVIKRSTUGSSGLP TMEVRINVSRQQVEKVFGLEFYWCQCVAWS SGTTKSQKAYRIAYLRKNFEQEPLAKEVSL EQGIVLPCRPPEGIPPAE MEPSLGQGMDLTCPFGVSPACGAQASWSIFG ADAAEVYGTRGHSQQEAAMPHIPEDEEPPGE PQAAQSPAGQQGPTVAGCSFTPTIVLTGDA TSPEGETDKNLANRVHSPHKRISHHLKVST ASLTSVDPAGHIDLVNDQLPDISISEEDKKKN LALLEERKLVSEFTLTRRGRKSRSPGDSPSA VSPNLSPSASFTSSRSNSLTYPTTPEGDAADA SPIPLGFENNYKGLADVSCSTPTIVLTGDA PVTNSSGKMALNSPQPGPVESLGKQLIKTG WGSSGFFNYFGLADAGVGPASQCRPAGEP MCPPASQCRFPASQCRPAGEP MCPPERNYFKCLINGKNDORKVSQGRLAP PVTNSSGKMALNSPQPGPVESLGKQLIKTG WGSSIFRSTTODAAGVGPPASQCRGPAGEP MCPPASQSKAELPPTVSRPPLLEGLSWDSGFE PGPRLQKVLAKLPLAEEKRRAQKAGKLAK APGLKDPQIQVQPVRMQKLTKLREHILLMRN QNLVALKLPLAEEKRRAGKAGGKLAK APGLKDPQIQVQPVRMQKLTKLREHILLMRN QNLVALKLPLAEEKRRAGKAGGKLAK APGLKDPGIQVQPVRMQKLTKLREHILLMRN QNLVALKLPLAEEKRRAGSAPD LTEKEVENVFVQLSSAFRNDSYTLESSRIQAE EKSGLDVPMTNISDVLRALREVHRSLFGSAPP LTEKEVENVFVQLSSAFRNDSYTLESSRIQAE EKSGLDVPMTNISDVLRALREVHRSLFGSAPP LTEKEVENVFVQLSSAFRNDSYTLESSRIQAE EKSGLDVPMTNISDVLRALREVHRSLFGSAPP LTEKEVENVFVQLSSAFRNDSYTLESSRIQAE EKSGLDVPMTNISDVLRALREVHRSLFGSAPP LTEKEVENVFVQLSSAFRNDSYTLESSRIQAE ERSTENTENTE ENFKASITSSALWHIEC	1	l l	1	1	}	1	SPMEPHALLVQLCGTYPPSYNLTFHS/SQAVE
OHYKVREKFYLLERGYFAGLTANDT TO REYCERSOFVYTSISNIKITVERHSDQSYTDT GETAEYLSYDSSDPCPGGFTCRTGRCREELR CDGWADCTDHSDELNCSCDAGHGFTCKNEF RCSNGKCISKSQQCNGKDDCGDGSDEASCP KVNVVTCKHITYRCHGLTSKGMPECDGK EPCSDGSDEKDCDCGLRSFTRQARVVGGTD ADEGEWPWQVSLHALGQGHICGASLISPNWL. VSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS QRSAPGVQERRLKRIISHPFFNFTFDYTDLALL ELEKPAEYSSMVRICLPPFNDFTFDVTDLALL ELEKPAEYSSMVRICLPDASHVPFPAGKAIWV TGWGHTQYGGTGALLQKGERVNNQTTCEN LLPQQTTPRMCVGFLSGGVDSCQGDSGGPL SSVEADGRFQAGVVSWGDGCAQRNKPGVY TRLPLFRDWKENTGV TRLPLFRDWKENTGV FVSGSFWRMDGSTERLEARRPAGRLPWSSRQ EMTRRPSLMAGRQHWSAQQSATVANPVPG ANPDLLPHFLGFEDVYIVKNFVLLVCKAV PATQIFFKCNGEWVRQVDHVERSTDGSSGLF TMEVRINVSRQQVEKVFGLEFWCQCVAWS SSGTTKSQKAYIRLAYLRKNFEQEPLAKEVSL EQGVUPCRPPEGIPPAE 450 1800 A 3620 1 2676 MEPSLGQGMDLTCFFGVSPACGAQASWSIFG ADAAEVPGTRGHSQQEAAMPHIPEDEEPPGE PQAAQSRAGQQFPTAGVSCSPTPTIVLTGDA TSPEGETDKNLANRVHSPHRLISHRLKVST ASLTSVPPAGHIDLVNDQLPDISISEEDKKN LALLEEAKLVSERFLTRGRKSRSSFGDSPSA VSPNLSPSASPTSSRSNSLTVPTTPFEGDEADVS SPHFEGETVFVKGLADRKGNDGRKVSQGRLAP RPPPVEKSKELAEQKENFIDLQVPETTPKGLA PVTNSSGKMALNSPOPGPVESELGKQLLKTG WEGSPLRSSTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLQYPETTPKGLA PVTNSSGKMALNSPOPGPVESELGKQLLKTG WEGSPLRSSTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLQTLERGLSWDSGPEE POPKLQKVLAKLYLAEEEKRAGKAGGKLAK APGLKDFQQVQVPWMQKLTKLREHHLMRN QNLVGLKLPDLSEAAEQEKGLPSELSPALEEB EKSGLDVMPNISVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKNQAE PROMT TENTITERE HERKASTISSASLWHHCE EKKSLDVMPNISVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKNQAE PROMT TENTITERE HERKASTISSASLWHHCE EKKSGLDVMPNISVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKNQAE PROMT TENTITERE HERKASTISSASLWHHCE EKKSGLDVMPNISVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKNQAE PROMT TENTITERE HERKASTISSASLWHHCE EKKSGLDVMPNISVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKNQAE PROMT TENTITERE HERKASTISSASLWHHCE EKKSGLDVMPNISVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESKNQAE PROMT TENTITERE HERKASTISSASLWHHCE ***********************************	İ	1	1.		1		LITLITNTERRHPGIFEATFFQLPKMSSCOOKL
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				•		// Alaine C-Cysteine
	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
EQ ID	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
10: of	peptide	1100	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
ucl-		- 1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
otide	seq-	1	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
eq-	uence		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
ence			714	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
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	\			peptide	-	/=possible nucleotide deletion, \=possible
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70 TD	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID IO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Crycine, r=Prisadans, I=Isoleucine, K=Lysine, L=Leucine,
ıcl-			USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagille, r=rolling,
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ence	1	1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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	1				462	TRAPASGREGAGLALSANAPDEGGHPGATEG
58	1808	Α	3663	154	402	DAGGI AHASGSARGTWRVRGRGSHGWERIV
		1	1	Ì		GAGGCANPVPALHSCASAPRGTGRVSALGPK
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150	1809	A	3664	902	135	SONALGKYNTSMALFESNSFEKTILESPYYVD
459	1003	11	1			LNQTLFVQVSLHTSDPNLVVFLDTCRASPTSD
	į.	1	1	ì	}	LNQTLFVQVSLH13DFNLVVID1GGHVGRF
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	1		}	1		QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRC
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				Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met ·	SEQ	beginning	nucleotide	I TO A
10: of	NO: of	hod	ID NO:	beginning	location	E-Dhenvisianine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	corresponding	Ly Tantanaina Vel veine Lei Glicille.
otide	seq-	1	USSN	location	to last amino	M-Methionine N=Asparagine, P=Proline,
eq-	uence	'	09/496	correspondi	acid residue	Character R=Arginine, S=Serine,
ence		l	914	ng to first	of peptide	T-Thereprine V=Valine W=1 [VDIODIMI]
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SEQ ID					m It and and	Amino acid sequence (A=Alanine C=Cysteine,
aru w I	SEQ ID	Mct	SEQ	Predicted	Predicted end nucleotide	D-Acportic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	E-Dhenvialanine, G-Glycine, H-Histidine,
nucl-	peptide		in	nucleotide	corresponding	I-Icoleucine K=I vsine L=Leucine
eotide	seq-	l	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	١.	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
испос	ļ	Į.		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ł		residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1	l	peptide		possible nucleotide deletion, v possible
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	į.	1	1	1	1	SGLIGPLKENTIKKWFSQHNHLKADYEKALR
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,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHTTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSDSE
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVDLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVALIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITTQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLIDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHE A SKI TDHNPKTYWESNGSTGSHYITLHM
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVALIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITTQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLIDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHE A SKI TDHNPKTYWESNGSTGSHYITLHM
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	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS I AGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQIITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG
	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS I AGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQILLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW
	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLNILLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEFMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP
	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGLSL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVRAGTEAGRGGIF LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ DPEFNNTDQDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITTQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL
	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS I AGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETQFFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLINR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLIDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL GKTCWEALVSPLVQNITSPDAEGVSALGWLL
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVALIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITTQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLIDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL GKTCWEALVSPLVQNITSPDAEGVSALGWLL
,	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS I AGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITTQ EIRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQALL GKTCWEALVSPLVQNITSPDAEGVSALGWLL DQYLEQRETSRNPLSRAASFASRVRLCHLL VHVEPPPGPSPEPSTRPFSKNSKGRDRSPAPSP
	1823	A	3746	3	500	*ISDKGLVSRICQELLRHLDAEQVSS IAGISL THASGGARSGAGWAGRGVRAGTEAGRGGIF LTLSILRITDLPSGAMSEGVLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLTVPAAVILMLN TEGCSSAARNGLLLLNLLLCNHHTLGDQITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLINR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLIDLERVLCREGSPGGAVRPLLKRL QQETQPFLLLRTLDAPGPNKTLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL GKTCWEALVSPLVQNITSPDAEGVSALGWLL

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	Date and the control of the control
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18.00	SEQ ID					nucleotide	D=Aspartic Acid. E=Glutamic Acid,
Second S	NO: of		hod				F=Phenylalanine, G=Glycine, H=Histidine,
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GLPINSTSDSRPKSSSPIRLPEMSGGOTINKTIE TEPOPTKKASGMISFRGTAGKSPDLSSQKRE TLRGADSAYYQVQOTGKEGTENQGVEQDE VDGGDTQKQLINPHYELQFSDANAKFYCRL YYAGEHRKMEVILDSSEEDFIRSLSHSSPWQ ARGKSGAAFYATEDDRFILKQAPFRLEVQSF LDFAPHYFNYITNAVQQKRYTALAKILGVYR] GYKNSQNNTEKKLDLLVMENLFYGRKMAQ VFDLKGSLRNRVKTDTGKESCOVVLLDENL LKMVRDNPLYRSHSKAVLRTSHSDSHFLSS HLIDYSLLVGRDDTSNELVVGHDVISTRYTWD KKLEMVVKSTGILGQQG*MVQLUENTYVQFLI KLEMVVKSTGILGQQG*MVQLUENTYVQFLI KLEMVVKSTGILGQQG*MVQLUENTYVQFLI KLEMVVKSTGILGQQG*MVQLUENTYVQFLI KLNNKDPATILDVYPNEVKNYVRTKTYTQMF WANFINAKSWKQFTHPSVRT ARARQPEPRILDVNQFKQLUENTYVQKSK KKMCLVVLVQTAILLCERIM*VYQKKSR KKMCLVXXR*G*GATTLITYTTINFTK KKMCLVXXR*G*GATTLITYTTINFTK KKMCLVXXR*G*GATTLITYTTINFTK KKMCLVXXR*G*GATTLITYTTINFTK KKMCLVXXR*G*GATTLITYTTINFTT KKMCLVXXR*G*GATTLITYTTINFTSLXMLLKDRI QEGCKM**KEKCKKKE KKMCLVXXR*G*GATTLITYTT			1	•	1		PSSIIAFALSCKEYRNALEELSKATQWNSAEE
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	1	1			}		RSRSRSQSRSQSQRPGQKRREEPR

						- v	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ	DIM	et S	EQ	Predicted	Predicted end	l w l A sid F= illitatnic Acid.
NO: of		- 1 -		D NO:	beginning	nucleotide	E-Dhenviolanine (1=(i)/Cine, n=nistionic,
nucl-	peptio		l i	n	nucleotide	location corresponding	1 v verlending Verl veine Leichtlich
eotide	seq-	_		JSSN	location	to last amino	1 A-Mathionine N=Asparagine, P=Profile,
	uence	.	10)9/496	correspondi	acid residue	O Characine D=Arginine, S=Settile,
seq- uence	GOLLO		9	914	ng to first	acid residue	I m mi V-Valine W=ITVDIODIJAII,
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20.10	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
QID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
O: of	peptide	1.00	in	nucleotide	location	F=Phenylaianine, O=Glytchic, IT Thistand, I=Isoleucine, K=Lysine, L=Leucine,
icl-	seq-	į	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
otide	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence	donot	1	914	ng to first	acid residue	T-Threenine V=Veline W=Tryptophan,
ciicc		1		amino acid	of peptide	V-Tyrosine X=IInknown, *=Stop codon,
	1	ļ		residue of	sequence	/=possible nucleotide deletion, \=possible
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L			3836	392	88	VAPSPMIMPDLYFYRDPEEIEKEE*AAAEKI
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				1	1	SVPIQQFPTEDWST*PTMNDWSATSTAQTT WVRITTEWP

WO 01/57188

				Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D-Amortic Acid F=Gillitamic Acid.
iO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I-Icoleucine K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	Correspondi	acid residue	O=Ghrtamine R=Arginine, S=Serine,
ence			914	ng to first	of peptide	T=Threonine V=Valine W=Tryptophan,
		ŀ	1	amino acid	sequence	V=Tyrosine X=I Inknown, *=Stop codon,
	i	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
		1		sequence		TPSDMNRAFETDTQSIGEKNRSPSEPDYFERK
493	1843	A	3838	19	380	KFKRS*EKAHIRYKIDQPEDIPLK\EFLCKHSK
173	1 .0.5	1	1			CTATLSMRNMSLMKKKCSFSEEF\LAFFPSLL
	ĺ	1			1	VCHLLAIKLGFYIBIHLTTFNNTF
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	1 3044	A	3845	2	352	FFFLRRSL/DSVAQAEAQWL\ELGLLQAPPPGF
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		1	ł	1	1	FTVLARMVLIS*PCDPPTLASQGTAITGMSYH
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	CEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
NO: of	peptide	1100	in	nucleotide	location	F=Phenylaianine, G=Grycine, ri=Frishdine, I=Isoleucine, K=Lysine, L=Leucine,
nucl-	seq-	•	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
00	uence	1	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
seq- uence		ł	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
UCITOC	1	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
1			1	residue of	sequence	/=possible nucleotide deletion, \=possible
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1	i	1		sequence		A DODE AT RIGVIKKKAMLHOEGHMDDALSL
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	LOECIN	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
NO: of	peptide	1100	in	nucleotide	location	F=Phenylaianine, G=Grycine, N=Instants, I=Isoleucine, K=Lysine, L=Leucine,
nucl- eotide	seq-	l	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T-Threonine V=Valine W=Tryptophan,
		1		amino acid	of peptide sequence	V=Turosine X=Unknown, *=Stop codon,
	ł	1		residue of	Sequence	/=possible nucleotide deletion, \=possible
i	1	1	1	peptide sequence		muoleotide insertion
			-	Sequence		CYFCRISRONQRSMFDHLSYLLENSGIGLGM
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						Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A-mortic Acid F=Glutamic Acid.
10: of	NO: of	hod	ID NO:	beginning	nucleoude	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	location	I Table 1 of the Landing Landi
otide	seq-		USSN	location	corresponding	M=Methionine N=Asparagine, P=Proline,
eq-	uence	1	09/496	correspondi	to last amino	Chromine R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
delice		l	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide		nucleotide insertion
	1	1		sequence		QFLLSCSEADENEMINCEEFANRFQEPARDIG
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						Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A-ordic Acid F=Ghutamic Acid.
	NO: of	hod	ID NO:	beginning	nucleotide	E-Dhanvialanine G=Glvcine, H=Histidine,
	peptide		in \	nucleotide	location	I v verlausing K=I veine I = Leucure.
ucl-	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
otide	uence	i	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
eq-	uence		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
ence			747	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
1			1	residue of	sequence	Y=Tyrosine, X=Unknown,
				peptide		/=possible nucleotide deletion, \=possible
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	0000 00	1/	CEO T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D-Accordic Acid. E=Glutamic Acid.
10: of	NO: of	noa	in in	nucleotide	location	E=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
пеисе	1	l	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
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	1	}	1	1		DLETCGQSGILRELEATIMSGSTMSLNHEAPT
		1	1		1	PRSPAGSDRPSFQERSSSRPHYSQTTRSNTLPS
	1	1	1		1	DVGRKSVTLRKMKQEIKEIMSPTPVELHKVT
	1	1				LYKDSDMEDFGFSVADGLLEKGVYVKNIRPA
		1		1		GPGDLGGLKPYDRLLQVNHVRTRDFDCCLV
	ł	ì		1		VPLIAESGNKLDLVISRNPLASQKSIDQQSLPG
	}	1995	1		ļ	D*SEONSAFFOOPSHGGNLETREPTNTL
		_		-	800	TEVOCUSCIMATERI AROLGLIRRESIAPANG
514	1864	Α	3967	833	1 000	NI GRSKSKOLFDYLIVIDFESTCWNDGKHHH
		1	İ	} .	}	SOEITEFPAVLLNTSTGQIDSEFQAYVQPQEHPI
Į.	1	1	[l .	I SEECMEL TOIKOAOVDEGVPLKICLSQFCK
1		1	1	1	ì	WIHKIOOQKNIIFATGISEPS/DF*SKIMCICYL
	1	\cdot				Up*RISYTY*SKHKSKGC
	1075	HA	3969	492	182	CRFWGISTHCDTCDPLSPQTTEG**EGDLWSL
515	1865	^	3303	452	1	DLLGPEFLARKPLFKTKTYQSTF*SISKNE/FTC
1		1		ļ.		PNFILEEGTDLIF*QVKHNPCHRLTPEEGTVQL
ļ		1		1	ŀ	NRADS CONTRACTOR OF THE CHARLES OF T
516	1866	A	3977	2	1357	KMLC/QKESNYIRLKRAKMDKSMFVKIKTLGI
210	1800	1				GAFGEVCLARKVDTKALYATKTLRKKDVLL
1	į.	1		1	1	RNQVAHVKAERDILAEADNEWVVRLYYSFQ
	•	1		j		DKDNLYFVMDYIPGGDMMSLLIRMGIFPESL
İ	1	{	Į.			ARFYIAELTCAVESVHKMGFIHRDIKPDNILID RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP
1		ł				RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA
}		- 1	1	}		ROHORCLAHSLYGTPNYIAPEVLLRTGYTQL
1	- 1	1		1	1	CDWWSVGVILFEMLVGQPPFLAQTPLETQM
1		}		1	ł	KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE
1		1	1	1		DDI CKNGADEIKAHPIF*NOFDFSO*PEUSKS
	1	- 1	- 1	1		AFKQFP*NHTTPTDTSNFDP\VDPDKLWSDDN
1		}	1			EEENVNDTLNGWYKNGKHPEHAFYEFTFRRI
1			1			PDDNGYPYNYPKPIEYEYINSQGSEQQSDEDI
	j	1			1	ONTGGEIKNRDLVYV
1					1000	FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY
517	1867	A	3980	1358	1022	LAGI DOMOL CHPGWSAVVOSOVI/VNLPPSWD
]				1	*RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA
1	- 1	١		}		OATEOPOPPKVLGLOV
1		L			- 100	SPEMESHPITOAGVOWHHLSSLQPLPPGFK*F
518	1868	A	3986	974	666	CEST PE+I GYRHVPPCLANSVFSVEMUVLH
		- 1		1		VGQAGLELLTSGDLPALASQSAGITG\SHRAR
]		Į			1	DENIGEENIE
					126	NOGI PHYGI CRTCL VNOMFASSILGKSHHHS
519	1869	Α	3994	751	120	LIGINOCHNALWKAAG\PLPLKAGYC\QSFSPQ
						DOLK A CHOMDEK DI TVPORDTHKRSVLK WIS
1			-	ì	}	LODGENI AVEMEEGHCLLILPLGTECLGIKVIV
1	ł	l		1	- 1	HLFSSEMGE\NRPMVG\ARHVYSNAALLSFTF
1	1	1				

	oro m	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
QID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
); of	peptide	1100	in	nucleotide	location	F=Phenylalannie, G=Glycine, 11 111111111111111111111111111111111
cl-	• •		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
ide	seq-		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
4-	uence		914	ng to first	acid residue	Q=Glutamine, K=Arginile, 3=3cinic,
nce			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			 	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1 1	peptide		/=possible nucleotide deletion, \=possible
		ì		sequence		nucleotide insertion
				Sequence		LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI
			1		1	A A PROPERTY I I ITTLES TYPEC
	1	1	l		(00	OSERI SI I SSWDYRHM*PRLANF*TVFCKDK
20	1870	A	3999	882	698	L OT ATT DDT VONGWPOAU PPKPPK V LULYI
20	10.0					FFF*ETVSCSAS*AGVRSHDNSSLQPPSPG\SSN
	1871	A	4011	1346	1178	PPTSASHVAGATGTHHHAWLLSV
21	10/1	1	1			QGIALLTRMGESVKHVTGGYKLRTRPLEFAA
	1000	A	4015	2	377	IGDYLDTFALKLGTIDRIAQRIIKEEIEYLVELR
22	1872	^	4015			IGDYLDTFALKLUTIDKIAQIGIKUBIST
	1	1	1		1	EYGPVYSTWSALEGELAEPLEGVSACIGNCST
	1	1 .	Į.		i .	AL*ELTDDMTEDFLFVLREYILYSDSMK
	1	1	1010	341	19	ERVIHNQIQQAQRSPHIFNARRSS/PRPNIVELP
23	1873	Α	4018	341	1	
			1	}	}	L*NRREWDEAIKVLKEKQULSKMV117AMEDI
	1	ţ	1	1	1	L ON TO STORE DAY
	1				743	- FEET DIVEL (DEVADAGVK WUNLUSLUAFFI OF
524	1874	A	4020	1067	143	I TOPEGOT OF DEGINITY REPORTS LANGUE TO THE POPULATION OF THE POPU
724	1	1				RQGFTVLARMVLIS*PHDLPASASQSAGITGL
			1		1	CITOCUIPT COII C
	1	1				- CONTREEL DECREVACIONOMINOSPICAL
-	1875	+A	4021	781	351	I POOT TO WIGHT SODSIWINY REVEYOUT
525	10/3	1 ^	1021			VETGSCQPCLQLLGSSNPPASASQSAGIAGISH
		ì	ì	1		QGQPE*SFDIRFACVIAALRETFQCLCSASRVN
		-	1	1	1	QGQPE*SFDIRFACVIAALREIT QCDCGT
	1	- 1	1		1	NKIINRPTHPVESSF
			1004	80	341	TPSSTSRGTEEQQSSKMAWQRREEKEHLNVR
526	1876	Α	4024	80	1	Decy EDGMK ADK BADGA 1 AGED UTT 11 21 1 4
		1	1	1		I
	1				230	- LDESG AMERICA GOMMTAVSLITRIVES VALE
527	1877	Α	4026	593	230	1 DATA STREET WALMING NAEKALI KU TIMBUN
		1	ı	4	l l	VCCCCPT *CHPTSKPALVFSUEQUAESCISIA
	1	1	1	ļ	l l	model chambar actual tributation
	l .	i	1			- LODGIANWGPAFPPRPGLALAPILQLI
528	1878	A	4028	1160	242	THE ACCUMENTARY PROPERTY AND ACCUMENTATIONS AND ACC
120	1 20.0		1		1	The ACT DEDICATESEPOPE IL PAGEULEULEUL
	.	- {	İ	1		POPODOTT CIADTUME ISSUIPEDED VIVEDO
	l	1	1	Ì		1 * CONTRACTOR ON DEPOVI PPRAPLOGELULI DO 1
	-			1	l	1 or or deposition to the participation of the part
	1	- 1	1			QLSVEEQMPF WNQTETTSKS\\GSMRNRWKF ETPVASQSSDKPSRDPETPRSS\GSMRNRWKF
		.	1	1		ETPVASQSSDKYSKDFETT KOSKOSKIII TI ROGKA
		l	1		1	NSKVL/GKSPLHPSCQDDNSPGTLTLRQGKA
	1	(1	ı		AFKPLSENVSELK\EGA\ILGTGR\LLKTEGRA
1	1	{		1		I ************************************
1	1				366	- TYPE OUT INTERNOSMITMIC POYL ETRICIPULI
529	1879	A	4039	2	1 300	
		1		1	1	II TIIVSIM*EHTFHNAGV*LSDIYPKIIVINGI V
1	1	ļ	1	1	1	I *#PPIZYP#X#EIXVI HVVV K I WAXUE
1	1	1				
520	1880		4057	358	3	PARTICOLD THE LEGISLAND RICH EN LA LIVING
530	1000	^	1,		İ	/DTDKWKDILCSWIRRIHMKDILCSWIGRTH
1	1	Ì	l	ł	1	/DIDKWKDILCSWIRGHIMAI
1		1	1	1	\	VKISILPKVNYRFYLISIKIIMAI VKISILPKVNYRFYLISIKIIMAI
				50	278	TQGTEEIYKISSCEWVQASFSTPLITLHDFKIY
531	1881	A	4061	1 30	7	I ame and process of the PORTURE OF A PORTUR
1		- }				IYDQFIFDKGEKIIQEKGNSFFNN/MCWKNW
	1	1	1	1	1	and very
		i				- STOUT ENEVEWEFERE LENINGTVIEKE IGG
532	1882	A	4069	19	368	convision to the contract of the contrac
334	1002	` ''		i		KLFQNTE/TEGRHPISLYEFRITLITIPNKDNIY
1		ı	1	1		LOSTER MOUGH MANILY IT K CP I
l		- 1	1			PIRKFTKVAG*KSNTPK*LAFLHINNEQFENI
			407	6 1	355	PIRKFTK VAUTASINTEN LATERATOR VTETT.I
	188	3 /	1 40/	• •		ITNI/PFIIASKRIKYSGISLTKEMKDLYTETLL KIKEDTNKWKDI/SCFWVGR/LNIVKMPK/VI
533	1					

				7 11.1.1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1 1			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	' '		1	residue of	sequence	/=possible nucleotide deletion, \=possible
	.		ì	peptide		nucleotide insertion
	}	1		sequence		IFNAIPIKMPMMCMAKIEKNSS
						IIDSSTRRMESERSPLYRQLIDLGYLSSSHWNC
534	1884	A	4088	3	1931	IIDSSTRRMESERSPLYRQLIDLG I LSSSITWIC
JJT	100.			į.	1	GAPGQDTKAQSMLVEQSEKLRHLSTFSHQVL
	1				1	QTRLVDAAKALNLVHCHCLDIFINQAFDMQR
				ļ		DLQITPKRLEYTRKKENELYESLMNIANRKQE
	ì	1	1	Į.		EMKDMIVETLNTMKEELLDDATNMEFKDVI
	1	i		ľ		VPENGEPVGTREIKCCIRQIQELIISRLNQAVA
	ļ	1	1	1		NKLISSVDYLRESFYGTLERCLQSLEKSQDVS
	1		1	İ	1	VHITSNYLKQILNAAYHVEVTFHSGSSVTRM
	l	1	1	1	· ·	LWEQIKQIIQRITWVSPPAITLEWKRKVAQEAI
	1	1	1			FSI SASKI AKSICSOFRTRLNSSHEAFAASLKQ
	Ì	1		1		I DACHGGRI FKTEDI WLRVRKDHAPKLAKUS
	İ	ľ	1	1	j	I POPOLODVI LHRKPKLGOELGRGOYGVVYL
	į.	1	1		1	CONWECHEPCALKSVVPPDEKHWNDLALEF
			ł	1		HVMD SI PKHERI VDI HGSVIDYNYGGGSSIA
ł	Ì	1	,	1	1	VI I IMPRI HRDLYTGLKAGLTLETKLQIALDV
		1 .	1	1	1	VEGIREI HSOGI VHRDIKLKNVLLDKQNKAKI
	1	1	Ì	1		TOI GECKPEAMMSGSIVGTPIHMAPELFIGK
ŀ		1			}	VDNSVDVVAFGILFWYICSGSVKLPEAFERCA
Ì	·	1		1		CKINHI WNNVRRGARPERLPVFDEECWQLME
	197	1	1	1		ACWDGDPLKRPLLGIVQPMLQGIMNRLCKS\
1		1	1	1		NSEOPNRGLDDST
					417	AT MPHEANYEEIFLKTDKDMDGFESGLEVKE
535	1885	Α	4090	2	417	IFI KTR/GLPSTLLAHIWALCDSKDCGKLSKD
1	ı	1	i	ł		LIEAL AFHILIT\OKLIKGIDPPLVLTPEKISPSNR
1	}	i	1	1	ľ	ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK
		1		1		HNRKRIWI.RA
					1 222	DHQK*KNIPCSWIGRINIVKMSILPKAIYRFSAI
536	1886	Α	4102	569	829	PIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK
		ì	1			EQNLEESHYLDFK*YYRAV
1		1	l			SIDCEHLIRRMLVLDPSKRLTIAQIKEHKWML
537	1887	A	4104	54	281	IEVPVQRPVLYPQEQENEPSIGEFNEQVLRLM
1 55.		1				
j	1.	į.		·		HSLGIDQQKTIE IRHIPLKIRSVVSHLKCFYKFILTFFFAGCSQPL
538	1888	A	4109	141	314	IRHIPLKIKSV VSHLKCI IITAI DVS
330	1000	1				VPRENITAWMNAIGLIITALPVS
539	1889	A	4111	268	1	ASRPWGHSYP*FNQQEVDTLKRPIASSEI*MM
1333	1007					I*KFAT\KKSPGPYRFTAEFSHTFKEDLVPILW
	1	1	1			PLFPKIYREGTLPHSFYEASITL
540	1890	A	4142	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE
340	1030	1^	1 112	1 7		AALGDFLGLHRRTQQPAVDRLLSDASAQWR
		1				VRGHGGVRESGRAPQQPGRRRGRRPRKRPR
1	1			•		GRWRREGCGAGGRGVCVAAWSQRSIAGNN
	1	1			1	DVRIFHKMSNSHPLRPFTAVGEIDHVHILSEH
	1	1		1		IGALLIGEEYGDVTFVVEKKRFPAHRVILAAR
		1		i		COVERALLYGGMRESOPEAEIPLQDTTAEAF1
1 .	j			1.	ł	MILKVIVTGRATLTDEKEEVLLDFLSLAHKY
1		1	1			GEPEL EDSTSEYLCTILNIONVCMTFDVASLY
1	1	1	-			ST PKT TCMCCMFMDRNAOEVLSSEGFLSLSK
		- 1]		TALL NIVERDSFAAPEKDIFLALLNWCKHNSK
	ļ	l		1		ENHAEIMOAVRLPLMSLTELLNVVRPSGLLSF
1	- 1	ł		l		DATEDATKVRSESRDMDLNYRGMLIPEENIA
1				i		MKYGAOVVKGELKSALLDGDTONYDLDHG
			1	1] .	FSRHPIDDDCRSGIEIKLGQPSIINHVRILLWDR
1	1	- 1	1	-	1	DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS
1		-	1	- {	-	WQKLYFPARVCRYIRIVGTHNTVNKIFHIVAF
-	- 1	ł	- 1	ł	1	WOKTALAKACKI KI AGILIMI AMATADOVAMI
1	1	1	1	1		ECMFTNKTFTLEKGLIVPMENVATIADCASVI
	1		1		1	EGVSRSRNALLNGDTKNYDWDSGYTCHQLG
		1			,	SGAIVVQLAQPYMIGSIRVLLWDCDDRSY
	1001	-+-	4146	282	778	GTLGYPNGARGQPQDNFFAHQ\VSHHPPISAC
541	1891	A	1 4140	202		

						Amino acid sequence (A=Alanine O=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-Americ Acid F=Glutamic Acid.
10: of	NO: of	hod	ID NO:	beginning	nucleotide	R-Phenylalanine, G-Glycine, H-Histidine,
ucl-	peptide		in	nucleotide	location	I-Icoloucine K=I.vsine, L=Leucine,
otide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	O-Clutomine R=Arginine S=Serine,
ience		ļ	914	ng to first	of peptide	T-Threonine, V=Valine, W=Tryptophan,
		-		amino acid	sequence	v=Tyrosine, X=Unknown, *=Stop codon,
ļ		Ì		residue of	Sequence	/=possible nucleotide deletion, \=possible
		1	l l	peptide sequence	ļ	analestide insertion
				sequence	ļ	UAESENEAEWODMKWKNKFWGKSLEIVPVG
		1			1	TUNIVE PRECIDIFEWNKYTSCHNYLSGUKW
	1		1	ł	1	TELLYCEVI IRNTODSSCHCKITFCKAKY WSSN
•		1	1	Į.	1	VHEVOGAVLSRSGRVLHRLFGKWHEGLYRG
	1	1	1			PTPCCCCTWKP
	<u> </u>	 	4147	44	433	SVDAYVCNDIVFSYRTTITLLEGA*LTHRYVA
542	1892	A	4147	1 **	1	QDPKQGQLRSLHLTCDSAPAGSQGTWSTSCR
				1		INHLIFRGGAQITFLATFDDSPKAVLGDRLLLT
	•	1		1		ANVSSENNTPRTSKTTFQLELSVKDAVYTVV
	1	1	ļ	ì		SSH SSH INDEED I DIMALDH
- 10	1893	A	4153	678	11	TISYPOCLTOMYFLISFANVDTFLLPIMALDH
543	1893	1^	1425	1	1	YVAICSALQ*CSIITP/ELCQGLPVLA*AGSSLIS PVHTVIMSRLAFCSSAQISHFYRDAYLLMKIA
		1	1		1	PVHTVIMSRLAPCSSAQISHI TIOTILIVSYIRIA CSHT*\NQHVFLGAVVLFLAPCALILVSYIRIA
		}	1]		AAILRIPSPTRRKACSICSSHLSLVTLFYGTV
		1	1	1		LGICI*PPDSFSAQDAIATIMYTVVTSMLNPFTY
		1	İ	Į.		SLMNKEVQEAVRRLFSRGSHSSWCW
	1	i .				TIVA OA GVO I NI SSI OPOPAGLKOSSHPSLP
544	1894	A	4158	3	538	SSWDYRYSTPHPANFFVEMEFHHVAQAGLEL
J44	1071	1		ı	1	L CCCDI PTCTCHSAGITGV\SHHAPPKLISSEUS
		1	. 1			LICHTICI PMVFPLLCVFVLISSSLAGEEAAU
		- [· I	-	LRVQKLWPAVVLSHLPVCWFHCSGIWSEVIE
	1	1		1		I I VVCDECHVI PWOAHVVBF
	1	1			1	UDI CI GI VPSEJESPODKKAADGSILAPARGE
545	1895	A	4160	1	412	DIEAGI KGGFMDGRLOASVSVIKIUKYOSAM
3.5				1	l	L COMA CA MOCT DVYPTSHCFMAGGKSKSQQW
	1	1			-	ELELSGEPAPGWQVLAGYTYTQARYLRDASE
ì		İ	}	1	}	LANDICODI PDV/DPR
1			- 191	1252	1190	TEOVERI ET REKTEFHSCCPGAVOWHULUSI
546	1896	A	4174	1232	1120	ODDDDD EK GESCL SLPSSWDYKHAPARIFAINE
	1	i	Ì			FLVETGFLHV\GQ\ASLELPISGDIPAS\ASQSA
ł		1				GITGVSHHA*PRASGRRCW
<u> </u>			4176	3029	1	AGPDGLAAPASCQGARGQTRVPGAFSWLAP
547	1897	A	4170	3027	1	COURT A CECT APGVPPA (ICIVSAUBLIAFF QUA
l		l l		1	Ì	WGLGAPPAAPRPESDEKRAGSDAVRSFSRGA
	.		- [1	RDSLGQRRLGGTRGAGPAGKGAQRTMGPAS
ļ	1	1	į .	- (1	GFHSFPPRPHQEPSPRSSCWQHLLWHCPWPC
	1	- 1	·	į		PSRLPRLTPAQLLQGPGVLAAPPGP*HVPGFL
1		- 1			1	AQSPWPLPSGPRSP*DPLHQGALVPLPQGGSI
		 				HTAPHCLPSVLSPAIQQPLLPTAST/SSRSPPA
1		- }				TMAPIPSALAVWEPAGSSPQLSSAPADSSVPL
1		- 1		1		ALPKVLPPWTQKPLLGCLCQSPLPLLSPPDQI RCPPACSPAAASSFSFESQPCPSAPSKASPAPA
1	1	1	- 1	İ	l	RCPPACSPAAASSPSPESQFCFSAI SICILIFIED
1	- 1	- 1	-		1	ALIVGPHHPP*SQQPQSQSVHPHGPGGPQPP AASSLFWMFCQPPPPHPQFLWHRPLPVTGK
	l	1	1	j j	ŀ	AASSLEWMECOPPPPHPOPLWING IN VIOLE
1 .	: [1		l l		LASSPLCFRPAPGSLRQTPLPPQFHIPRPGLSA
	.	- 1				PPPASGTSDSSDSRSPSASAARVWPPA\SPPP
Ξ.		1	1		1	AARHRPHPPEYFLSPCPFSCGFPRLLGRPRRI
1	-	1	1		ı	ALQTPRAWDLPPGSSPAPLCSGPELP*APPPI
1	- 1	- 1	1	1	1	PFPRVA*LGSGHPPSAQVPGLW*RCV*GHPU
1			1	ŀ	1	RPVGHS*SGPPHSPPL*APPQAWPLELPPSRQ
1		1	1	1		LQPLHLRAAQPLDPCCSLSPPGPPLPVPALPS
	1	- 1	1			WPGRP*SPSPASSQPPYHAGLPGPQSSPLPPC
			1	1	1	PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSI
1		l		- I ·	1	PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVO
	1	1		1		TPSRSASSLPEVVLASSLPKIPQSSGSVPLGPT MP*CFHRPSPPLP/LSSPFPA/LRPQAPQFPLH
				- 1	İ	MP*CFHRPSPPLF/LSSITIADIQ C. L.
						P*PPAPSPGCPLPPLAQQHQPSPPSPHARSTL PPLWPSLALLP*PLPPPPPVPSFSASLLCSLPA

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	I To A mortio Acid Fest illiamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	E-phenylalanine G=Glycine, H=Hisudine,
nucl-	peptide		in	nucleotide	corresponding	I verte leveling K=I veine L=Leuchie.
eotide	seq-		USSN	location correspondi	to last amino	NA-Methionine N=Asparagine, P=Profine,
seq-	uence	<u>'</u>	09/496	ng to first	acid residue	O-Clutemine R=Arginine, S=Settine,
uence		1	914	amino acid	of peptide	T-Theonine V=Valine W=ITVDtOphan
		1	1	residue of	sequence	V-Tyrogine X=Inknown, *=Stop couon,
1		1	1	peptide	554	/=possible nucleotide deletion, \=possible
	İ	1	1	sequence	1	nucleotide insertion
				Sequence		GTPASPGLGRSCLGKPQTLPWISFWPPSGRLA
	}	1				PGTWQPW/PVSPAPLSCLSAWDPWELPSPQPQ PGTWQPW/PVSPAPLSCLSAWDPWELPSPQPQ
1		1	1	ł		VCSTAELPTSCLLSSPGPPAFQPPRFGCL*GPP
		1		Ì		GPPGLPPLQSSLSFPPPPPPVPQPPAPPALQWG
1	· ·				1	1 nccnrrv
			1.00	2369	844	RIHREEDFOFILKGIARLLSNPLLQTYLPNSTK
548	1898	Α	4180	2309		
		1		ł	ì	GEQLPQ*PGGRDSVRLRGVGQSCPSLELSPLG
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Gutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
	peptide	1	in	nucleotide	location	Fernenylalanine, U-Olycine, II-Tusine,
nucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}	ł	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	1	ì		soquonos	/=possible nucleotide deletion, \=possible
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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	I to A control A cid Feet illustante Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	E-Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide location	corresponding	I r_reglerighe K=I vsine L=Leuchile
eotide	seq-	1	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O-Chytomine R=Arginine, S=Serine,
uence		l	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
į.		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide		/=possible nucleotide deletion, \=possible
}	1	ı	1	sequence		nucleotide insertion MGIFHNEDLKHILQLIEPSVFKEAATPEEESDT
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SEQ ID No. of hod							Amino acid sequence (A=Alanine O=Cysteine,
NO. of No. of USSN	LOEO ID	OI ORZ	Met	SEQ	Predicted	Predicted end	
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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	- A
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	r-phenylalanine G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	v_v_loucine K=I vsine FLEUCINE,
eotide	seq-		USSN	location correspondi	to last amino	NA-Methionine N=Asparagine, P=Profine,
seq-	uence		09/496	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	1		peptide	boquan	/=possible nucleotide deletion, \=possible
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						(A=Alonine C=Cysteine
	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
SEQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, b=Glutamine, H=Histidine, F=Phenylalanine, G=Glycine, H=Histidine,
NO: of	peptide	nou	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
nucl-	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
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	1			1	_	ETYTLSSKMGPDSKPSEGDVFPRTSE RNSRPLWCSPPASOPROAPVSQSCCCPLPSSSS RNSRPLWCSPPASOPROAPVSQSCCCTIMI.P.
L		-	4288	83	406	PPSALLAPTKPRALGTLRLYECSPELGTTMLP
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			A 120	0 2012	1843	COKEL TITPIVLYFLTSFYTKYDQIHF VLNI VC
568	191	8	A 430	00 2012	1843	SRKFLTITPIVLYFLTSFYTKYDQIHFVLNIVS LMSVLIPKLPQLHGVRIFGINKY WTFCLFL/WWVPESARWLLTQGHVKEAHRY

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	l to_A mortio Acid F⊨Ghrtamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	R-Phenylalanine G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I I-Icoloucine K=I vsine L=Leucine.
eotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine N=Asparagine, P=Proline,
seq-	uence			ng to first	acid residue	O-Glutomine P=Arginine, S=Senne,
uence			914	amino acid	of peptide	T-Threanine V=Valine W=Tryptophan,
			1	residue of	sequence	V-Tyrosine X=I inknown *=Stop codon,
				peptide	304	/=possible nucleotide deletion, \=possible
			i	sequence	i	nucleotide insertion
				Sequence		LLHCARLNGRPVCEDSFSQEVRVNVCVSMHI
			l	ł		CVWWGVGCVKCLPPRAHHIWQEKPLGPIKI
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574	1924	_ A	4346	333		LTT VEDICTSDVRVWDLLLLIPNVLFLIFLLWA
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576		1 - 1		1	ì	GPQAQSHAACQPEPEPPRVLLDPTAARGGVQ
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576	1,520					GPUAQSHAACQPELDTIKYDDD
576	1,720					GPQAQSHAACQFEI BITTOTHTPWPQSGRLPCAS GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCAS EPLPLGGIRPTPGLEPKGRDLM

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
QID	SEQ ID	Met	SEQ	Predicted	nucleotide	
); of	NO: of	hod	ID NO:	beginning	location	n phandalanine (intivelle, n-nisuumo,
	peptide		in	nucleotide	location	l · -: V-I veine L=Laucille
cl-	seq-	- 1	USSN	location	corresponding	1 \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
tide	uence		09/496	correspondi	to last amino	La con de la Dara Arconomo Nacionales
q-	UCITOC		914	ng to first	acid residue	l m mi
nce			7.	amino acid	of peptide	1 to the same Very Introduction - Duble vouces
		•		residue of	sequence	/=Iyrosine, A=Olikilo /=possible /=pos
			l	peptide		/=possible nucleonide defenda, \ \ possible
		1	١.			nucleotide insertion
				sequence	502	nucleotide insertion SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW
77	1927	Α	4366	785	302	I LOW TOD A CODD VIA COLL TARY DANKE TO DESCRIPT
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	1928	A	4367	1	221	SRLSLLSSWDYRHP/HAANFCIFSRDG\VSPYW
78	1520	1		1		
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		4	4383	1	224	FETESHSV TQAGMQWINLESHSV TQAGMQVSP FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP
79	1929	A	4383	1 *		FSCLRLQSSWDHRHAFTILLAIM OM ON
	1			1	l .	CWPGWSSTPDLK
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580	1930	A	4397	410	177	I ARTITITITE CONKERSTATINOT LEGGS
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	1	- 1				- L
			4439	1	628	
584	1934	Α	4437	1 -		
l			1	1		GOOLWNRMKPAPGTVEVSSSTSRSDPLLLPPR
1		- 1		1	1	GQQLWNRMKPAPGTCFKVONHSGSSAR
i		- 1		1	1	GQQLWNRIVITAL OF STATE ALAPTQRASTVVLAPSPT/SEKVQNHSGSSAR ALAPTQRASTVVLAPSPT/SEKVQNHSGSSAR ALAPTQRASTVVLAPSPT/SEKVQNHSGSSAR
!	1	ı	1	1	1	GNLSGKPDDWP/LGHERVCGALLHRL*VGGG
1	1	1	- 1	ļ		QGPHGKAAQGGAAGAAGRLGLYH
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585	1935	A	4463	10	144	
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					- 1 - 1 - 4	Amino acid sequence (A=Alanine C=Cysteine,
QID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	Last Anial Cartinismic Acid.
0: of	NO: of	hod	ID NO:	beginning	location	r-phenylalanine G=(ilVcine, n=nistante,
icl-	peptide	1	in	nucleotide	corresponding	l v vlensing V-l veine LELEUCHE
tide	seq-		USSN	location	to last amino	1 \ A-3 dechioning N=A sparaging, P=Proling,
q-	uence		09/496	correspondi	acid residue	1 O-Clistomine D=Aroinine, S=Senile,
ence			914	ng to first		m Theoring V=Veline W=ITVDIODIBIL
SIICC	1			amino acid	of peptide	Y_T-moine Y=I Inknown. *=Stop codon,
	1 1		[residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		4 113- in continu
	1			sequence		1
		 -			1	DTPNACATFNFLCHEGRVTGAALIPPPGGTSL
	ł	1	ł	1	1	DIPNACATRIFECIMORETO
		1	1			TSLGQAAQ FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT
		 	4492	1	472	PFFFETESRSVAQAGVWACLEGEP PFSCLSLPSSWDYRRPPLRPANFFVFLVETGFP
90	1940	A	4472	1 ^		PFSCLSLPSSWD TRRTTLEATH THE TRY
	1	1	1	1	1	RFSRDGLDLL1/S/GDFF1SAS/GDFRVTS ARPKRIGEPRRKCGNAVVWPSTSLGDHRVTS
	į	1	1	1	1	ARPKRIGEPRIKCGNAVV WF515DGD121
	ł	1		i		VPHQGLPGPIRVAPSSAGQREASQGPPGR
	i	<u> </u>	1	1444	1116	VPHQGGLPGPIRVAF SSAQCELLER IAARFTLAKTWNQLKRPTMIDSIKKTR\YTYT IAARFTLAKTWNQLKRPTMIDSIKKTR\YTYT
591	1941	Α	4495	1444	1110	
	1	1				LKDNWVEDTIPQGAVPCTATAEGMAREETTA
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593	1943	1.0		1		1 4
	l	i		l l		C KMAGGVRPLRGLRALCRVLLFLSQFCILSGG
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594	1944	1^	1 430.			
ì	ļ	- 1			İ	NMTCRFCWQLPETDYECTNSTSCMTVSCPRQ
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l	[- 1			1	GOYKWYYGLWLLRHHPRWGLGADRFYYLGP
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595	1945	A	4512	333		FFFKMESYSVARLECSGARUHTQQIFVLLVQMRVF SPASASRV/AGNIGARUHTQQIFVLLVQMRVF
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		17.4	CEO I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
		Met hod	SEQ ID NO:	beginning	nucleotide	D-Americ Acid E=Glutamic Acid.
0.0.	210.02	.nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
٦ ١	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	İ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1		Joquelles	/=possible nucleotide deletion, \=possible
- 1				peptide		nucleotide insertion
1				sequence	<u> </u>	PRREMOSOSVMLALRRGDAVWLLSHDHDG
						YGAYSNHGKYTTFSGFLVYPDLAPAAPPGLG
ı			1	ļ		ASELL
1			1			MGQPAPYAEGPIQGGDAGELCKCDFLVFTSP
99	1949	Α	4526	366	776	NPEAVCEAGTPAMFQTAWRQMESCSI/AQAG
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Į.				1	· ·	HAPPHPANFCIFSRDQVSPCWPGWSRSLDLVI
		1			1	
i		(PPPWLPKVLGLQA
	1050	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPG\SS
500	1950	A	4329	1 '''	1	DPPASASRVAGTTGARHHTQLIFVFLVETGFH
		1		l	į	\MLARDGLKLLTSSDPPASASQSSWDYRREPP
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602	1932	^	75.0	1		VSGGLPKPANITFLSINMKNVLQWTPPEGLQG
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						VKTVGSVVSSVALTGVLSGNGGTNVNMPVS KPTSWAAIASKPAKPQPKMKTKSGPVMGGC LPPPPIKHNMDIGTWDNKGPVPKAPVPQQAI

						Amino acid sequence (A=Alanine C=Cysteine,
·	SEQ ID	Met	SEQ	Predicted	Predicted end	I —: A aid te-filitigmic Acid.
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	E-Dhenylelenine G=Glycine, H=Histidiie,
nucl-	peptide		in	nucleotide	location	l - v 1i.a Verl veine Lei zucille.
eotide	seq-	1	USSN	location	corresponding	1 14-14-thioning N=Asparaging, P=P1011110,
seq-	uence	1	09/496	correspondi	to last amino acid residue	1 0 Clustomine R=Arginine, 0=3crille,
uence		l	914	ng to first	acia residue	Thereprine V=Valine W=1rvplopnan,
uciioc	1	1		amino acid	of peptide	1 1/ Tunging Y=I Inknown, *=Stop codon,
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				I You distant	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
QID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-A specie Acid F=Glutamic Acid.
of	NO: of	hod	ID NO:	beginning	location	E-Dhenvialanine G=Glycine, H=HISTIGING,
cl-	peptide		in	nucleotide	corresponding	I-Icoleucine K=Lvsine, L=Leucine,
tide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
	иепсе	1	09/496	correspondi	to last amilio	O-Glutamine R=Arginine, S=Serine,
q-	001100	l	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
nce		ļ	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł	1 .	residue of	sequence	Y=1 yrosine, A=0iiAilowii, =0iip eeee,
	l	l	1	peptide	1	/=possible nucleotide deletion, \=possible
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	1		l	sequence		TIENOTETI DPDSFOHI PKLERLFLHNNKITHL
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WO 01/57188 PCT/US01/03800

EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutainic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	.location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, 1-110ine,
eq-	ualco		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			[[amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	·			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	•	/=possible nucleotide deletion, \=possible
	1		1	sequence		nucleotide insertion
	1061	<u> </u>	4571	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT
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				D 41 + 4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
ichico				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	residue of	sequence	/=possible nucleotide deletion, \=possible
	Ì		!	peptide		/=possible nucleonde deletion, \-possible
	1	ł	!	sequence		nucleotide insertion
	 _					GLAYGHFSYEFSNHRDVVVDLQGWVTGNGK
	ł			ł.		GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFN
		1				NOHVECNEICHRLSLTRPSMEKPCKS
	1000	 	4606	1	2415	MERLWGLFQRAQQLSPRSSQTVYQRVEGPR
620	1970	Α	4000	1 '	1	KGHLEEEEEDGEEGAETLAHFCPMELRGPEP
	1	l	1	l .		LGSRPRQPNLIPWAAAGRRAAPYLVLTALLIF
		1	ł	(TGARLI GVVAFRGSCOACGDSVLVVSEDVN
		1 '			1	VEDDI DEHOGRI YWSDLOAMFLOFLGEGRL
	1	}	1		ł	EDTIDOTSI RERVAGSAGMAALTOUKAALS
	1	1	1	i		DOK! DHVWTDTHYVGLOFPDPAHPNILHWV
	1	1	1		1	DEACK VOEOLPLEDPDVYCPY SAIGNVIGEL
	ì		1			VYAHYGRPEDLQDLRARGVDPVGRLLLVRV
		1	1	1		GVISFAQKVTNAQDFGAQGVLIYPEPADFSQ
	1	ł	1 .	1	1.	DPPKPSLSSQQAVYGHVHLGTGDPYTPGFPSF
	1	1	1	1	1	NOTOFPPVASSGLPSIPAQPISADIASRLLRKL
		1	1	}	1	KGPVAPQEWQGSLLGSPYHLGPGPRLRLVVN
	1	1				NHRTSTPINNIFGCIEGRSEPDHYVVIGAQRDA
	Ì	}		1	-	WGPGAAKSAVGTAILLELVRTFSSMVSNGFR
	1	1	1	1		PRRSLLFISWDGGDFGSVGSTEWLEGYLSVL
	1	ı	1	1	}	PRRSLLFISWDGGDFGSVGSTEWEDGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEG
	1.	1	1			HLKAVVYVSLDNAVLGDDKFHAKTSPLLTSL
6	1	1	1	1		IESVLKQVDSPNHSGQTLYEQVVFTN\PSWD\
		1.	1		1	AEVIRPLPM\DSSAY\SFTAFVGVPAVEFSFME\
		1	ì	i		DDQ\AYPFLHTKEDTYENLHKVLQGRLPAVA
	1	1	- [1		QAVAQLAGQLLIRLSHDRLLPLDFGRYGDVV
	Í	1	1	į.	1	I DUTCHT NEESCOLKARGLTLOW VYSAKODY
	1	-	1	1		IRAAEKLRQEIYSSEERDERLTRMYNVRIMRV
	1	1	- {		1	FEYFL SOYVSPADSPFRHIFMGRGDHTLGALL
		ì				DHIRLLRSNSSGTPGATSSTGFQ\ESKFKKQL\
)		}	1	i	1	AT TATWO ACKGA ANALSGDV WNIDNNF
					334	TISPVDDEVGSGIANVILAVAIFSIPAFARLVKG
621	1971	Α	4610	793	334	NTT VI KOOTFIESARSIGASDMTVLLRHILPG
(l	ì	GSSTAVEETMRIGTSIISAASLSFLGLGAQPPIP
	1	1	1	1		EWGAMLNEARADMVIAPHVAVFPALAIFLT
		- 1	1	1		T AFAIT I GDGLRDALDPKIKG
1						LVYVMIAIFCIASAMSLYNCLAALIHKIPYGQ
622	1972	A	4614	2	820	CTIACRGKNMEVRLIFLSGLCIAVAVVWAVF
V22				1		RNEDRWAWILQDILGIAFCLNLIKTLKLPNFK
1	- 1	- 1	j	1	1	SCVILLGLLLYDVFFVFITPFITKNGESIMVE
1		- 1		1		AAGPFGNNEKNDGNLVEATGQPSAPHEKLPV
1	1		1	}	1	AAGPFUNNEANDUND VEATUGE SALIEBRUE
1				l		VIRVPKLIYFSVMSVCLMPVSILGFGDIIVPGL
1	1	ì	\ ·			LIAYCRRFDVQTGSSYIYYVSV\TVAYAIGMI
	1	1	1		1	TFVVLG\LMKKGQPALLYLVPCTLITA/CQFV
1	1		1			AWETVREMKKFWERVTS
L			4619	17	691	TLVSVVEFVRRADLTREDLAPSSVDSGQAGF
623	1973	A	4019	1 "	1 55.	COCCESCI PNTMPSAFSVSSFPVSIPAVLTQT
1		- 1		1	1	DWTEPWI MGLATFHALCVLLTCLSSKSYKL
1		1		i		TOURT CT VII VYCAEYINEAAAMNWRLFSKY
}	- 1	}	1	ì	1	OVEDSEGMEISTVESAPLLVNAMILVVMWVW
1		1	1			VTI NVATDI KNAOERRKEKKRRKED*GAA
	ļ	- 1	1	1		AAWSLRPSRPPSAAPSAAVCVAWASFQLTH
1	1	- [1			LKNRCFI
1	1	1				VSCYTALQSIMNQPESANDPEPLCAVCGQAF
624	1974	A	4622	164	668	SLEENHFYSYPEEVDDDLICHICLQALLDPLD
024	17/4	1"		1		SPEENHL 19 1 LEEA DADPICHICE CATEGORIES AND REL
	}	J	1	ł	1	TPCGHTYCTLCLTNFLVEKDFCPMDRKPLVI
1	- 1	- [-1	1	1	QHCKKSSILVNKLLNKLLVTCPFREHCTQVL
1	1		1	}		QRCDLEHHFQTSQAWGTHL*SQLLGRLRQE
	- B	1		1	1	CLSPGVHHCSEV
		- 1		l		CLOPUVINCODV
625	1975	A	4625	474	473	CFLSPSPLLPPLLLSSSSSPSFPLPPPPTLLPSTI PPLLIPSS*LSP

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
QIQ	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	Data and Acid PaGlutamic Acid.
O: of	NO: of	hod		nucleotide	location	E-Dhenylalanine G-Glycine, H-Histidine,
ıcl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M-Methionine N=Asparagine, P=Proline,
- P	uence		09/496		acid residue	O-Chatamine R=Arginine, S=Serine,
ence			914	ng to first amino acid	of peptide	T-Thronging V=Valing W=Tryptophan,
					sequence	V-Tyrosine X=I Inknown, *=Stop codon,
				residue of	Sequence	/=possible nucleotide deletion, \=possible
	l		ì	peptide		
	1			sequence	<u> </u>	VIVONECECVHCNVCIFLMIKK*GLFLC*IYFI
26	1976	A	4629	249	3 .	LFFET*SHSFTRLECSGTISAHCSLQLQGSSNSP
20	1]		1)	ASASQVAGIAGTHH
		(l		FFFFETKPFFAPQAGGQGPSRGSLNPLPTGLK
00	1977	A	4635	1	301	QFSGLTLSRSGNNGPRPPPRVNFGILRGNGVP
27	1977	1.				PGGAG*PRPPDLRGPPGLAPPQGGNNGGDPP
	1	1	}	ì		
	1	i	1]		ARAYL
		 	4648	1357	782	KLFSSQRLFGPHIQAINPSFLLLSFFPS*LLAMR
528	1978	Α	4048	1337	1.0-	THE THE PROPERTY OF THE PROPER
		1		1	1	AND AND AND AND AND AND AND AND AND AND
		1		1	1	1 ADORNINI AIGHT WPKT I OSLIFH VDF CGFLFIA
	1	1			1	VEVICETEFLLFLYFL*LFIIKVSCSII*CSTICVF
		1	1		1	LONGGEAUTEEVONTREFSFGF
		1_			1000	TRIED LITER I ONPERVE TREE ODVNYSLEAV
629	1979	A	4660	18	999	I VENTE TO A
02)	1		1		1	DEL TECOECEVUKNTASASSWYYF33AWN 11
	1	1	1			1 ACRESTOCK TARVEREDHISCATORNALISO
	. l	1				KHYWEVESRDSLEVAVGVCREDVMGITDRS
	1	1	1		ł	KMSPDVGIWAIYWSAAGYWPLIGFPGTPTQQ
	į.	1		1	1	EPALHRVGVYLDRGTGNVSFYSAVDGVHLH
	ł	ļ		·	ļ	TFSCSSVSRLRPFFWLSPLASLVIPPVTDRK*G
	}	1		1	1	TFSCSSVSRLRPFFWLSFLASLVIII TVIDIAL
	ł		1		İ	FSSPDQNSFPVVQLRDTHPWALFCPSCLYPG
	İ	1	1		1	WSIFWVSLTVPFGICPLCASQEAVPWEVGLA
	l	1	1			NGDGTGNFPRRFWEIFL
			4669	2	358	FFFFETESHSVAQAGMQWRNLGSLPAPPPG
630	1980	A	4009	12	-	TPFFCLSLLNGWDYRRPPPHLANFFVLLVETO
	1	1		ł	ì	FHDVGODGLDLLTS*STPSASQSAEITGVSTIC
	j			ì	1	TO VVIDEAK CHVEFFESHVE
	i			052	614	TODO CATO DE LIFECT VOEYSAGKNICL RPGAV
631	1981	Α	4674	953	014	ATTECNIBETT GGRGRWIT*GSGVUDQPGFTW
		1				NPVFLERRPRALHSSPGLTTQRILWAQGLWV
	İ	1	- 1		İ	LOACOTOCSPGPRGEGVFREG
						DOTTI A COMISPSEGEMGHLLRLEFEILPSTPN
632	1982	A	4678	34	314	*I DOVOCE A ACSSI ISHLOTESPOLKGV YOLF
032	1-2		İ	ļ		ASGLAPVPTHWTVSELSRSPVATATFC
		- 1				RTLGMEGERRASQAPSSGLPAGGANGESPG
(22	1983		4696	1	1365	GAPFPGSSGSSALLQAEVLDEDEDDLEVF
633 ·	1703	^		ł		GAPFPGSSUSSALLQAE VEDEBEDEDEDE
		1	1		ľ	KDASLMDMNSFSPMMPTSPLSMINQIKFEDI
		1	1	1	1	DLKDLFITVDEPESHVTTIETFITYRITKTSRO
Ì		1	- 1			EFDSSEFEVRRRYQDFLWLKGKLEEAHPTL
1	1	- 1		1		I DOT DEVELOK CIMVERENDURIE I KAKAMAMA
1		- 1	1		i	LADIADUPTI TENEDEKIELIAUAWELSSIAA
1			1	1		L CDCT I CDMGOTVRAVASSMKUVNINGEELI
ļ		1	1	l		TARRETET ESOKINI IDKISOKI Y KEEKE I FUI
1	1	1	- 1	1	- [LAWEVCDILIII WSASEEDLVDILKDVASCIDI
1	\ \	1		1	1	LOWATER DINGGI SEALL PVVHEY VLYSEML
1	1	I			1.	CARAMED DOLOAFI DSKVEVLI YKKADIDE
}	1	-	}	ì		I DEPLOY EDVVECANNALKADWEKWAYNA
1	1	ĺ	- 1		1	QNDIKLAFTDMAEENIHYYEQCLATWESFL
1	1	- 1		1		SQTNLHLEEASEDKP
		1				SYWVGEDYTYKFFEVILIDPFHKAIRRNPDT
131	1004		4708	421	158	SYWVGED I I KFFEVILIDITHING THE FKDR
634	1984	^	17,00	1		WISKAVYKHREMCGLTSTGRKSHGLEKDR
1	- 1	1	}	1	{	FPHAIGGSCRAA*RRKTLQFPCYH
L				42	341	
635	1985	A	4709	42	1 37,	POUROAPCHWEDYGRGDNFYLFRYDFOOT
		1				WNIFNRMPIARKNITDGEHHEYLIEVPRLFH
1	1	-		1		cen
1		.				EVENUEDE CTSFIHEPRRPN*GDLVHCLGG
					351	I DOLDINATED OF STANDARD CO.
636	1986	A	472	2	1 221	RSTTVTVA*LMQKLNLSMNDAYYIVIMKM

				- 1: 1: 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	I D. A mortio Acid F=Glintamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	T=Dhenvialanine G=Glycine, H=Mistidine,
nucl-	peptide		in	location	corresponding	I Licelancine K=1 vsine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O-Clutamine R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T-Threonine V=Valine W=Tryptophan,
	}		۱ ۱	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
\	1	1		peptide	0042000	/-possible nucleotide deletion, \-possible
	1			sequence	1	nucleotide insertion
	<u> </u>			Sequence	ļ	ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK
	1	į	1			MYFTTPSNHNAYQVDSVQST
		 	4726	664	253	NTGLTCSIQRKCGETQLYRREENRLILLLQDH
637	1987	A	4/20	1 007		LKSESFQVLTLSPRLEFSGLISAHCNLRLPGSS
1	1			l		DSSASSRAAGITGVHHHAWLIFFFLVETGFL
ì		1	1	1		HAG*AGLELLTSGDPPASASRSAGITGVSHHA
	İ	1	1			RPRETRFL
		 _ _ _ _ _ 	4734	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG
638	1988	A	4/34	124		TLERGHWNNKMEFVLSVAGEIIGLGNVWRFP
}	i	1		ł		YLCYKNGGGAFFIPYLVFLFTCGIPVFLLETAL
	Ì	1	1	1	l .	GOYTSOGGVTAWRKICPIFEGIGYASOMIVIL LNVYYIIVLAWALFYLFSSFTIDLPWGGCYHE
	1	ı	1	1	1	LNVYYIIVLAWALF ILFSSFIELD W GGGTEFW
	-					WNTEHCMEFQKTNGSLNGTSENATSPVIEFW WNTEHCMEFQKTNGSLNGTSENATSPVIEFW
	1000	A	4743	1040	699	QGLTLLPRMECSATITAHCSLELPGSIDLPTSA
639	1989	ΙΛ.	7/73	1 20.0		S*VARTTGTHHIPWLILVLLL*TWGSYYVAQ AGLELLGSSNLPAAMVSQSAQIIGHDHCAWA
1		1	1	İ	İ	AGLELLGSSNLPAAM VSQSAQIIGIIBIIGI
1 .			1.	1		TSNHVLYTQEGLRRGKEG GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN
	1000	- A	4771	527	2	WIRRPCLPSGCLKMNREIGPLQHSLCCPGWS
640	1990	Α.	4//1	1		WIRRPCLPSGCLKMINKEIGFEGIBLEGE QTPGLKAILLRQPPK*LGLQMESHSCPPAWSA
	1	- 1		l	1	QTPGLKAILLROFFK-LGLQMLSMS
			1	l	ł	PDHEQQPLSWVLPPPQKDMNPREQQVALGP
1	1		1	į.	1	PDHEQQPLS W VLPPP QRDING TO CEPR
		1		1		QAAALPWAVWRNDCFPR RPSSQCGGIPTGWKKGLAPELSSELSSPPLPAR
1	1991	A	4780	16	473	LQLAASPYFSPSWAECPQPVPAGTHATWCLA
641	1991	1.	. .,,,,			RVWARMTPPGPAGIPSHPLPPPPPERSVPIPSP
1	1	1		1		FPARDSGSRQGHSTDRYKHTDAPRDAHRRVP
1	- 1	1	\	ŀ	ŀ	QRDTDTGVHTGSGTHTHAHTPPEK
		1	1.			GYSFRCDIVDYSRSPTALRMARTCWLYYFSK
642	1992	A	4798	1	487	PRETA DETECTO DEKNSOVIFILHVERIGITAL WILL W
042	1772	1		1		TOTAL CONTROL OF THE PROPERTY
1	- {			ì		A STRUCT GAT GRAVOK YI.WWKK ILIOLOLULY QA
	1	1	1			VIVAIHISQFFFMEDCKYQFPVFACIIMSYSFM
1		1	- }			
İ		1	1	1		- TAKER ALIGGE VVI.KIKTKIYSYFSMLNFLL
643	1993	A	4799	2	391	L COUNT OF IT DISCOPPING NING KINNER CERTIFI
1 373				-		A A TOTAL CENTRICING CONTROL OF THE PARTY OF
	1	- 1	ł	- 1		WEKAIROALMPYTPQASVCISPUQUADIDA
1	1	-	1			Los A SVCTSPGOGKDHSKU
1	- 1	1			101	- I TYPE EAVIDVITECVAGVVGRAYLLCALFEL
644	1994	A	4800	488	101	T CEL CACA YEBESNKE GARSSIE M APPEA
			1		1	AVAMLCKEOGITVLVRAATWLGPAPSVCPTI
1	1	1	1	1	1 .	CONTINUOWPCI.CGVI.HAYLPLLV
1					126	- I VECTOR COTPARPOSTMIHLGHILFLILLEV
645	1995	A	4805	458	126	A A A OTTOCER SSI PAPYPGI SUSCOCCOSCOS
1						PLLAGLVAADAVASLLIVGAVFLCARPRESF
1		{	1	1		LACEDGY VVINMPGRG
1	1	·			1022	- I VOCETIVALI SEI SHESRI HGGVPGRULLEUNL
646	1996	A	4817	47	1033	* ODG A DCLITIMTSIPFPGDRLLUYDG VILCULI
1 5.5	1	1			1	TITE A MOOT REPROVABLATER VERSING
1		1	1	ł	1	TO A STOCK GOER TAVSLVIAL PURPOSCYSY I
1				l		DODUE*CON*KRIANGI.GFSFVOMERESCOME
1			- 1	1		Vedi vdikbi Ebühbaeengalaagulluku
	l l	1	Į.	1	Į.	LAURCORY A SSSRCRGSWAMULSVUAGFSFAS
-	1	1				A STEAT OF TREATMENT OF THE PROPERTY OF THE PR
	1					DELECTROTORISADKEFTRATCIDSCISFIL
		1				GSRGOLGGTVPPQMQGKAWGLRPESSQAAM
}				1		POTMACA ETERDI GPVP
١		1				PRVRGDWPLEKKKSNSNIHPIPSWCGSTDSKD
647	199	7 A	485	1044	335	1 KYROD II.
1 047	1 200					

						Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A mortio Acid F=Glutamic Acid.
10: of	NO: of	hod	ID NO:	beginning	nucleotide location	E-Phenylalanine, G-Glycine, H-Histidine,
ucl-	peptide	I	in	nucleotide	corresponding	1-Icoleucine K=Lvsine, L=Leucine,
otide	seq-	- 1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496	correspondi	acid residue	O-Chromine R=Arginine S=Serine,
ience			914	ng to first amino acid	of peptide	T-Threonine V=Valine W=Tryptophan,
				residue of	sequence	V-Tyrosine X=I Inknown, *=Stop codon,
				peptide	Sequence	/=possible nucleotide deletion, \=possible
1			1	sequence		nucleotide insertion
				sequence		IVMPTYDLTDSVLETMGRVSLDMMSVQANT
	1				Ì	GPPWESKNSTAVWRGRDSRKERLELVKLSRK
	{ ·		Í		Į.	HPELIDAAFTNFFFFKHDENLYGPIVKHISFFD
	}					FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK
	1	ł	1	1		QDSIYYEHFYNELQPWKHYIPVKSNLSDLLEK
		1			1	LKWAKDHDEEAKKIAKAGQEFARNNLMGD
	ì	1			*	DIFCYYFQTFPRNMPIYK
	1000	A	4867	2030	837	AGMLPAVGSADEEEDPAEEDCPELVPMETTQ
648	1998	^	4007		1.	SEEEKSGLGAKIPVTIITGYLGAGKTTLLNYI
		1	1	ł	1	LTEQHSKRVAVILNEFGEGSALEKSLAVSQG GELYEEWLELRNGCLCCSVKDNGLRAIENLM
	1	1	1			QKKGKFDYILLETTGLADPGAVASMFWVDA
	1	1	1		1	QKKGKFDYILLETTGLADFGAVAGIAN ELGSDIYLDGIITIVDSKYGLKHLAEEKPDGLI
	\	1	1	i	1	NEATRQVALADAILINKTDLVPEEDVKKLRT
		1			1	TIRSINGLEQUILETQRSRVDLSNVLDLHAFDSL
	İ	1	1			SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG
	l	1 .		1		NAKEEHLNMFIQNLLWEKNVRNKDNHCMEV
	ł	1	1 .	1	1	I DI ECI ASIKUKSUUAIAOGAHELIDEETLA
	}	1	1	1.	1	SWKDDTERTNRLVLLGRNLDKDILKQLFIAT
		1	1			L EPPTRICOUTTUEKEDOVCI
		1		<u> </u>	100	- DOVELLI BYL GVOWAOYWAHWOPPLPURKK
649	1999	A	4873	226	189	POOT OF DOCUMENT APPHRAPALATE
						GQAGLELRTSGDPPASASQSAGITGVSHLA*P
ĺ	-	Į.	1			L TO AND I DECODI CVVI
				- 2	437	PERI DESEARVACIAGVOWCDLGSPOPLPFGF
650	2000	A	4874	12	1731	V*ECCT CT DCCWDYRHAPPPCPS*FLIF**AQQ
1					\	TOTAL A DI AN NG PHOLPTSPSUSAEIRU VOLIN
		1		ļ		CPASFYLFLKYYLEAKFCA*GECAPSAGVOA
l	1		1	Į.	Ì	1 CVVPCUVSCLLINCVVOI
		A	4898	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATR
651	2001	A	4070	1		PHMEPKASCPAAAPLMERKFHVLVGVTGSV
		1		1		AALKLPLLVSKLLDIPGLEVAVVTTERAKHFY
	• .	1			i	SPODIPVTLYSDADEWEMWKSRSDPVLHIDL RRWADLLLVAPLDANTLGKVASGICDNLLTC
1	1	1	1		ŀ	VMRAWDRSKPLLFCPAMNTAMWEHPITAQQ
1	i	1	1]		VMRAWDRSAFLEICU AMKLVCGDEGLGAMA VDQLKAFGYVEIPCVAKKLVCGDEGLGAMA
}	-	1.	1			LEVICTIVIDEVICEVI FOHSCHOOSTOISVING VI
Ĭ.		1	1			LYSEWVQAKSVKMDVGKIGGYPHLLNGGPA
1		- 1		l		LSLPRGQACSRLNWTEGPGLSFFQPGEAAA
1		ı				
652		- 	4927	1	611	ODET DO A GNIDT A FGGT, IFPCAPL VP TPAPPOT LI
1 (1)	2002	_ A		1	1	
032	2002	A		1		DARCCADDDD AHTHSRTHPSAPLVPAPSSAAA
032	2002	A				PAFSCAPRPRAHTHSRTHPSAPLVPAPSSRAR
032	2002	A				PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAA GQSPIPSRASSPSCSWAQVPGVALARCAGVC
032	2002	A				PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAA GQSPIPSRASSPSCSWAQVPGVALARCAGVC
032	2002	A				PAFSCAPRPRAHTHSRTHPSAPLVRAPSSKAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI
032	2002	A			202	PAFSCAPRPRAHTHSRTHPSAPLVRAPSSKAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA
653	2002	A	4965	2	283	PAFSCAPRPRAHTHSRTHPSAPLVPAPSSKAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR
		6	4965	2	283	PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R
		6				PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHLAILVLNS*PQVICPPWPPKVLTLQA
		6	1000		283	PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAA GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI RPAVGLGALGVIPPVRVPDRPPTORSQGRGW
653	2003	A	1000			PAFSCAPRPRAHTHSRTHPSAPLVRAPSSKAK GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHLAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW
653	2003	A	1000			PAFSCAPRPRAHTHSRTHPSAPLVRAPSSARAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTILAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLF PPCLTHLAAASCVVVWCGRWKRDSAECQCI
653	2003	A	1000			PAFSCAPRPRAHTHSRTHPSAPLVRAPSSARAK GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHLAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEFGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLF PPCLTHLAAASCVVVWCGRWKRDSAECQCI
653	2003	A	4968	3	437	PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAA GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP PPCLTHLAAASCVVVWCGRWKRDSAECQCI HSCSAVSQQEDRCRSSSCS
653	2003	A	4968	3		PAFSCAPRPRAHTHSRTHPSAPLVRAPSSARAK GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHLAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLF PPCLTHLAAASCVVVWCGRWKRDSAECQCI HSCSAVSQQEDRCRSSSCS MNNNTTCIQPSMISSMALPIIYILLCIVGVFGN
653	2003	A	4968	3 .	397	PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAA GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTHLAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP PPCLTHLAAASCVVVWGRWKRDSAECQCI HSCSAVSQQEDRCRSSSCS MNNNTTCIQPSMISSMALPIIYILLCIVGVFGN TLSQWIFLTKIGKKTSTHYLSHLVTANLLVC
653	2003	A	4968	3 .	437	PAFSCAPRPRAHTHSRTHPSAPLVPAPSSAAR GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPE QSFRGAWGPSFWGSWKSQRELSAGGAQAWI LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTLAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGI IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP PPCLTHLAAASCVVVWCGRWKRDSAECQCI HSCSAVSQQEDRCRSSSCS MINNTTCIQPSMISSMALPIIYILLCIVGVFGN TLSQWIFLTKIGKKTSTHIYLSHLVTANLLVC
653 654	2003	A	4968	3 201 3 332	397	PAFSCAPRPRAHTHSRTHPSAPLVPRFSSAAA GQSPIPSRASSPSCSWAQVPGVALARCAGVC KPGDSWRVAACISGRCCSRGRRRGSGPRNPI QSFRGAWGPSFWGSWKSQRELSAGGAQAW LLGSAGSGLRGEA FFFFI*DGVSLCHPGWNAVARSWLTATSASR VQAVSCFRLPSSWDYRHATMPG*FF*YF**R WGFTILAILVLNS*PQVICPPWPPKVLTLQA RPGIPGRRFRRSWFCQLP*EPEPGLESLATPG IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW DPERDPGCRVQVSRGPRFGBQKTPGLQGCL PPCLTHLAAASCVVVWCGRWKRDSAECQC HSCSAVSQQEDRCRSSSCS MNNNTTCIQPSMISSMALPIIYILLCIVGVFGI

				N - 1: 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D_A coeffic Acid F=Glutamic Acid.
10: of	NO: of	hod	ID NO:	nucleotide	location	E-Dhenylalanine G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	r_relevating K=1 vsing L=Leucine
otide	seq-		USSN	correspondi	to last amino	N=Asparagine, P=Proluie,
eq-	uence		09/496	ng to first	acid residue	Carolintamine R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T-Three vine V=Valine W=Irvotophan,
	۱ ۱			residue of	sequence	V_Tyrocine X=IInknown, *=Stop codon,
			'		Soquenoo	/=possible nucleotide deletion, \=possible
	į į			peptide		analostide incertion
	1		<u> </u>	sequence	 	TOTT DUTCESHIGGVI LKIVEOINRKODWSDH
						ATWWEOKROWLLOTHWILDKYGILADAKLF
	1	1	1		}	PCDOUDPVII RI PNRRALKLX*
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658	2008	A	5017	1	292	TWDESCT STI SSUMVRCAPPHPANEVILVEIUF
050	1		1			THE ACACIVITE SANLGLS ISLIPLING
		}	1			TRANSPORTED TO CATEGORIAN CONTRACTOR OF THE PROPERTY OF THE PR
659	2009	A	5018	17	338	T*NSLVSPVLGKWSPCLQGPGLSAVHTWPWL
027	2005			1		MAACWAVHVKTHMRPGLAVLPRLVLNSWS
	1	l .		1		MAACWAVHVKIIIVIIG OLITVEITE
		ł		1		*AIILLWPPKALGLQA SRVDDFVGERRGGCDECLCGHRGLRAVPLG
550	2010	A	5028	2	310	SRVDDFVGERRGGCDECECHROUNG ST HPGHLCLQPPGGPA*FLDYCRGCCPHPVPGST
660	2010	10	3020	1 -		HPGHLCLQPPGGPA-FLDTCKGCGFWIYORGEPH
	-1	1			1	AGSCPROKKTTPGPTVLCVCSFWIYQRGEPH
	1	1 .		1	_	HRTGARWNH
	 	+	5050	752	431	RQSCSSTQAKVQWFHYGPLQSQPPGLKQSSQ
661	2011	Α	3030	1,52		LSLPNSRDHRHVPPRLAIFSFAETGSPYFAQAS
		1		1		LELLGSSHPPTSASQSARITGVSHRAWPLK*F
		1	Ì	1	1	LATATOMOTE TMN
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662	2012	Α	3034	140	1	1 - A ACOCOUT AT DIT I SCHOOL NAVIDUITY 11
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		1		1	1	WDTPLPGAGHQSTQKLE*LFAMVEIWQ
	_L			951	580	- I I TO SICK CRATICA SVVK HHY MIDGUIPULT V 33A
663	2013	A	5066	931	1 500	LADY DECAYAVCCDSPAFFCRKHRLPAFVFFSCA
		1		l	1	ODATOSTTICTOLATMAAPPHLVHABLEPSST
	ì	- 1	}	1	1	THE POT TOTAL AND AVESTS LYRY LYNSY
ł	i				-	- LY OFFENT SYMEOVNIKTVVREFVVLGFSSLAKLY
664	2014	A	5071	550	1.	OVERVIEW I VI FTI GTNAIISTIVLDKALITE
		1		1		LARGET ATT CCCETCVTFVIVPK MLVDLLSQAA
1	\	1		1		CONTROL CONTONESE FEGSSHSFLLAAMUIDA
ſ	1	1.			1	VALATONPI RYSVLMGHGVCMGLMAAA WAX
ì	l	l	1	1	ł	OPPUSE VITTS VEHI PEHSSNOHE
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665	2015	A	5074	496	092	DI STORCE DEFNSI FGHSLKUSUHEES VQLUS
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1		1		1	1	PropersyllyDPGITARRC
1		l				IMLLSTSS*VYFQSSTKDSHFFLFDFQKTGPPI
666	2016	-	5080	408	248	LUCDE ACT SET OF OPCLYKER
1000	20.0	{ ``	1			DLTNSHFFLFDFQKTGPPLGGPKAQFSSLQL
667	2017	A	5081	129	247	DEINGREEDI GETGITAGO
00/	2017	1		į		PCVY*RR NIKSNDRWVQIKTAYKYFF*KNGDNYNWVI
160	2018	A	5086	852	233	NIKSNDRWVQIKTATKTTI KINGSQPFYLGHT RALPTTFADIENLKYLLFTRDASQPFYLGHT
668	2018	A	1 3030			RALPITEADIENLA ILLETADAGGI TOGIT
1	1	1.	1	1	1	IFGDLEYVTVEGGIVLSRELMKRLNRLLDNS
1	- 1	i		1		TCADQSVIWKLSEDKQLAICLKYAGVHAEN
1	- 1	1	1	1		EDYEGRDVFNTKPIAQLIEEALSNNPQQVVE
		1		1		CCSDMAITFNGLTPQKMEVMMYGLYRLRA
		1	1			CITYENIDTI VELPPVGSEND
		l_			329	DCDDTDDDI I TI LAHVSPEPAGPSCDSLAQPO
669	2019	A	5101	1	323	L CONTROLINGUIPPI L CGSOCLSEP V PUSITUE
	1	1		1		RGCQHEAAPCPRGPGSDGLHHASAACASLF
	1					,
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			5102	3	547	SPILPVLLPELGPL DAWGNRCAVGAAPRLIHLHLCCTPADPSRK

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	DA enertic Acid F=Cilutemic Acid
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	E-Phenylalanine G-Glycine, H-Histidine,
nucl-	peptide	1	in	nucleotide	corresponding	I-Icoleucine K=Lysine L=Leucine
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O-Chitamine R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine V=Valine W=Tryptophan,
	1	1	Į.	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
1	ļ	ļ .		peptide	504	/=possible nucleotide deletion, \=possible
1	Ì	}	Ì	sequence	ì	nucleotide insertion
		 	 	Sequence	 	DEL*NMNGRVDYLVTEEEINLTRGPSGLGFNI
		1				VGGTDQQYVSNDSGIYVSRIKENGAAALDGR
		1		1		LQEGDKILSVNGQDLKNLLHQDAVDLFRNA
1	1	1	1			GYAVSLRVQHRLQVQNGPIGHRGEGDPSGIPI
1	1	1				FMVLVPVFALTMVAAWAFMRYRQQL
	0001	A	5105	672	400	RDGREELCLQQEPTLPSRICSSAPLLYFLFICPF
671	2021	^	1 3,03			VLLLLLISLLCLYWKARKLSTLRSNTRKEKA
1						LWVDLKEAGGVTTNRMED*EEDECN
	2022	A	5148	72	314	IIYFSYNIFLKITELLNDVERLKQALNGLSQLT
672	2022	^	1 3.10	'-	}	YTSGNPTKRQSQLIDTLQHQVKSLEQQLAVS
1	1.	1	1	1		NQAHGALQEYVLAPCS REILCSRIGRLNIV*MSLFPNLTCRLNAIPIKIPA
(02	2023	+A	5152	210	335	
673	2020	1"			_	NHFVEVT LTEDQPFDILQKSLQEANITEQTLAEEAYLDA
674	2024	A	5153	3	2953	SIGSSQQFAQAQLHPSSSASFTQASNVSNYSG
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İ		1	1			GTQQFFCQAQKKCLNQTSPISAPKTTDGLR
		ł			l l	QAQIPGLLSTTLPGQDSGSKVISASLGTAQPQ QAQIPGLLSTTLPGQDSGSKVISASLGTAQPQ
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	1	1		1		MVMIDRMFNQEERASLSRDKRLALVDPEGFQ
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			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
		Met	SEQ ID NO:	beginning	nucleotide	The Americ Acid F=Glutamic Acid.
10.0-	NO: of	hod	in No.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	peptide	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	- 1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence			ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence		}	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
l l	}			peptide	Soquesion	/=possible nucleotide deletion, \=possible
}				pepude		nucleotide insertion
				sequence	306	TEET DOSE AT SPRPDCGLOWRNLGSLOAPPPG
676	2026	Α	5155	2	300	ETDESCI SI PSSWDVRRPPPRPANFLYF**KKG
			į			FTLLARMVSIS*PHDPPASASQSAGITGVSHRA
			1	1	1	PPT
		· ·			7.40	FELISYDLI AL FOSKTEYKPDWFDIVESEVKCC
677	2027	A	5167	97	740	L VE A VCVIDMQQFTFFFITS (GDUALE VLQ I LF
0,,				Į		CAINT DVDVGHIVHTGMLNEGGGYENDCSIAK
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	l	l	1	ł		NLLLEDVTWKYTALNLIGPRAVDVLSELSYA
		1	1	į		PMTPDHFPSLFCKEMSVGYANGIRVMSMTHT
		l		1	1	GEPGFMLYIPIEYRWGFTMLSTLVSNS
	Ì	ļ				PALCRLRDDMTVCVADFGLSKKIYSGDYYRQ
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	ľ	1	})	}	VTMWEIATRGMTPYPGVQNHEMYDYLLHG
	1	1				HRLKQPEDCLDELCKI**SPQSP
		 	5190	39	499	RESOVKHFKMRKIDLCLSSEGSEVILATSSDE
679	2029	A	2190	1 37		KHPPENIIDGNPETFWTTTGMFPQEFIICFHKH
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681	2031	A	5207	10	247	KNESPLPGTLAHTCNTSTLGGRGRWIT*GREF
002				ł	İ	I TOTOMANIMATE POLITIK
	1					- PERCTECUCITOA GVOWPNLSSLKTLPPGPK*F
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002		1		1	}	MEGMERTEDIS
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LEQQHHEKKSTYNLNEDELTHYGGSLADE KIHANDYDSDADROTIJSGELTAAHFGGGG GILHKKTQGGEREKPKSRKELIEELLASK QEKRERQAQREDALELTEKLDQDWKEIQTLL SIKITYKSENRDKKEKPKPDAYDMMYRELGF EMKAQPSNRMKTEAELAKEEQHILRKLEAB RIRRMIGKDEDENVKKYKHMSADDLNDGPV LDKDDRRILSYKDOKMNVEEDVQEGQSKEA SIPPESNEEGGSSGGEDTESSPDSHLDLES NVSSEEBHEKPAKEQROTFGKGLISGKERAG KATROLPYTPAAPESYEELBILGRSMEEQ LILVVERIQKCNHPSLAEGNKAKLEKLFGFLLE YVGDLATDPPPILTVIDKLVYHLYHLCOMFP ESASDAIKFYLRDAMHEMEEMETKGRAALP GLDVLIYJKITGLJEYTSDFWHVVTTPALVCL SQLITKCPILS,QDVVKGIFVCLFLEYVALS QRFIPELINFLLGILVIATPNKASQGSTLVHFFR ALGKNSELLVVSAREDVATYCLLFLYALVCL SQLITKCPILS,QDVVKGIFVCLFLEYVALS QRFIPELINFLLGILVIATPNKASQGSTLVHFFR ALGKNSELLVVSAREDVATYCLLFLYALVCL SQLITKCPILS,QDVVKGIFVCLFLEYVALS QRFIPELINFLLGILVIATPNKASQGSTLVHFFR ALGKNSELLVVSAREDVATYMLVSLLUGSSLSERWA SRLRAPTSTEANHHRLSCLAVGLALLKRCVLM YGSLPSFHAIMGPLRALLITHALDCSHPQELQ ELQGSTLTEMBSOKQLCRPLTCEKSKPVJKL FTFRLVKVLEFGRKQGSSLSERWA SRLRAPTSTEANHHRLSCLAVGLALLKRCVLM YGSLPSFHAIMGPLRALLITHALDCSHPQELQ ELQGSTLTEMBSOKQLCRPLTCEKSKPVJKL FTFRLVKVLEFGRKQGSSLEEQERKRLIHKHK REFKGAVREIRKDNOFLARMQLSELMFERDA KRKVKVGLTNSLATDEGGEWKALIKKKKKKK FFFFFLKSSKPLONTINATHOLOSHPQELQ ELGGSTLTEMBSOKQLCRPLTCEKSKPVJKL FTFRLVKVLEFGRKQGSSLEEQERKRLIHKHK REFKGAVREIRKDNOFLARMGLSELMFRUND FKRTFPLLKSSSTEPTLIVLKFYLVTLT SFVK 691 2041 A 5261 1 304 FFFFTLKSSSLSTYDKEIFPILIVLKFYLVTLT SFVK 692 2042 A 5282 56 1268 OMEPYGCGECRGSSVDPRSTFVLSNLAEVV EVLSSFFFFFLKFSVKPONN 693 2043 A 5301 362 507 EMEKERGEGCDRVTGNFILARCN EVKDDDLFHSVTTIMALHLGSSK 694 2044 A 5310 1 204 KVLTANHTLKENLRKFYKGKKDRFLDLRPK KVTANHTRLNHLEENLKTKCQHREGULK EVKEDDLFHSVTTIMALHLGSSK 695 2044 A 5310 1 204 KVLTANHTLKENLRKFYKGKKDRPLDLRPK KVTANHTRLNHLEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHRKERLYPL RKYAMKRALNHHEENLKTKKQHKKERLYPL RKYAMKRALNHHEENLKTKKQHKKERLYPL RKYAMKRALNHHEENLKTKKQHKKERLYPL RKYAMKRALNHHEENLKTKKQHKKERLYPL RKYAMKRALNHHEENL	i	1	1	l		I	DDKCNVFRDKRFGEYNSNMSPEEKMMKKFA
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693 2043 A 5301 362 507 EEIKERFGPGLVIYWYGFIQELDCNRERGILLK ACFPTNIVTLCHSIA 694 2044 A 5310 1 204 RVLTAINHTLKENLRKFYKGKKDKPLDLRPK KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA 695 ETRSTAVKSEVQVCISLLCLEDRTMPKKAKP	ı				1		KFFPSVPLFGFFGNGEIGCDRIV I GNT ILARCH
694 2044 A 5310 1 204 RVLTAINHTLKENLRKFYKGKKDKPLDLRPK KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP			1				EVKDDDLFHSYTTIMALIHLUSSK
694 2044 A 5310 1 204 RVLTAINHTLKENLRKFYKGKKDKPLDLRPK KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP				6201	362	507	EEIKERFGPGLVIYWYGFIQELDCNRERGILLK
694 2044 A 5310 1 204 RVLTAINHTLKENLRKFYKGKKDKPLDLRFK KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA 1596 ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP	693	2043	A	2301	302	1 20.	A CEPTNITUTI CHSIA
KTRAMRRINMHEENLKTKKQHRKERLYPL RKYAAKA 1596 ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP						204	DVI TAINHTLK ENLRKFYKGKKDKPLDLRPK
RKYAAKA 1596 ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP	694	2044	Α	5310	1	204	KTRAMRRRLNMHEENLKTKKQHRKERLYPL
1596 ETRSTAVKSEVQVCISLLCLEDRTMPKKAKP		1				ļ	DETANEN
605 2045 A 5315 125 1596 EIRSTAVESEVQV-GISEREE		}					ETPSTAVKSEVOVCISLLLCLEDRTMPKKAKP
	605	2045	A	5315	125	1596	DIKSTAVKSBVQ COLORES

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspertic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide ·		in	location	corresponding	T=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		}	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	·	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	1		peptide	boqueine	/=possible nucleotide deletion, \=possible
	•	1	1	sequence		nucleotide insertion
	 	 		Soquence		TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP
	1 .			l	i	SSLFESLISPIKTETFFKEFWEQKPLLIQRDDPA
		1	1	1	İ	LATYYGSLFKLTDLKSLCSRGMYYGRDVNV
l		1	 			CRCVNGKKKVLNKDGKAHFLQLRKDFDQKR
	Į.	1		l	1	ATIQFHQPQRFKDELWRIQEKLECYFGSLVGS
	Į.	1	1			NVYTTPAGSQGLPPHYDDVEVFILQLEGEKH
	1	1.		j	1	WRLYHPTVPLAREYSVEAEERIGRPVHEFML
	1	1		1		KPGDLLYFPRGTIHQADTPAGLAHSTHVTIST
	1			1	1	YQNNSWGDFLLDTISGLVFDTAKEDVELRTG IPRQLLLQVESTTVATRRLSGFLRTLADRLEG
		1		1		TKELLSSDMKKDFIMHRLPPYSAGDGAELSTP
!		İ	1	1	İ	GGKLPRLDSVVRLQFKDHIVLTVLPDQDQSD
ļ	ł	i	1			ETQEKMVYIYHSLKNSRETHMMGNEEETEFH
ļ		ì	1	1	1	GLRFPLSHLDALKQIWNSPAISVKDLKLTTDE
]			1			EKESLVLSLWTECLIQVV
		1		 	742	I MKYVI FAAFLGEISDIHTKLLRLSSSQGTIET
696	2046	A	5318	1476	142	STODIDSRI SPGGSLADAWAHQEGTHPKDRN
		1				VEKLOVILNOMTEIYYOFKKUKAERKLAYN
1	1	1	1	ł		FEOTHKEDKOKLYYHATKAMTHETDECVKK
1		1		ì	. 90	VEARI NKSEEWIRKMLHLRKOLLSLINQCIDI
		1		1		EEEVSKYQEYTNELQETLPQKMFTASSGIKHT
			i i			MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE
	ł	İ			_	LAENNHILESGGSLTMDGGLRNVDCL
697	2047	- A	5320	244	478	LDYNFFLFEMTFGLVSQAGVQWHDLGSLQPP
057	2047	1			ì	PPGFKQFSCLSLPSSWDYRHLPPHLANFSREG
		1				VSPSWPGWSRTPDFR LPIRKSLRSVRSGFPTSQSPITRNLDGTASGSC
698	2048	A	5324	266	714	LAKTYTGSLFRINVGLRGLVAGGIIGALLGTP
1 ***		-			ļ	VGCLI MAFOKYSGETVOERKOKDRKALHEL
1	1		1	Ì	1	KLEEWKGRLQVTEHLPEKIESSLQEDEPENDA
	ĺ					L WEIT AT I.MI.PRNPSVIDKODKD
				699	277	DDHGHT VCISSSAGLSGVNGLADYCASKFAA
699	2049	Α	5334	699	12"	FGFAFSVFVETFVOKOKGIKTTIVCPFFIKTGM
	1	- 1				EECCTTGCPSI I PII EPKYAVEKIVEALLUEKIVI
1		ļ				YLYMPKLLYFMMFLKSFLPLKTGLLIADYLGI
1		1	1			I HAMDGFADOKK
600	2050	A	5344	+3	614	PTAFFMSSLTPESSPELAKRSWFGNFISLDKEE
700	2030	^)3944	1		QIFLVLKDKPLSSIKADIVHAFLSIPSLSHSVLS
1	- [1		QTSFRAEYKASGGPSVFQKPVRFQVDISSSEG
1				1		pepsparingsggggiysvirilisurskkrkkv
		- 1		1		VETIQAQLLSTHDQPSVQALADEKNGAQTRP
		- 1		1	I	AGAPPRSLQPPPGRPDPELSSSPRRGPPKDKK
1		1		<u> </u>		LLATNGTPL HASVLFCRVMAASKTQGAVARMQEDRDGSC
701	2051	A	5346	3	1383	STVGGVGYGDSKDCILEPLSLPESPGGTTTLE
1	1 202.			1		GSPSVPCIFCEEHFPVAEQDKLLKHMIIEHKIV
1	1	- 1			1	IADVKLVADFQRYILYWRKRFTEQPITDFCSV
1	1	· I		1	1	RINSTAPFEEQENYFLLCDVLPEDRILREELQ
l l	ì	- 1	ł	-		KQRLREILEQQQQERNDTNFHGVCMFCNEEF
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i		- 1	{		1	CTLOKKI DNI OCLYCEKTFRDKNI LKDHMK
					1	LECTED KINDKNREYDRFYVINYLELGKSWEE
		1		1		VOI EDDREI LDHOEDDWSDWEEHPASAVCL
		- 1		i		ECEKOAFTIEKI YVHMEDAHEFDLLKIKSELU
1	·	ļ				I NEVOOVKI VNFIRROVHOCRCYGCHVKFK
		1				KADI RTHMEETKHTSLLPDRKTWDQLEYYFI
		- 1		1.	ł	TYENDTLLWTLSDSESDLTAQEQNENVPIISE
	1	l l	1		ĺ	DTSKI VALKOSSILNOLLL
				2500	1540	MAAATRGCRPWGSLLGLLGLVSAAAAAWD
702	2052	A	5356	2502	1540	

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D_Accordic Acid E=Glutamic Acid
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	E-Phenylalanine G=Glycine, H=Histidine,
nucl-	peptide	- 1	in	nucleotide	location	1-Icolencine K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		- 1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uctice		1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	} }		1	peptide		
	1		ĺ	sequence		nucleotide insertion
				Soquette		LASLRCTLGAFCECDFRPDLPGLECDLAQHL
	1				ì	AGQHLAKALVVKALKAFVRDPAPTKPLVLSL
		į				LICTUTCTCK SYVSSLLAHYLFOGGLKSPKVII
		ļ				TIPEDVI LIEDUDCHIERYKKDLKSWYOGNLIA
	1	i .		ľ		CGP SI FI EDEMDKMPPGLMEVLRPFLGSSW V
	1		1			VOCTNIVER ATETETSNTGGEOINOVALEAWKS
	1		ł	i		RRDREEILLQELEPVISRAVLDNPHHGFSNSGI
	1	1	Ì	<u> </u>	1	MEERLLDAVVPFLPLQRHHVRHCVLNELAQL
	1	1	1	l · ·		GLEPRDEVVQAVLDSTTFFPEDEQLFSSNGCK
	Ì	l		Ì		GLEPRDEVVQAVLDSTITTEDDQDIOSITO
	1	1	1			TVASRIAFFL
	L	 	5380	278	657	LFLQKLRMKTEEEARTHTEIEMFLRKEQQKL
703	2053	A	2300	2,0	1	PERI PENARK VOKOTEMKONELNALKA IKA I
	1	1	1	1	İ	COLARI ODLAKMIRE YEOVIEDKIEKEROKA I
	l	1	1	1		KVKQDLLELKSVIKLQAWWRGTMIRREIGGF
		1	1	i	1	V14
		1	1	<u> </u>	1003	FRORATIVMAAVVEVEVGGGAAGERELDEV
704	2054	A	5381	1 .	1003	DAGDI ODEEOWRVEHARMHAKHRGHEAMH
70.	1	1				A DARKET TO TACT VVAOLITIVOWKOKHPROIN
1	1	1	1	1	1	MVTLFQMWVVPLYFTVKLHWWRFLVIWILF
1	1			1	1	SAVTAFVTFRATRKPLVQTTPRLVYKWFLLIY
1	(4)	, }		i	1	KISYATGIVGYMAVMFTLFGLNLLFKIKPEDA
	ļ		1			MDFGISLLFYGLYYGVLERDFAEMCADYMA
	1	1	1			MDFGISLLFYGLY TOVERDITALIACIDETIC
i .	1	1	1			STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV
1	1		1	1	į	SEEGIENTYRLSCNHVFHEFCIRGWCIVGKK
l		1	1	l l		QTCPYCKEKVDLKRMFSNPWERPHVMYGQL
	į.	1	ł	į.		I TOWN BY VAWOPVIIGVYUGINYILULE
					675	TYPE DE OLATRA GOPL DINMA GEPK PYRPKP
705	2055	A	5396	3	073	CINTER DE CAT VRI ESKEPFLSVGGY VIDYDY I
				1		PODEVNIRI EDVHGRVPPPPRAVIPLKKPKVA
1	į.	1				VTTTDDCKCVFSMKGGSRSTASGSTGSKLKS
1	- {		1	1		DELOTIKKEL TOIKTKIDSVLGRLDKJEKQQA
1	ļ	1				LABADAOKKI I RESI VI IOEECVSEIADHSI EEF
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	· .		1	ł	ł	
1	1	1	1	1		GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI
	2056	A	5410	2	98	GRVGLNLEGRGCSBPKWRACITIWAIDQDS
706	2056	^	74.0	1-		S
		A	5415	6	287	PFKLTPSFLSHAFSSGQERKVFIELNHIKKCNT
707			3413	١٥	-	
	2057	1 ^				VRGVFVLEEFGNYTILLLGLDSHOSHSHDOM
Ì	2057	1		l		VRGVFVLEEFGNYTILLLGLDSHGSNSNLGAP EEGLGAGRKRTSVEKSGGAGVTRKKRDP
	2057		<u> </u>		201	EEGLGAGRKRTSVEKSGGAGVTRKKRDP
708	2057	A	5423	3	291	EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPG PAITLTVRVCGFIPEVSKTTNPLGRTNNS
708			5423	3	291	EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS CCTEVTYTT TARSTASLLKSVRPRTHQKE
708			5423			EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS CCTEVTYTT TARSTASLLKSVRPRTHQKE
	2058	A	5423	3 679	291	EEGLGAGRKRTSVEKSGGAGVTRKKRIDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFTPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE
708						EEGLGAGRKRTSVEKSGGAGVTRKKRIDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKHKGG
	2058	A				EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK
	2058	A				EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWECPBCVOEKRKKK
709	2058	A	5424	679	347	EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK
	2058	A				EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPTTPSSSFRSSTPTGSEYDEEEVDY
709	2058	A	5424	679	347	EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKKKKK QESLKKKQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSSFRSSTPTGSEYDEEVDY EEGDSDESWTTESAISSEALLSSMCMNGGEEK
709	2058	A	5424	679	347	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK
709	2058	A	5424	679	347	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK
709	2058	A	5424	679	347	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV
709	2058	A	5424	679	559	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV
709	2058	A	5424	1073	347	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ
709	2058	A	5424	1073	559	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP
709	2058	A	5424	1073	559	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD
709	2058	A	5424	1073	559	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD
709	2058	A	5442	1073	347 559 319	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD LYRDIPELQGF
709	2058	A	5424	1073	559	EEGLGAGRKRTSVEKSGGAGVTRKRRDP SSSNPLGSPSTLWKLCSFVLHNKSCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD

PCT/US01/03800 WO 01/57188

					31 1 1 1 1	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	~~~	Predicted	Predicted end nucleotide	D-Acceptic Acid E=Glutamic Acid
IO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	corresponding	I-Icoloucine K=I vsine L=Leucine.
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	O-Glutamine R=Arginine, S=Serme;
ence			914	ng to first		T-Threonine V=Valine W=Tryptophan,
.01.00				amino acid	of peptide	V=Tyrosine X=Unknown, *=Stop codon,
		'		residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ			peptide		tootide incertion
	ł	l	·	sequence		KAPELLQGQSEDEQPDASQMHVYSLGMTLY
						WSAGFHVPPHQPLQLCEPLHSILLTMCEDQPH
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					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	ned enorgic Acid F=(ilutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	E-Dhanviolanine G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	corresponding	I I-Tealeroine K=I vsine L=Leucine.
eotide	seq-		USSN	location	to last amino	Nathioning N=Asparagine, P=Proline,
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uence		}	914	ng to first	acid residue	T-Threanine V=Valine W=Tryptopnan,
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					N 3' 4-34	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	I manage A sid ReGinternic Acid.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	E-Dhenvialanine G-Glycine, H-ristiume,
nucl-	peptide	}	in	nucleotide	corresponding	I I Tooleycine K=I vsine L=Leucline
eotide	seq-	Ì	USSN	location	to last amino	Manufactionine N=Asnaragine, P=Proline,
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
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	l .	1	1	1	1	GIPFLEYKHFVTRTFFPKCSSLYEERYVLPSQT
1.	-	l			1	LNSQGSSQAQETHPLLGEWKIPESCRPNMEE GISLFSSLLDNKHFLIVFVHALEQQKDFAVRD
	3	1			1	RCSLASLLTIALHGKLEYYTSIMKELLVDLID
1	1				1	ASAAKNPKLMLRRTESVVEKMLTNWMSICM
1			1	1		YSCLRETVGEPFFLLLCAIKQQINKGSIDAITG
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		İ	1		1	SOWPRAEDVDLEWFASSTOSYILRDLDD1SV
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730	2080	A	5744	3	292	QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ VANGKGNQRNMGSPQPSLLAFERNLELQIMO
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731	2081	·A	5747	1	382	LKD FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC FRVDEVNWTTWNTNVGINEDPGNCEGVKR

		17.4	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D-Aspartic Acid. E-Glutamic Acid.
O: of	NO: of	nou	in ID NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T=Threonine V=Valine W=Tryptophan,
			['		sequence	V=Tyrosine X=Unknown, *=Stop codon,
			1	residue of	Sequence	/=possible nucleotide deletion, \=possible
				peptide	İ	nucleotide insertion
•		İ		sequence	ļ	I SESI RSSRVSGRHWKNFALVPLLREASARD
					ł	ROSAQPEEVYLROFSGSLKPEDAEVFKSPAAS
		ļ	Į.		l	
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732	2002	\ ^*	1			PGKLQAQLPCPSPVRFTSARIPPASRPQTKS
·	0002	A	5754	2	2223	AAGPPGLEAEGRAPESAGPGPGGDAAETPGL
733	2083	A	3134	1 ~	_	PPAHSGTLMMAFRDVTVQIANQNISVSSSTAL
	1		Ì		1	SVANCLGAQTVQAPAEPAAGKAEQGETSGR
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	1	1	ł	1		NKLQKQAAHQREVFLFNDLLVILKLCPKKKS
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	1	1	1	1		TPLSGSEKKQVLHFCALGSDEMQKFVEDLKE
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	ł	1	l		1	QQTPPLPPPPPTPPGTLVQCQQIVKVIVLDKPC
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1		1		l l	1	KSFKFLPQLPGHTKRRIRPSAVYVCGEHRTVV
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737						DGANFIVNHMRDQNNTNEERDOWN
737						VDRLCLFVVTPVMVVGTAWIFLQGVYNQPPP
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			5881	1	1160	VDRLCLFVVTPVMVVGTAWIFLQGVYNQPFP QPFPGDPYSYNVQDKRFI
737	2088	A	5881	1	1160	VDRLCLFVVTPVMVVGTAWIFLQGVYNQPFP QPFPGDPYSYNVQDKRFI LVVTAITAILAFPNEYTRMSTSELISELFNDCG LLDSSKI CDYFNRFNTSKGGELPDRPAGVGV
		A	5881	1	1160	VDRLCLFVVTPVMVVGTAWIFLQGVYNQPFP QPFPGDPYSYNVQDKRFI

					- 11 × 1 × 1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-Acportic Acid E=Glutamic Acid
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F-Phenylelanine, G-Glycine, H-Histidine,
nucl-	peptide	i	in	nucleotide	location	I-Isoleucine K=Lysine, L=Leucine,
eotide	seq-	- 1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence	"""		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uence	1			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
				sequence		wcsQGADcitpgLyamvgaaaclggvtrmt
	ļ					VSLVVIMFELTGGLEYIVPLMAAAMTSKWVA
	1	İ	Į.	1		VSLVVIMFELIGGLE ITVILIVADATITIEST
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	1	1		1		SETTYSGFPVVVSRESQRLVGFVLRRDLIISIE
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						LYDYQGGRLGVARGAWYMEAPDIRQGDM GAPHTDWAWAPTPMSGLGSGRGRQGTLASS PLSLPLLLAGVTGILATELFDQMARPAACMV CCALAWUMI II VGLGFPFIMEALSHFLYVPFL
						LYDYQGGRLGVARGAWYMEAPDIRQGDM GAPHTDWAWAPTPMSGLGSGRGRQGTLASS PLOT BY LLAGYTGILATELFDOMARPAACMV

NO: of nucleotide sequence NO: of peptide sequence NO: of nucleotide in nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NE: OF NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NE: OF NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NE: OF NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NE: OF NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NE: OF NO: of nucleotide location corresponding to last amino acid residue of peptide sequence NE: OF NO: of NO:	Hycine, H=Histidine, ne, L=Leucine, paragine, P=Proline, inine, S=Serine, ne, W=Tryptophan, iown, *=Stop codon, deletion, \=possible
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nucl- cotide seq- uence USSN 09/496 914 USSN 09/496 914 IOSATION 10 Location correspondin ng to first amino acid residue of peptide sequence 1 LOSSN 09/496 914 IOSSN 10 Location correspondin ng to first amino acid residue of peptide sequence 1 LOSSN M=Methionine, N=As Q=Glutamine, R=Argi T=Threonine, V=Valii Y=Tyrosine, X=Unkn /=possible nucleotide nucleotide insertion RCARHGACQRSCL RGSGGTDVDQAGN SGPGDSAYGVRRD	ne, L=Leucine, paragine, P=Proline, inine, S=Serine, ne, W=Tryptophan, iown, *=Stop codon, deletion, \=possible
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vence 914 ng to first amino acid residue of peptide sequence 746 2096 A 5971 3 ng to first amino acid residue of peptide sequence 1343 AQTARRIGLELDTI RCARHGACQRSCL RGSGGTDVDQAGN SGPGDSAYGVRRD	inine, S=Serine, ne, W=Tryptophan, own, *=Stop codon, deletion, \=possible
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VQTPQLYTTFLPPP	EGVPPPELACLPTPESTPE
LPVKHLRAAGDPW	VEWNQNRNNAKEGPGRSR
GGHAAGGPAPRVL	VRPPPPGCPGQAVEVTTL
EELLRYLHGPQPPF	RKGAEPPAPLTSRALPPEP
APALLGGPSPRPHE	ECASPLRLDVPPEGRCASA
PARPALSAPAPRLO	GVGGGRRLPFSGHRAPPAL
LTRVPSGGPSRYSC	GPGKHLLYLGRPEGYRG
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747 2097 A 5998 2 754 DHASLPCSWNHRF	DVETRHVFIGDHSGQVTI
1747 2097 A 3550 2	FRGHTGGVTALCWDPVQ
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DRVOALSYAOHTI	ROLISCGGDGGIVVWNMD
VEROFTEWLDSD	SCOKCDOPFFWNFKQMW I
DSKKIGLROHHCR	KCGKAVCGKCSSKRSSIPL
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749 2099 A 6002 2 447 GRPDRSELVRMHI	AQRPGPMELVEKNILPVDSS
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DOPA SOF SOG SAA	ASPSEPKVSESPSPVTTNTP
AQFASVSPTVPEF	KTPPTAD
TI TOAMI VI PHR	POWFTPGPRLQAQGPCQEG
750 2100 A 6004 2 427 LLTQAMLVLPHR	PEDEDLNKRRVPQAKPDAV
	PEPVIEEVDLAKLAPRKPD
QEKYKEQLEAAK	EKLLKRTQRAIAELIRERLK
WDLKKDVAKKLE	ATEHETE
GQEDSLDSAVDA	TIDEAEDVETVOTODINDE
751 2101 A 6007 33 1280 TDQAKVDNQPEK	LVRSAEDVSTVPTQPDNPF
1751 SUPPLICEMENTS	VPAFLQDESDDRETDTASE
SSYQLSRHKKSPS	SLTNLSSSSGMTSLSSVSGS
VMSVYSGDFGNL	EVKGNIQFAIEYVESLKEL
HVFVAQCKDLAA	ADVKKORSDPYVKAYLLP
DKGKMGKKKTL	VVKKTLNPVYNEILRYKIEK
QILKTQKLNLSIW	HRDTFKRNSFLGEVELDLE
TWDWDNKQNKQ	LRWYPLKRKTAPVALEAE
NRGPMKLALOYY	YPEPVPGKKLPTTGEVHIW V
VECI DI PLI RGSI	ILNSFVKCTILPDTSRKSRQ
KTRAVGKTINPIE	NHTMVYDGFRPEDLMEAC
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752 2102 A 6028 108 1283 KEIFSPFELISVKP	HLVFILPSLMLLIPHILLENF IMLDNNTGSGNETGILSEDA

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-A sportic Acid E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ıcl-	peptide		in	location	corresponding	I=Icoleucine K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
:q-	uence		09/496	ng to first	acid residue	O-Clutomine R=Arginine S=Serine,
ence			914	amino acid	of peptide	T=Threoning V=Valing W=Tryptophan,
			1	residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
			1	peptide	Soquesia	/=possible nucleotide deletion, \=possible
			1	sequence		analestide incertion
				Sequence		LLRISIPLDSNLRPEKCRRFVHPQWQLLHLNG
						THISTSEADTEPCVDGWVYDQSYFPS11V1KW
				}		DLVCDYOSLKSVVOFLLLTGMLVUGIIGGHV
	ì	(1		1	SDRFGRRFILRWGLLQLAITDTCAAFAPTFPV
		ļ				YCVLRFLAGFSSMIIISNNSLPITEWIRPNSKAL
		ļ	1	1	1	VVILSSGALNIGQIILGGLAYVFRDWQTLHVV
	1	1	1	İ	ŀ	ASVPFFVFFLLSRWLVESARWLIITNKLDEGL
	Ì	ì	1	İ		KALRKVARTNGIKNAEETLNIEVVRSTMQEE
	ľ	i		İ	Ì	LDAAQTKTTVWDLFRNPSMRKRICILVFLRK
	1	1				KNLKEKA
1	0102	A	6043	1	1470	DSFESILRLIFEIHHSGEKGDIVVFLACEQDIEK
753	2103	\ ^	~~~	1		VCETVYQGSNLNPDLGELVVVPLYPKEKCSL
	-2.	1				FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN
	1	[1	SVRFVIDVGVERRKVYNPRIRANSLVMQPISQ SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTP
	1	1		1		SQAEIRKQILGSSSSGAFFCDTTELFABROUTE LKPAEMQEANLTSMVLFMKRIDIAGLGHCDF
	ì	İ				LKPAEMQEANLTSMVLFMKRDIAGDISTS MNRPAPESLMQALEDLDYLAALDNDGNLSE
	1	1	1			MNRPAPESLMQALEDED TECHDOVDEVLTIA FGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA
	1	1		1	1	AMVTAPNCFSHVPHGAEEAALTCWKTFLHPE
		1	į		1	GDHFTLISIYKAYQDTTLNSSSEYCVEKWCRD
		1	-	1		YFLNCSALRMADVIRAELLEIIKRIELPYAEPA
	1	1				FGSKENTLNIKKALLSGYFMQIARDVDGSGN
	1	1			į	YLMLTHKQVAQLHPLSGYSITKKMPEWVLF
	1	1			1	I TIVEGICENNIVIR ITSEISPELFMULVPUY YFONL
		į.	1	İ		PPSESKDILQQVVDHLSPVSTMNKEQQMCET
		}			1	CPETEORCTLO
					394	VVALHHWPFPDLLCOTTGAIFQMNMYGSCIF
754	2104	Α	6055	2	394	I NOT TATUTOR VA ATVHPLRLRHLRRPR VARLLU
	1	į.				I CVWALIT VEAVPAARVHRPSRCKYRDLEVK
	İ	1		ļ		LCFESFSDELWKGRLLPLVLLAEALGFLLPLA
	1			1		ANTIVES
		-	6059	3	1795	LGLGSGTLLSVSEYKKKYREHVLQLHARVKE
755	2105	A	0039	"	1	RNARSVKITKRPTKLLIAPESAAPEEALGPAEI
	1	[İ	į	· I	PEPGRARRSDTHTFNRLFRRDEEGRRPLTVVI
		- 1		ļ		QGPAGIGKTMAAKKILYDWAAGKLYQGQVI
	1		1	1	Ī	FAFFMPCGELLERPGTRSLADLILDQCPDRGA
		1		1	1	PVPQMLAQPQRLLFILDGADELPALGGPEAA
		- 1	ļ		1	CTDPFEAASGARVLGGLLSKALLPTALLLVT
		- 1	- [1	RAAAPGRLQGRLCSPQCAEVRGFSDKDKKK
	}	- 1	1			YFYKFFRDERRAERAYRFVKENETLFALCFV PFVCWIVCTVLRQQLELGRDLSRTSKTTTSV
	1		1		Į.	PFVCWIVCI VLKQQLELGKDLSKISKI I ISV
		1		ì		LLFITSVLSSAPVADGPRLQGDLRNLCRLARI
				1	ļ	GVLGRRAQFAEKELEQLELRGSKVQTLFLSK KELPGVLETEVTYQFIDQSFQEFLAALSYLLE
		-		1		DGGVPRTAAGGVGTLLRGDAQPHSHLVLTT
		- 1	Ì	- 1	l	DGGVPRTAAGGVGTLLRGDAQFHSHLVETT RFLFGLLSAERMRDIERHFGCMVSERVKQEA
	1	- 1			i	RFLFGLLSAERMRDIERHFGCMV3ERVRQEF LRWVQGQGQGCPGVAPEVTEGAKGLEDTEI
	1	l	1			PEEEEGEEPNYPLELLYCLYETQEDAFVRQ.
Į.			1			LCRFPELALQRVRFCRMDVAVLSYCVRCCP.
ļ		1			}	GQALRLISCRLVAAQEKKKKSLGKRLQASLO
1	1				1	
ì				1		GG SGRPTRPAKPTGQGMGRFMLTLVCQGSIMM
751	2106	-	6060	12	436	SGRPTRPAKPTGQGMGKPMLTLVCQGSIVINARDLIMNNLTELQPGLFHHLRFLEELRLSGN
756	2100	14	5556			LSHIPGQAFSGLYSLKILMLHNNQLGGIPAQA
	-		- 1			LWELPSLQSLRLDANLISLVPERSFEGLSSLR
		- 1	1	\		LMETAPOTAT LEDGE
1		١.	i			LWLDDNALTEIPS ITPLGLGAADMCAFPWLLLLLLQEGSQRRI
	j	1				
757	2107		6063	54	419	ITPLUCCEEUTAM OFFICE DE REPUBLICANI
757	2107	A	6063	54	419	WRWCGSEEVVAVLQESISLPLEIPPDEEVEN WSSHKSLATVVPGKEGHPATIMVTNPHYQG

					N. Hatad and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ			1	amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			}	residue of	sequence	/=possible nucleotide deletion, \=possible
1	{	1	1	peptide		nucleotide insertion
	<u> </u>		ļ	sequence	 	OTLTMLLRSLOOPSASWPRDCSSSCSW
				105	438	IGISCPATIFVPMFSHSLIGIGEEYQLPYYNMV
758	2108	Α	6066	125	430	PSDPSYEDMREVVCVKRLRPIVSNRWNSDEC
	1]		1	1	LRAVLKLMSECWAHNPASRLTALRIKKTLAK
1		1		1		MVFSODVKI
					650	PGRRFRPAALEERAMEKLREKVPFQNRGKGT
759	2109	A	6072	3	630	LSSIIPNNSDTRKATETTSLSSKPEYVNPDFRW
i		i		ļ	ì	SKIDPSSKSGNLLETSEVGWTSNPEELDPIRLA
· ·		1	1			LLGKSGLSCOVGSATSHPVSCQEPIDEDQRISP
1	1	i	1	•	1	KDKSTAGREFSGOVSHOTTSENQCIPIPSSIV
		1	1	1.		HSSVADMONMPAAVHALLTQPSLSAAPFAQ
1	1	ł	ļ	1		DVI GTI PSTGSTTLPOCHAGNATVW
		 	6077	3	730	PLRITLMEEVLLLGLKDREGYTSFWNDCISSG
760	2110	A	00//) 3	1,20	I PCCM JELPLRGRLOLEACGMRRKSLLTRK
	1	ŀ	}		1	VICKSDAPTGDVLLDEALKHVKETQPPETVQ
1		1	1	1	1	NWIELL SCETWNPLKLHYOLRNVRERLAKNL
1		ł			ļ	VEKGVLTTEKQNFLLFDMTTHPLTNNNIKQR
1	1	1		1 .		I TKKVOEAVLDKWVNDPHRMDRKLLALIYL
	1		1	1		AHASDVLENAFAPLLDEQYDLATKRVRQLLD
]	1	1	1			LDPEVECLKANTNEVLWAVVAAFTK
761	2111	IA	6078	833	390	IVSFHLSGFKKFVRPFSFLSVHGLQVDEYHSV
/01	2111	1	1 00.0	1		HQKLSADMADHSNLIRSLLVGAEDARLMRD
	1 .	1	1	1	}	MKTMKSRYMELYDLNRDLLNGYKIRWNNH
İ				1	ì	TELLGNLKAVNQAIQRAGRLRVGKPKNQVIT
ł					<u> </u>	ACRDAIRSNNINTLFKIMRVGTASS KKAITCGEKEKQDLIKSLAMLKDGFRTDRGS
762	2112	A	6079	2	2686	HSDLWSSSSSLESSSFPLPKQYLDVSSQTDISG
			1			SFGINSNNQLAEKVRLRLRYEEAKRRIANLKI
l	1	1		ì		OLAKLDSEAWPGVLDSERDRLILINEKEELLK
	Ì	1	ł	i		EMRFISPRKWTQGEVEQLEMARKRLEKDLQ
	-	1	1	1		AARDTQSKALTERLKLNSKRNQLVRELEEAT
		1	1	}		ROVATIHSOLKSLSSSMOSLSSGSSPGSLTSSK
		i		1	1	GSLVASSLDSSTSASFTDLYYDPFEQLDSELQ
1		1			-	SKVEFLLLEGATGFRPSGCITTIHEDEVAKTQ
1		ŀ]	1		KAEGGGRLOALRSLSGTPKSMTSLSPRSSLSS
Í		-		Ì		DODDCODI MADPLILAGDAFLNSLEFEDPELSA
1	1	1	1	Ĭ		TI CELSI GNSAOERYRLEEPGTEGKQLGQAV
1		1	}			NTA OGCGLK VACVSAAVSDESVAGDSGVYE
		1		1		ASVORI GASEAAAFDSDESEAVGATRIQIALK
j			1	1		VDEKNKOFAILIIOLSNLSALLQQQDQKVNLK
		1	1	1		VAVI PCSESTTCLFRTRPLDASDILVFNEVFW
		1		1	1	VSMSVPALHOKTLRVDVCTTDRSHLEECLGG
				1	1	A OISLAEV CRSGERSTRWYNLLSYKYLKKUS
1				Į		PELKPVGVMAPASGPASTDAVSALLEQTAVE
		1			1	1 FKROEGRSSTOTLEDSWRYEETSENEAVAE
		- 1		1	.	FEFFEVEFEEGEEDVFTEKASPDMDGYPALK
		1		1		VDKETNTETPAPSPTVVRPKDRRVGTPSQGPF
	1	1	1	}	1	LRGSTHRSKTFSPGPQSQYVCRLNRSDSDSST
				1		LSKKPPFVRNSLERRSVRMKRPSPPPQPSSVK
	1		ĺ		1	SLRSERLIRTSLDLELDLQATRTWHSQLTQEIS
	1	ļ	1	1	\	VLKELKEQLEQAKSHGEKELPQWLREDERFR
Ì	1	[-		1	LLLRMLEKRMDRAEHMGELQTDKMMRAAA
1	-		1			KDVHRLRGQSCKEPPEVQSFREKMAFFTRPR
					<u> </u>	MNIPALSADDV
763	2113	A	6082	3	1558	PHPIRFSKLCVSFNNQEYNQFCVIEEASKANE
103	2113	1.,	1	1		VLENLTQGKMCLVPGKTRKLLFKFVAKTED VGKKIEITSVDLALGNETGRCVVLNWQGGGG
	l l	- 1	1	1	1	I VCK PIFITSVIII ALGNEIGKUV VLN W QUGUU
		1	1	1	i	ACCULATION DAY DELLE DEL
1					ļ	DAASSQEALQAARSFKRRPKLPDNEVHWGSII IQASTMIISRVPNISVHLLHEPPALTNEMYCLV

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					W . 1' . 1. 2 3	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Aspartic Acid F=Glutamic Acid.
10: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	1=teoleucine K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	l	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence	{		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	l	l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		i	Į.	peptide	coque	/=possible nucleotide deletion, \=possible
	i	1		sequence	l .	nucleotide insertion
		 		sequence	 	VTVQSHEKTQIRDVKLTAGLKPGQDANLTQK
		1	1			THATT HOTEL CDESYPALLTDIPVGDLHPGEQ
	1	1	1]		LEKMLYVRCGTVGSRMFLVYVSYLINTTVEE
		ì	1	}	1	KEIVCKCHKDETVTIETVFPFDVAVKFVSTKF
		İ	1			EHLERVYADIPFLLMTDLLSASPWALTIVSSE
		ļ	1	ŀ	1.	LHLAPSMTTVDQLESQVDNVILQTGESASECF
		l	}	\	1	CLQCPSLGNIEGGVATGHYIISWKRTSAMENI
	1	1	1	1	1.	PHITTVITLPHVIVENIPLHVNADLPSFGRVRES
	-	1	1	1		LPVKYHLQNKTDLVQDVEISVEPSDAFMFSG
		1	1			LKQIRLRILPGTEQEMLYNFYPLMAGYQQLPS LNINLLRFPNFTNQLLRRFIPTSIFVKPQGRLM
	1		1		1	
	1	1				DDTSIAAA AAADLANSNAGAAVGRKAGPRSPPSAPAPAP
764	2114	A	6093	1	1422	PPPAPAPPTLGNNHQESPGWRCCRPTLRERN
,,,	,					ALMFNNELMADVHFVVGPPGATRTVPAHKY
		1	1	ļ	1	LVI AVGSSVEYAMFYGDLAEVKSEIHIPDVEPA
	ļ		}	1 .	1	ART II I KYMYSDEIDLEADTVLATLYAAKKYI
	1		1	1		VIDALAK ACVNELETSLEAKNACVLLSQSKLF
			ł	1		PEDEL TORCWEVIDAOAEMALRSEGFCEIDK
	Ì		ł			OTLEUVTREALNTKEAVVFEAVLNWAEAEC
		1	1		ļ	KROGI PITPRNKRHVLGRALYLVRIPIMILLE
		l	į		1	FANGAAOSDILTLEETHSIFLWYTATNKPRLD
		i	-	Į.	1	LDI TKRKGI APORCHRFOSSAYRSNQWKYKU
	ł	1	-			RCDSIQFAVDRRVFIAGLGLYGSSSGKAEYSV
	1	1				KIELKRLGVVLAQNLTKFMSDGSSNTFPVWF
			1	t		EHPVQVEQDTFYTASAVLDGSELSYFGQEGM
	1	1	1	1		TEVQCGKVAFQFQCSSDSTNGTGVQGGQIPE
		1				LIFYA SGFTHYAIYDFIVKGSCFCNVHADQCIPVHGF
765	2115	A	6099	1	1150	RPVKAPGTFHMVHGKCMCKHNTAGSHCQH
,,,,		1	1	1	}	CAPLYNDRPWEAADGKTGAPNECRTCKCNG
	1	1				HADTCHFDVNVWEASGNRSGGVCDDCQHN
	ł	- 1	Ì		1	TEGQYCQRCKPGFYRDLRRPFSAPDACKPCS
		١	- [1	ł	CHPVGSAVLPANSVTFCDPSNGDCPCKPGVA
		1				CRRCDRCMVGYWGFGDYGCRPCDCAGSCD
İ						PITGDCISSHTDIDWYHEVPDFRPVHNKSEPP
ļ		-	1		\	WEWEDAOGESALLHSGKCECKEUTLUNAKA
		- }	ı	1	j	FCGMKYSYVLKIKILSAHDKGTHVEVNVKIK
	}	ı		1	1	KVI.KSTKI.KIFRGKRTLYPESWTDRGC1CPIL
	ì	l		l		NPGLEYLVAGHEDIRTGKLIVNMKSFVQHWI
1		1		1	1	PSLGRKVMDILKRECK
766	2116	+	6103	- 2	384	MTAAATATVLKEGVLEKRSGGLLQLWKRKE
766	2110	A	1 0103	1		CVLTERGLQLFEAKGTGGRPKELSFARIKAV
Į .	}		1	1		CVESTGRHIYFTLVTEGGGEIDFRCPLEDPGW
	- 1	1				NAQITLGLVKFKNQQAIQTVRARQSLGTGTL
1	1	- 1				VS PROPORTED PLOSEDOTEL LAGMOST.
767	2117	HA.	6106	1	542	SGSSHASDGSGFQELRICSEDQTPLIAGMCSL MARYYIIKYADQKALYTRDGQLLVGDPVAL
1 ""	"""	1				NCCAEKICTLPNRGLDRTKVPIFLGIQGGSRC
1			- 1	1	1	NCCAEKICTLPNKGLDKTKVFIFLOIQUGGKC LACVETEEGPSLQLEDVNIEELYKGGEEATR
1				1		TFFQSSSGSAFRLEAAAWPGWFLCGPAEPQC
1	- (ı			PVQLTKESEPSARTKFYFEQSW
1						FILQAVLQLSSQEARYKAFGTCVSHIGAILAF
768	2118	A	6109	3	292	YTPSVISSVMHRVARCAAPHVHILLANFYLL
		1				PPMVNPIIYGVKTKQIRDSLGSIPEKGCVNRE
1		· [RHEPSCSNGVASTKSKQNHSKYPAPSSSSSS
769	2119	A	6110	1	711	CCCCCCCCCCVNVSRSNSTDSTKSOHHSSTSNU
1	1					ETSDSEMEMEAEHYPNGVLGSMSTRIVNGA
		- 1	ı	1	1	E I OLO DE IVILIA LO LA LA LA LA LA LA LA LA LA LA LA LA LA
1		· · ·		1		KHEDLQTDESSMDDRHPRRQLCGGNQAATI

SEQ IID NO: of nucleotide peptide colide sequence wence when the colide sequence were colide sequence when the colide sequence were colided sequence when the colided is sequence when the colided sequence when the colided is sequence when the colide					- W. I	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of non-colide could could in in in incleotide could sequence when the country is uncleotide could sequence when the country is uncleotide uncleotide in its in in ingular in the country in the count		SEQ ID	Met	SEQ	Predicted	Predicted enu	D-Americ Acid E=Glutamic Acid.
mucle cotide sequence Sequence			hod			location	F=Phenylalanine, G=Glycine, H=Histidine,
cetide sequence were proposed as the sequence of the sequence							I=Isoleucine K=Lvsine, L=Leucine,
sequence where with the sequence of peptide sequence sequence of peptide sequence of peptide sequence of peptide sequence of peptide of p						to last amino	M=Methionine, N=Asparagine, P=Proline,
uence amino acid residue of peptide sequence peptide sequ	~~	uence					O=Ghitamine, R=Arginine, S=Serine,
residue of peptide sequence	ience	1		914			T-Threonine V=Valine W=Tryptophan.
Popsible Popsible	ì		'	1		sequence	V=Tyrosine, X=Unknown, *=Stop codon,
nucleoidde insertion RIILFGREI QALSEQLGREYGKNI.AH AFSLLAYSDPWSCPVGQQLDPIQREF NSALLESQNLPKQFPLMLALGQASEC. RAGIGSCSRARVDVLH 770 2120 A 6125 2 570 YFGINLHVQHLGNNVFLUQTLFGAV VPQEMQMLREVLATLGLGASALANI GNEVPTITRARAMGINATFANIAGAL LISVYSPPLPWITVGVFFFISGFAFLLL PLEDTIQDEKNERKDPBEFKQEDPRV RDYCNILAFSRNSTNIHVALRDIGNQL LTKEDTGWYWCGIQRDFARDDMDF DDKGTLANDFWSGKDLSGNKTRSC RKADRSRISLLICLITGLGIISVISHLI QRNRRVGRTLKPFSKVLIFKEMAPT 772 2122 A 6148 7 810 FVLGILALSHTISPFRNKFFFASFPRR KADRSRISLICLITGLGIISVISHLI QRNRRVGRTLKPFSKVLIFKEMAPT GLGITIFIMHIFKHAQPALIV CVICLG WYLLRKHWIANNLFGLAFSLNGVEL UNTLERKHWIANNLFGLAFSLNGVEL GLGITIFIMHIFKHAQPALIV LVAC ALAKGEVTEMFSYESSPKKDPAAVT RASASKGLEKKEK COPMLYTEKNIFEKLLRRTESVAEK FTFILLYKFILESAGEPLEMIY CARK PIDATIGRARYSLSEDKLIRHLIDYKI NFENENAPEVYVSGLDCDTGTQAXI AVKGVPYSGRKAADMDLEWRQG QDEDVTTKIDNDWKRINTLAHYQV ALVPKQTSAYNISNSSTIFTSISSRVE SSPDJRSRTPMITPDLESGTKLWHI LDQREODRGSKMVSETVLTRLLATK VDDLFETIFSTAHRGSALFLAIKYMF ADKHQHDADVRHTWKSNCLPLIFF NCFYPDILKRSITDALCSVV NCFYPLIFNSTIPALCSVV NCFYPLIFNSTIPALCSVV NCFYPLIFNSTIPALCSVV NCFYPLIFNSTIPALCSVV NCFYPLIFNSTIPALCSVV NCFYPLIFNSTIPALSV N	ì	Į.		Ì		J. J. J. J. J. J. J. J. J. J. J. J. J. J	/=possible nucleotide deletion, /=possible
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					[S . P. A. J and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	·Met	SEQ	Predicted	Predicted end	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
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	1	ĺ		1		PQVL\SEPN*RSGGCFSAPSFEVPPWTGEVKP/
1	1	1	1	-	i	SPQRDGGALG\QGPLGIPSDSILALLKKQT*RA
		1		ì		LLNWPLGSLRRSSCFGGQDGQDLKPRSGLGC
ļ			1			NSFRYRR
	10,00	A	6249	420	36	ARAPSPSFSVRDVELSDPARERGEMPVAVGP
779	2129	1^	1 0247	1		YGQSQPSCFDRVKMGFVMGCAVGMAAGAL
	İ				ļ	FGTFSCLSSILVSSSG/SGMRGRELMGGIGKTM
	1	1	1		İ	MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH
1		Ì			1	QSQPMY
1 700	2130	A	6263	415	1380	RIMRMCDRGIQMLITTVGAFAAFSLMTIAVG
780	2130	1				TDYWLYSRGVCRTKSTSDNETSRKNEEVMT
1	1	1	1	I	ì	HSGLWRTCCLEGAFRGVCKKIDHFPEDADYE
1			1			QDTAEYLLRAVRASSVFPILSVTLLFFGGLCV
		}	1		•	AASEFHRSRHNVILSAGIFFVSAGLSNIIGIIVYI
1	1.	1				S\ANAGRTPGQR\DSKKSYSYGWSF/YFSGAFS FIIGR/IIC*GVGLPWHIYIEKHQQLRAKSHSEF
	ì					FIIGR/IIC*GVGLPWHITEKHQQLKAGSIOLI LKKSTFARLPPYRYRFRRRSSSRSTEPRSRDLS
1	ł	1	1	1		PISKGFHTIPSTDISMFTLSRDPSKITMGTLLNS
1	1	1	1		1	DRDHAFLQFHNSTPKEFKESLHNNPANRRTT
1		1	1	ì	j	
1	1		1	·		PV RIIKVKDLKQTLAIKTAYPRCKCLVEMDQIFH
781	2131	A	6274	832	318	LQVKQKQLACLCTWQARDPDCPPSTKVVL/L
1				1		VCDCMCCMVALFODSIAWSNKSMPSSLSALS
1		ľ	1	1		OSPCOVOAPEGPSSFHLPTLSFTTCLSWQGGD
1	1	1		1		LEFLGDLKGCSELKNFQELITQSALVHPKADV
		1				WWYCGRPLLGTLPSN
		ــــــــــــــــــــــــــــــــــــــ			393	WIST PSSLI CRKNGSSAEDDRR\GEPSAEEAEG
782	2132	Α	6281	1324	393	EPEDWGIGSA*SVGAVSKVPSARF*RTYPS\E
				1		DEFEVTHOKSSSSDSNSEEHRKKKTSRSKNK
ļ			Ì	1		LAKBKNK SZKRKHRKYSDSDSNSESDTNSDSD
1 .	ļ	Į.	}			DDKKRVKAKKKKKKKKKKKKKKKKKKKKKKK
1		1	 			PSSDSSCKDSEEDLSEATWMEQPNVADIMUL
1		l				TODE A PITHT SODEKPLKYGHALLPGEGAAMA
}	1	1		1		EVVIK A CKRIPRRGEIGLTSEEIGSFECSGY VM
1		-	1	1		CCCDHDDMEAVRLRKENOIYSADEKKALASE
	1		1			MOFFREKRESKILASFREMVHKKIKGKUUK
	-	- , -	6305	201	1032	TWODYPOGAL RRREAAEGLHFLGPPGRVKGQ
783	2133	A	. 6363	29.	1	I RGITGPA WYCHSPSHSLLSAFCHLPTPSKCP
	1	1			1	AMARPPVPGSVVVPNWHES/RRGQGVPGLHS
	1	ļ		1	1	A OEDDA GVWA A * AASAAAA\LSIDTASYKIFV
		- 1		}		SCKSGVGKTALVAKLAGLEVPVVHHETTGIQ
		1		i	1	TTVVFWPAKLOASSRVVMFRFEFWDCGESA
	1	- 1		1		LKKFDHMLLACMENTDAFLFLFSFTDRASFE
1	f	- [- 1	1	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT
ļ	1					DVPERDLTAFRQAWELPLLRVKSVPGRRLG
	- 6:50		6308	86	96	CCCDDDASI ITMKNODKKNGAAKOSNPKSSP
784	2134	A	0308	1 80]	GOPEA GPEGA OERPSOAAPA VEAEGPGSSQA
ŀ		İ	1			DDKDEGAGARTAOSGALRDVSEELSKQLEDIL
ĺ	- [- [STYCVDNNQGGPGEDGAQGEPAEPEDAEKSR
	1		- [1	1	TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR
		l	1	-		QSDEVGDRDHRRPQEKKKAKGLGKEITLLM
1				ĺ		QTLNTLSTPEEKLAALCKKYABLLEEHRNSQ
1		1		1		KQMKLLQKKQSQLVQEKDHLRGEHSKAVLA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ŀ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ł	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		ļ	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	İ	ļ		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
		ì	1	peptide	1	nucleotide insertion
		<u> </u>		sequence		RSKLESLCRELQRHNRSLKEEGVQRAREEEE
				l		KRKEVTSHFQVTLNDIQLQMEQHNERNSKLR
İ	1	ļ		1	ì	QENMELAERLKKLIEQYELREEHIDKVFKHK
}	}	1		ł	l	DLQQQLVDAKLQQAQEMLKEAEERHQREKD
i	l	1			1	FILKEAVESORMCELMKOOETHLKQQLALY
	1	İ	ļ			TEKFEEFONTLSKSSEVFTTFKQEMEKMTKKI
l]	}		ļ	KKIEKETTMYRSRWESSNKALLEMAEEKTV
		1				RDKELEGLOVKIQRLEKLCRALQT/GAQ*PVR
1	1	ì				I GORWGSHRTSAVRIFS
	0126	+	6319	1493	889	L SPOGPLLRSVSPVSAGASSVTPGGAQPGVTTT
785	2135	A	0313	1475	1	PPSI.VAVAPAPGSAAGPAAGWQ*HAGCR/WT
}	1	l	1	ľ	Ī	KI PWSWGMRPMKIFFSEEYRSISTRISHDAL*
1	1		1	1		FKCTOPAKPLSMIR\TGSSVSPG/PLVKWNWT
		}		1		RREFRNSGTRVVSSCCGMSCMYSFLGHCSV/S
1		1	1	}	1	QDLPLVHVDVGWQPPLGPTVGLRPGLLPLHD
		1	ļ	1		TTPCQKLVVDDLDWA
786	2136	$+_{A}-$	6320	551	135	RWLPVAECDSSCVGCTGEGPGNCKECISGYA
'00	2.50	1				REHGQCADVDECSLAEKTCVRKNENCYNTP
1	1	1.				GSYVCVCPDGFEET/RRCLCAAGRG*SHRRRK PDTAALPRRPVMCRTYPLNYSEGCPVENVAL
1	-	ł	1	1		PDTAALPRRPVMCKI TPLN I SEGCI VENVAL
1						RMPSPAVDSGGERLPAL DYVLTAELHRQRSPGVSFGLSVFNLMNAIMG
787	2137	A	6330	1693	227	SGILGLAYVMANTGVFGFSFLLLTVALLASYS
	1.	1		1	1	VHLLLSMCIQTAYLGP*TNYFMVLPAH*LTCL
1		1	İ	1		PLIEFLQSL*NSL*AVTSYEDLGLFAFGLPGKL
		1	1.	\	ł	VVAGTIIIQNIGAMSSYLLIIKTELPAAIAEFLT
1		ł	1	1		GDYSRYWYLDGQTLLIIICVGIVFPLALLPKIG
		1	1	ļ.	1	FLGYTSSLSFFFMMFFALVVIIKKWSIPCPLTL
1	1	ĺ	1 .		\	NYVEKGFOISNVTDDCKPKLFHFSKESAYALP
1	1		l	1	İ	TMAFSFLCHTSILPTYCELQSPSKKRMQNVTN
l	1			ļ	l .	TAIAL SELIVEISALEGYLTEYD/GTTKAQRGE
1	1			i	ĺ	VTCHRIKDKVESELLKG***IP*SHDVVVMT\V
	-	1				KLCILFAVLL\TVPLIHFPARKAVTMMFFSNFP
i		ļ				FSWIRHFLITLALNIIIVLLAIYVPDIRNVFGVV
	1	1	1	1		GASTSTCLIFIFPGLFYLKLSREDFLSWKKLGV
			-	1	1	GCFC/LLSFKTSILRNSLSVYIILPASRKSIYFKI
788	2138	A	6351	1	6622	PRSLCFSLWAEAAVLADGGLRRRRLLRGTM
1	1			ļ		SASFVPNGASLEDCHCNLFCLADLTGIKWKK
-		1			j	YVWQGPTSAPILFPVTEEDPILSSFSRCLKADV LG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLF
1	1	1		1		TMTYQKKKMECGRMDFPMNAVLCFSKAVH
	1	1	1			NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN
				1	1	KSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
1		ı				LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQ
1		1			1	AFKMSDSATKKLIGEWKOFYPISCCLKEMSE
1				l		FKOFDMDWEDDSLAAVEVLVAGVRMIYPAC
1				1		FVI VPOSDIPTPSPVGSTHCSSSCLGVHQVPAS
				1	ļ	TROPAMSSVTLTPPTSPEEVOTVDPQSVQKW
	1	ı	- [VKESSVSDGFNSDSTSHHGGKIPRKLANHVV
		İ	1	1	1	DRYWOFCNMNRAONKRKYSASSGGLCEEAT
	1	- 1		1	1	AAKVASWDFVEATORTNCSCLRHKNLKSRN
	1	1		- (1	AGOOGOAPSI GOOOOILPKHKTNEKQEKSEK
- [1	1	POKRPI TPFHHRVSVSDDVGMD\ADS\ASQKL
	.	- 1		1		VICAPIDSO/VRFSNIR/TNDVAK/TPOMHGTE
	l	-	1.		1	MANSPOPPPLSP\HPCDVVDEGVTKTPSTPQS
-	1	1	j	1	1	OHEYOMPTPDPLVPSKPMEDRIDSLSQSFPPQ
		1			-	VOEAVEPTVYVGTAVNLEEDEANIAWKYYK
	1	ì		1	1	EPKKKDVEFI PPOLPSDKFKDDPVGPFGQESV
	1	- 1		1		TOUTEI MUNCKKPI KUSDELVOOYOIKNOCL
1	1	1		i	Í	SAIASDAEQEPKIDPYAFVEGDEEFLFPDKKD
1						

				B 134.1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
1	ł			residue of	sequence	/=possible nucleotide deletion, \=possible
	1			peptide		nucleotide insertion
		1		sequence		RONSEREAGKKHKVEDGTSSVTVLSHEEDA
						KUNSEKEAGAATAVEDOISSVIVESILEDA
i '	1	i				MSLFSPSIKQDAPRPTSHARPPSTSLIYDSDLA
1	J	1	}	}	ĺ	VSYTDLDNLFNSDEDELTPGSKRSANGSDDK
		1				ASCKESKTGNLDPLSCISTADLHKMYPTPPSL
1				ł		EQHIMGFSPMNMNNKEYGSMDTTPGGTVLE
		1	i	•		GNSSSIGAQFKIEVDEGFCSPKPSEIKDFSYVY
		1	ļ	1	1	KPENCQILVGCSMFAPLKTLPSQYLPLIKLPEE
	1			1	1	CIYRQSWTVGKLELLSSGPSMPFIKEGDGSNM
	1	ł	ļ			DQEYGTAYTPQTHTSCGMPPSSAPPSNSGAGI
		1	1	1		LPSPSTPRFPTPRTPRTPRTPRGAGGPASAQGS
1	1	1	Ì	Į.		VKYENSDLYSPASTPSTCRPLNSVEPATVPSIP
į		1				EAHSLYVNLILSESVMNLFKDCNSDSCCICVC
1			Ì			NMNIKGADVGVYIPDPTQEAQYRCTCGFSAV
	1	1				MNRKFGNNSGLFFEDELDIIGRNTDCGKEAE
		1	1			KRFEALRATSAEHVNGGLKESEKLSDDLILLL
		1	1			QDQCTNLFSPFGAADQDPFPKSGVISNWVRV
ļ				İ	İ	EERDCCNDCYLALEHGRQFMDNMSGGKVDE
		1	1			ALVKSSCLHPWSKRNDVSMQCSQDILRMLLS
1		1			Į	LQPVLQDAIQKKRTVRPWGVQGPLTWQQFH
		1			l	KMAGRGSYGTDESPEPLPIPTFLLGYDYDYLV
			1	1		LSPFALPYWERLMLEPYGSQRDIAYVVLCPE
	1	1	1		1	NEALLNGAKSFFRDLTAIYESCRLGQHRPVSR
	1	1	1	1		LLTDGIMRVGSTASKKLSEKLVAEWFSQAAD
1	1	1	1			GNNEAFSKLKLYAQVCRYDLGPYLASLPLDS
İ		1	1	i	1	SLLSOPNLVAPTSQSLITPPQMTNTGNANTPS
1	}	1			ì	ATLASAASSTMTVTSGVAISTSVATANSTLTT
		i	Ì			ASTSSSSSSNLNSGVSSNKLPSFPPFGSMNSNA
	.					AGSMSTOANTVOSGQLGGQQTSALQTAGISG
	l l			1	1	ESSSLPTOPHPDVSESTMDRDKVGIPTDGDSH
		ł	1			AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTL
		1				GLLRCFLEMVOTLPPHIKSTVSVQIIPCQYLLQ
1		-				PVKHEDREIYPOHLKSLAFSAFTQCRRPLPTS
l l		ŀ	İ	1		TNVKTLTGFGPGLAMETALRSPDRPECIRLYA
ł	ł	ł	1	1		PPFILAPVKDKOTELGETFGEAGQKYNVLFV
	{	İ			1	GYCLSHDQRWILASCTDLYGELLETCIINIDVP
ŀ		1 .	1	1		NRARRKKSSARKFGLQKLWEWCLGLVQMSS
	1 .	-	1			LPWRVVIGRLGRIGHGELKDWSCLLSRRNLQ
	1		1	1	1	SLSKRLKDMCRMCGISAADSPSILSACLVAM
ì			ĺ	1		EPQGSFVIMPDSVSTGSVFGRSTTLNMQTSQL
		1	1	1		NTPODTSCTHILVFPTSASVQVASATYTTENL
		J	1	1		DLAFNPNNDGADGMGIFDLLDTGDDLDPDII
-	'	1		,		NILPASPTGSPVHSPGSHYPHGGDAGKGQSTD
i			1	1	1	RLLSTEPHEEVPNILQQPLALGYFVSTAKAGP
1			1			LPDWFWSACPQAQYQCPLFLKASLHLHVPSV
				1	1	OSDELLHSKHSHPLDSNQTSDVLRFVLEQYN
		1		1	1	ALSWLTCDPATQDRRSCLPHFVVLNQLYNFI
				1		MNML
1						TGTLTEDGLDVMGVVPLKGQAFLPLVPEPRR
789	2139	A	6359	1	2002	LPVGPLLRALATCHALSRLQDTPVGDPMDLK
		1				LYVGYLLKALATCHALSKLQDIF VODIVIDLA
			1		1	MVESTGWVLEEEPAADSAFGTQVLAVMRPP
	1	1			1	LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM
			1		1	SVVVAWPGATQPEAYVKGSPELVAGLCNPET
	1			1	1	VPTDFAQMLQSYTAAGYRVVALASKPLPSVP
		-	ļ	ļ	1	SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP
1	1				1	QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA
1		1	Ì	1	1	RGCGMVAPOEHLIIVHATHPERGQPASLEFLP
			1		I	MESPTAVNGVKDPDOAASYTVEPDPRSRHLA
						LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP
.			1	1_		FORTELVCELOKLOYCVGMCGDGANDCGAL
		1	1	1 -	1	KAADVGISLSQAEASVVSPFTSSMASIECVPM
l						

						/ N. I. C. C. C. chains
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Thrennine, V=Valine, W=Tryptophan,
	1	1	ł	residue of	sequence	V=Tyrocine X=I Inknown, *=Stop codon,
		ļ.	1	peptide	Sodinouse	/=possible nucleotide deletion, \=possible
	1	ļ		sequence	1	nucleotide insertion
		ļ	 	Sequence		VIREGRCSLDTSFSVFKYMALYSLTQFISVLIL
	1	1			ł	YTINTNLGDLQFLAIDLVITTTVAVLMSRTGP
,			1	ĺ	i	ALVLGRVRPPGALLSVPVLSSLLLQMVLVTG
		1 .	1		ļ	VQLGGYFLTLAQPWFVPLNRTVAAPDNLPNY
	İ		1	ł		ENTVVFSLSSFQYLILAAAVSKGAPFR\RPLTN
•	1	1	1		}	NVPFLLASAL*SSVLVVLVLSPGLLHGPLALR
	ì	1	1	1		NITDTGFKLLLVGLVTLNFVGGLHAGERARP
	ì	1	1		ļ	VPPRLPAPPPAQAG\SKKRFKQLERELAEQPW
1		İ	1			PPLPAGPLR PPLPAGPLA ARVINDI I PERPAGA AR
700	2140	A	6380	76	1059	SSAGSARKLQVMALAARLWRLLPFRRGAAP
790	2140	1 ~	0500			GSRLPAGTSGSRGHCGPCRFRGFEVMGNPGT
1	1	1	1			FKRGLLLSALSYLGFETYQVISQAAVVHATA
ľ		l	1	Į.	į.	KVEEILEQADYLYESGETEKLYQLLTQYKESE DAELLWRLARASRDVAQLSRTSEEEKKLLVY
		1			1	EALEYAKRA/L/EKNESSFASHKWYAICLSDV
	ì	1		ì	1	GDYEGIKAKIANAYIIKEHFEKAIELNPKDATS
	1			Ì	1	GDYEGIKAKIANA TIKESII EMUMENTA IIKISII E
	1		1	ì	ì	*FPPYEKALG\YFHRAEQVDPNFYSKNLLLLG
		1		1	1	KTYLKLHNKKLAAFWLMKAKDYPAHTEED
		Į.	1	1	1	KQIQTEAAQLLTSFSEKN
1.			İ		1	IALLIVDGLAWDDQGGLALLHISPSKLIL*QDS
791	2141	A	6434	3	1460	1 COMPANIATION AFFKSLLCHICOYSIGPQ
{ '''						*VT\CPGODACKE*KSTAN*GG*RE**PQVLFF
1	1		1) ·		A ET SNIPA VK FGRMSKKORDSLY A EV QKHQQ
1		ļ		i		PLOFOROOOSGEAEALARVYSSSISNGLSNLN
1				l l	1	NETSGTYANGSVIDLPKSEGYYNVVSGQPSP
	1	1		-		DOSGL DMT\GIKOKOEPIYDLTSVPNLFTY\SS
1		1			1	ENDIGOT APCITAMTEIDRIAONIIKSHLETCUY
1		- 1	ſ	1	1	TAGET HOLAWOTHTYEEIKAYQSKSREALW
		1	\	İ	1	OCATOTHAIOYVVEFAKRITGFMELCUNDU
1	1		- 1	1		ILLLKSGCLEVVLVRMCRAFNPLNNTVLFEG
				1	1	KYGGMQMFKALGSDDLVNEAFDFAKNLCSL
1		1				QLTEEEIALFSSAVLISPDRAWLIEPRKVQKLQ
		1				EKIYFALQHVIQKNHLDDETLAKLIAKIPTITA
			1	1	l ·	VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF
		-				NPDCATACK SRGTFRCFCRDFFPCFSNMRLFLWNAVLTLFV
792	2142	A	6440	92	781	SRGTFRCFCRDFFPCFSNMKLFLWNAVETEL TSLIGALIPEPEVKIEVLQKPFICHRKTKGGDL
132	~.~~					MLVHYEGYLEKDGSLFHSTHKHNNGQPIWFT
	1	1		l	1	MLVHYEGYLEKDGSLFHSTHATINGGTWA LGILEALKGWGPGA*K/DMCVGEKRKLIIPPA
		- 1	- 1		ì	LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH
1		ļ	1]	1	ESFQEMDLNDDWKLSKDEVKAYLKKEFEKH
1	1.	1		-		GAVVNESHHDALVEDIFDKEDEDKDGFISAR
1	ľ	1		1	1	EFTYKHDEL
		1				PRLKRLVVTEEDGGARPEALGKIAPRTPAELG
793	2143	A	6446	3201	152	AD A DORI WTAI MCDLRRPAAGGMMDLAY V
1.75					1	CEWEKWSKSTHCPSVPLACAWSCRNLIAFTM
	i	1			1	DLRSDDQDLTRMIHILDTEHPWDLHSIPSEHH
		- 1	1			EAITC\LEWDQSGFPGFLFSRWPTGQIK\CWS
1	1		1	1		MGVSTLA\NSWE\SSVGSL\VEGGPHLWALS\
1		1		-		WLH/NGVKLALHVEKSGASSFGEKFSR\VKFS
1	-	1		1		DIGITI FIGGNAMEGWIAVTVSGLVTVSLLQV
1		- 1	1	ŀ		SGQVL\TST\ESLCRLRARVALADIAFTGGGNI
		- 1		1		ANATADGSSA\SPVOFYKVCVSVVSEKCRIDI
						DII PSI EMRCTTDI NRKDKFPAITHLKFLAKU
1		-	-	ı		MSEOVILICASSOTSSIVECWSLRKEGLPVNNI
1	1	- 1	1.	. [FOOTSPYVGDKOPTILKWRILSATNDLUKVSA
	ļ	-	- 1	1.	1	MAI PKI PISI TNTDLKVASDTQFYPGLGLAL
1	i					A PUT COVETVER LSLOTMANTYSSAAPRIND
1	1		1			EPAMKRPRTAGPAVHLKAMQLSWTSLALVG

			050	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	le soleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	,		ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	l		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	1		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Ì			peptide	Soquesion	/=possible nucleotide deletion, \=possible
}				sequence		nucleotide insertion
				Sequence		IDSHGKLSVLRLSPSMGHPLEVGLALRHLLFL
			l			I EVCMVTGYDWWDILLHVOPSMVQSLVEKL
l		ł	ł		ĺ	HEEYTROTAALOOVLSTRILAMKASLCKLSP
	l		1	ì		CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT
1		l				PDKSPGDRLTEICTKITDVDIDKVMINLKTEEF
1	}		ì	ì	! .	VI DANTI OALOOLLOWYGDFVLYLLASLPN
	}	ł	1	1	1	OPCPTSEPCPTSEPSPTSEPSPTSEPSSP*SLC\G
	1	1		Ì		SI I RECHSFI ROGTSLGMLRELMVVIRIWGLL
Ì		1		ì	1	V DSCI PVYTATSDTODSMSLLFRLLTKLWICC
		1		•		RDEGPASEPDEALVDECCLLPSQLLIPSLDWL
}		1	1		1	PASDGLVSRLOPKOPLRLOFGRAPTLPGSAAT
1	1	1	1			I OI DGLARAPGOPKIDHLRRLHLGACPTEEC
	}		1			KACTROGOVTMLKSPNRTTAVKQWEQRWIK
1	{	1		1		NOT VEWAL VAGAPOLPLSPAAPOLLLSYPSA
		1	1	1		APERGCCKSHRSPWTLLGAVNLSPPCRAVEG
1	1	1	ì	1	}	RGPDACVTSRASEEAPAFVQLGPQSTHHSPRT
{	İ	ſ		1		PDGI DHI HPEDRP
				410	585	NGDKADLENESCRAOVLMPVVPALWEAEGG
794	2144	Α	6490	418	1 363	COMPRINI RLO*AVITPL\TPAWVTQ
1	<u> </u>		1 2100	205	1027	VII WI PPHSEOKRSPLYHPOGPSGTTPSAP\FS
795	2145	A	6499	395	1027	SUSPERSILLOA/PSIAAFLRTHGHISASGPLRMP
	1		1			FPH/H*NAFILLVFPGORSQLTS/PSHYLCREVFP
	-		1		· .	DHIHHHI CRI SLESSPLFHHRVLFCVPKQNVN
1	-		1	1		STRACIFCL FVHIVGCRCINTFPLHLFRLHLWL
	ŀ	1	1	1	1	HFLOIPLCKKNKSVKLGKTVVGRGCQSAAGS
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796	2146	A	6303	100	1	DI OFONSSEMEK IPE IGKFGEKAPPAPSHVWK
ì				1		PAALFITLICLLLIGLGVLASMFHVTLKIEM
1	1	Ì	1	į	1	KKMOJKI OMISEELORNISLOLMSNMNISNKIK
1		ļ			1	NI STEI OTIATKI CRELYSKEOEHKCKPCPKK
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			ĺ	[1	ASLLKINNKNALEFIKSQSRSYDYWLGLSPEE
	-	1	Ì		1	DS/YSWYESG*YNQ\PSAWVIRNAPDLNNMY
	1	1				CGYINRLYVQYYHCTYKQRMICEKMANPVQ
		i		1		LGSTYFREA
797	2147	A	6507	1	881	PGSTHASARSQVPRSAGEAAPHSRRPPGLLPH
197	2147	1	0307	1	1	APRAASAQLEERMRDPHPGMTLQEGDCRGS
	1				1	QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ
1	1	1			1	ESALAKLLLTCCSALRPRATQARGSSRLLVAS
				l		WVMQIVLGILSAVLGGFFYIRDYTLLVTSGA
	}	1		1		AIWTGAVAVLAGAAAFIYEKRGGTYWALLR
1		1	1		ļ	TLLALAAFSTAIAALKLWNEDFRYGYSYYNS
1 .	,			1		ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM
1	}	1		1		DMLKALFRTLQAMLLGVWILLLASLTPLWL
1		1	1 .	1		/SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG
1	1	Į.		ı	1	STHASARSQVPRSAGEAAPHSRRPPGLLPHAP
1				ı		RAASAQLEERMRDPHPGMTLQEGDCRGSQT
		1		1	1	VSLTMGTADSDEMAPEAPOHTHIDVHIHQES
	1	1		1	1.	ALAKLLITCCSALRPRATQARGSSRLLVASW
	1 .	Į.		1	}	VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI
	1	1				WTGAVAVLAGAAAFTYEKRGGTYWALLRTL
	1 '	- 1		1	1	LALAAFSTAIAALKLWNEDFRYGYSYYNSAC
		- }		1	1	RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM
		- 1	1	1		LKALFRTLQAMLLGVWILLLLASLTPLWLYC
	1	1	1			WRMFPTKGVSP
700	2148	A	6528	912	2287	VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAP
798	2140	^	10020	1		RFLVAFAYWNHYLSCTSPCSCYRPLCRLNFG
					1	LNVVENLALLVLTYVSSSEDF/TWVPG*GRSG
- 1	1	- 1	1			

EQ ID						// Marina Constains
	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	C=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	of peptide .	T=Threonine V=Valine, W=Tryptophan,
}		}		amino acid	sequence .	V=Tyrosine, X=Unknown, *=Stop codon,
į		i .			Sequence	/=possible nucleotide deletion, \=possible
}		į	1	peptide sequence		nucleotide insertion
		!	 	sequence		EVFPEGTGLPLPHSDLPTSWCGHSLQCGSQSS
					1	EDPAINENAFIVEIASSLEHMLLTCILWRLTKK
		1	Ì			HTVSOE\DGLSLAGAPROPRRKSRTSVLKIKV
	ļ	1		 		MVRWELSSNGNPGRGVLGLGLGLGNKLRVV
	ļ		i	}	l	GQNLGL*HCVWVVWETGE*KRWRLQMGIE*
	ļ	1	1	1		GVASRRQ*VRNSVRGLVCHNSSAPPMYMGFF
	ļ					SPTVFGGGVGG*LHVTFILHPPEVEAAGIPLLL
	1		1			GPSLPQRQGREHIVVILAAPACAPFHDR*WEP
		1	1		ĺ	REIRPSP*ELGLRGEPTLSYPASCRVIRQPIP*D
		1	1		1.	RKSYSWKQRLFIINFISFFSALAVYFRHNMYC EAGVYTIFAILEYTVVLTNMAFHMTAWWDF
	1	1		1	i	EAGVAILLAIDEALA
	1					GNKELLITSQPEEKRF FFFFQRINFIEHSGSVSLLALACDLGWCEDWS
799	2149	A	6529	1	874	CCL VOGGGDLVDVVOTNHGEDEAGGDIDSV
		1	1	ŀ		DEADCKESOOFAOFNI.REDLCLESFAKUKIL
	1	1				OURGSPREHEETRTKOAALDGEPLGGGQLIA
		1				VIJI HPSKEOOGOEGGERORGARTHHWKUW
		1	1	1		LEKCOR VRI RPPSGKLRADOPVRKLGGP1PS/1
	1	l			ì	FI PGI OPHAPTPHTA/PATPTYSPAPDTPNPPY
	1		1		1	RWKCPLPVEPRTROLCRERTRKACPPKPKPFL
	}		1	1		GLPGDPTGPVTHHAPPVSPTGASGQERRAEP
	1					GAVSYAHASATK TO THE TOTAL OF TH
000	2150		6544	2	662 .	SAQRWAAVAGRWGCRLLALLLLVPGPGGAS
800	2150	^	05.77	1	Ì	EITFELPDNAKQCFYEDIAQGTKCTLEFQVITG
1	1	ı		ł	Ī	GHYDVDCRLEDPDGKVLYKEMKKQYDSFTF
	}		ì			TASKNGTYKFCFSNE\FSTFTHKTVYFDFQVG E\THLCFLVR/DRVSALTQMESACVSIHEALKS
	\	1			1	VIDYQTHFRLREAQGRSRAEDLNTRVAYWSV
İ	1	1		1		GEALILL VSIGQVFLLKSFFSDKRTTTTRVGS
		1	_			TPCMECIKGEGLREPQNLSGSQREPQTEGSM
801	2151	A	6556	1	1319	DGWRRMPRWGLLLLLWGSCIFGLPIDTITF
		- 1	-			LADIEL KEWDSIREST KERGYDWAKTOLE MOOL
		1		1	1	MKRI TI GNTTSSVILTNYMDTQY YGEIGIGIT
ļ		1	Ì	1	1	POTEK V V FDTGSSNV W V PSSKCSKLYTACV 1
			1			LIKI FDASDSSSYKHNGTELTLRYSIGIVSGFL
ľ	ì	· •			1	CODITYGGITYTOMFGEVTEMPALPFMLAER
	1	- 1	1		1	DOVUGMORIEGAIGRVTPIFDNIISQGVLKED
1]	1			1	VESEVVNRISENSOSLGGOIVLGGSDPQHIE
1	1			1	1	CVIERALM IKTOAMOLOWKOASARPO
	İ	1	1		j	DOCT AT VITTGASYIS(IS) SSIEKLMEALUAN
			1			KRLFDYVVKCNEGPTLPPTFLFLLGGKDTPLT
1		1	1			SADYLFQESYSSKKLSTLAIHAMYIPPTGPTI VALGATF\IRKFYTEFDRGNNPHGFALAR
1	1			L		MCLGRMGASSPRSPEPVGPPAPGLPFCCGGS
802	2152	A	6567	13	6147	MCLGRMGASSPRSPEPVGFFAFGLFFCCGGGG LAVVVLLALPVAWGQCNAPEWLPFARPTNI
802		177			ł	TDEFEFPIGTYLNYECRPGYSGRPFSIICLKNS
	-			1	1	VWTGAKDRCRRKSCRNPPDPVNGMVHVIKO
		- 1		1	1	IQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIV
1		1				DNETPICDRIPCGLPPTITNGDFISTNRENFHY
1				1	1	CONVITYD CNDGSGGRKVFELVGEPSIYCISNI
	1			ļ	1	DOVGINGGPAPOCIIPNKCTPPNVENGILVSD
1		1	1	1		Americal MEVVEERCOPGFVMKGPKKVKCQ
	1	-	- 1	1		I TAIL THE DEL DOCORVOOPPPDVLHAEKT QKUM
	1		1	1	}	DATESPECIFICATION
1		- 1	- 1			DIVIGIDA A PTOPVIK SODDEMGOLLNGKYLFFY
					Ì	NI OI GAKVDEVCDEGFOLKGSSASYUVLAU
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESLWNSSVPVCEQIFCPSPPVIPNGRHTGKP
						NI OI GAKVDEVCDEGFOLKGSSASYUVLAU

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NO: of mole- orida seq- uence NO: of mole- orida seq- uence NO: of seq- uence NO: of seq- uence NO: of seq- uence NO: of seq- uence NO: of seq- uence NO: of seq- uence NO: of seq- uence NO: of seq- populate seq- seq- seq- seq- seq- uence NO: of seq- populate seq- uence NO: of seq- populate seq- seq- seq- seq- seq- seq- seq- seq	SEO ID	SEQ ID	Met			Predicted end	Amino acid sequence (A=Alanine O=Cysteine,
meric winds (9/96 controlled to controlled t	NO: of		hod				E-Dhenvialanine G=Glycine H=Histidine.
### designation of the control of th	nucl-	peptide				location	I=Isoleucine, K=Lysine, L=Leucine,
uence 1914 signification of peptide residue of peptide residue of peptide sequence peptide sequence	cotide					to lest amino	M=Methionine, N=Asparagine, P=Proline,
uence Paptide sequence Ta-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Valkonow, Y-Sip codon, Paptide sequence Sequence	seq-	uence					O=Glutamine, R=Arginine, S=Serine,
residue of peptide pep	uence			914			T=Threonine, V=Valine, W=Tryptophan,
Peptide sequence		{		i			Y=Tyrosine, X=Unknown, *=Stop codon,
sequence Sequence STICLDBL/WSSPRDVCKRKSCKTPPDPVNG MVHVTIDIQVGSRNYSCTTGHBLIGHSSAED LSGNAAHWSPPICQRPGLPPTIANGDER TNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGAPQCIIPNICTPINV ENGIL VSDNRSLFSLNEVVERCQPGVMXGP RRVKCQALMK WPEPLSSKVCQPPPVMCIP RRVKCQALMK WPEPLSSKVCQPPPVMCIP RRVKCQALMK WPEPLSSKVCQPPPVMCIP RRVKCQALMK WPEPLSSKVCQPPPVMCIP RRVKCQALMK WPEPLSSKVCQPPPVMCIP RRVKCQALMK WPEPLSSKVCQPPPVMCIP RRVKCQALMK WPEPLSSKVCQMPPVMCIP RRVKCQALMK WPEPLSSKVCQMPPVMCIP RRVKCQALMK WPEPLSSKVCQMPPVMCIP RRVKCQALMK WPEPLSSKVCQMPVMCIP RRVKCQALMK WPEPLSSKVCQMPVMCIP RRVKCQALMK WPEPLSSKVCQMPVMCIP RRVKCQALMK WPEPLSSKVCQMPVMCIP RRVKCQALMK WPEPLSSKVCQMPVMCIP RRVKCQALMK WPEPLSSKVCQMPVMCIP RRVKCQALMK WPEPLSCSRVCQ GFVMKGRRVKCQALMK WPEPLSCSRVCQ GFVMKGRRVKCQALMK WPEPLSCSRVCQ GFVMKGRRVKCQALMK WPEPLSCSRVCQ GFVMKGRRVFCQALMK WPEPLSCSRVCQ GFVMKGRRVFCQALMK WPEPLSCSRVCQ FPELLIGIBETTSNDDQVGTWSGAPACCAVSCODF LGQ.Pp.GRVLPILNQLGAKVSFVCDEF RRVKCQALMK WPEPLSCSRVCQ FPELLIGIBETTSNDDQVGTWSGAPACCAVSCODF GMTPMLGGSTRGTSDFPMGVSVYSCERGY GMTPMLGGSTRGTSDFPMGVSSPARCC LSVRAGHGTTSSDDFVGSSTVTYCGERGYTCKMSSVSTVTYCGH RRVKCQFGFFFMGMVWSSPARCC LSVRAGHGTTSSDDFVGSSTVTYCGERGYTCKMSSSVSTVT RRKKCQFGFFFMGMVWSSPARCC LSVRAGHGTTSSDDFVGSSTVTYCGH RRKSCQFGFFFMGMVWSSSPARCC LSVRAGHGTTSSDDFVGSSTVTYCGH TGPDGGLFELVGRSSTTCTSSDDQVGVWSSPARCC GSCPFTTISNOFFSTVTYCGH TGPDGGLFELVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGLFELVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDFELVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDFELVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDFELVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDFTCLVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDFTCLVGRSSTTCTSSDDQVGVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDFTCLVGRSTWTCTSDDQVGCWFTSSTTCTSDDQVGCVWSSPARCC CSCPFTTISNOFFSTVTYCGH TGPDGGCDVAAMARVPORTSTSTTCTTCTTCTTTCTTTCTTTCTTTCTTCTTCTTCTT		1				Joques	/=possible nucleotide deletion, \=possible
SITCLDIN. VSSPRIVCKSR. KIPPP-VIOL MYNYTDIQVOSRINYSCTTGIRLIGISSAGE LSGNAAHWSTKSPTCQRIPCGLPTIANGDPIS THRENPHYGSVYTTKCPROSGGRKYCELVGE PSYTCTSNDDQVGIWSGPAPQCIIPKCTPTNV ENGILVSDNRSLISLINEVVEFRCQPGYMKGP RRVKCQALNKWFELEPSCSRVCQPPPDVLHA BETORDKDNFSPGOEVYSCEPGYDLRGAS MCCTPGODWSPAAPTCEVKSCDDFNGQLLN GRVLFYVNQLGAK VDFVCDGGFGLKGSSAS YCVLAGMESLWISSVPVCEGIFCSSPVIPNG RRTCKPLEVFFGKA VNYTCDPHDPRGTSFD LIGESTIRCTSDPQORIOVWSSPAPCGLIGHC QAPDHFLFAKLKTQTNASDPIGTSLKYCECP PYGREPSITCLDIN. WSSPKDVCKKKSCKTP PSPVNGMYHYTDIQVGSRNYSCTTGIRLIG HSAGCLSGNTAHWSTKPFCQRIPCGLPTI ANGDPISTNRENPHYGSVVTYRCNLGSRGRK VEEL VGEFSIYCTSNDDQVGIWGSPAPCGLIPN KCTPPNVENGILVSDWRSLFSLINEVVEFRCQP GFVMKGPRRVKCQALMKWPEPLESCSRVCQ PPPELHGBHTSHQDNVGSVGAYSCDDF LGQLPGRVLFFLNLQLGAKVSFVCDEGFRL KGSSVSICVLVGMRSKJKWNSVSVCDEGRC PSPSSICVLVGMRSKJKWNSVSVCDEGFRC KGSSVSICVLVGMRSKJKWNSVSVCDEGFRC KGSSVSICVLVGMRSKJKWNSVSVCDEGFRC LSVRAGHCKTFEOFPASPITIPNDFEFFVGTS LNYCAGHCKYFLOFPASPITIPNDFEFFVGTS LNYCAGHCKYFLOFPASPITIPNDFEFFVGTS LNYCAGHCKYFLOFPASPITIPNDFEFFVGTS LNYCAGHCKYFLOFPASPITIPNDFFTYGTS LNYCAGHCKYFLOFPASPITIPNDFFTYGTS LNYCAGHCKYFLOFPASPITIPNDFFTYGTS LNYCAGHCKYFLOFPASPITIPNDFFTYGTS LNYCAGHCKYFLOFPASPITIPNDFFTYGTS LNYCAGHCKYFLOFPASPITIPNDFFTYGTS LNYCAGHCKYFLOFT COMPANIANGACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTYCAGHCCHACHTY		i .				}	nucleotide insertion
LISGNAAHWSTKPPICQRPCGLPPTIANGDPIS THRENFIYGSVUTTKE/PGGGGGRYFELVGE PSIYCTSNDDQVGJWSGPAPCQLIPKCTPINV ENGILVSUNRSIJSIJNEVVEFKCQFGPYMKGP REVKCQALINK WEPELPSCSRVCQPPPDVLHA BETORDENDRISPGGVEYSCEPGYDLRGAAS MRCTPQGDWSPAAPTCEVKSCDDFNGQLLN GRVLFYVILQLGAKX VDPVCDGGFGLKGSAAS YCVLAGMESLWNSSVPVCEGFGCSPVPING RHTCKPLEVFFGKAVNYTCDPHDPRGTSFD LIGESTIRCTSDPQONGVWSSPAPRCGLIGHC QAPDHFLFAKLKTQTNASDPIGTSLKYPCCR BYYGGPFSITCLDIN WSSPKDVCKRKSCKTP PSPYNGMYHYTDDQVGSRNSYSCTTGFRLIG HSAGCLSGNTAHWSTKPPCQRFTCQLPTI ANGDFISTNERNFHYGSVVTYRCKLGSRGKK VEEL VGFSIYCTSNDDQVGTWSGPAPCGLIFN KCTPPNVENGILVSDWRSTKPFCQLPTI ANGDFISTNERNFHYGSVVTYRCKLGSRGKK VEEL VGFSIYCTSNDDQVGTWSGPAPCGLIFN KCTPPNVENGILVSDWRSLFSLNEVVEFRCQP GFVMKGFRKVKCQALMKWEPELPSCSRVCQ PPPELHGBHTSHQDDNFSIGOEVFYSCERGY DLRGAASH.HCTPGGDWSFAPRCCK KGSSVSICVLVGMRSLWNSSYPVCEDEGFRL KGSSVSICVLVGMRSLWNSSYPVCEDEGFRC LSYRAAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFEFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPEOFFASPTIPNDFFFVGTS LNYRAGHCKTPTT LNYRAGHCKTPTT LNYRAGHCKTPT LNYRAGHCKTPT LNYRAGHCKTPT LNYRAGHCCHTT RTTT RTTT RTTT RTTT RTTT RTTT RTT		 	 		boqueste		SITCLDNLVWSSPKDVCKRKSCKTPPDPVNG
THRENFHYGSVYTYRCNPGSGGRKYEL/GE PSYCTSDDDQVGINSGPAQCIBNKCTPINV BNGILVSDNRSLFSLNEVVERCQFGFVMKGF RVKCQALNKWEPELPSGSRVQCPPDVLHA ARTORDDXPSFGGEVFYSCEPGYDLRGAAS MRCTPQDWSPAAPTCEVSKSCDDPHQGLIAN GRVLFVNLQUGAKVDFVCDEGFQLKGSAS, YCVLAGMESLWNSSVYVCEGFCSPVPVIPNG RITGKFLEVFFFGKAKVNTCDPHPDRGTSFD LIGESTIRCTSDPQGNGVWSSPAPKCGLIGHG QAPPHELPAKLKTUTNASSPPIGTSLKYECRP EYYGRPFSITCLDNLVWSSPKDVCKKKSCKTP PDPVNGMVHVTIDQVGSRNYSCTGIGRLIG HSSAECLISGNTAHWSTKPFICQRPCGLPFTI ANGDISTIRRENFHYGVVTYRCHLGSRGK VFELVGEPSIVCTSNDDQVGIWSGPAPQCIIFN KCTPPNPGGILLSPNSSLSSLEVEVERCQP GPVMGGPRRVKCQALNKWEPELPSCSRVCQ PFPELHGBHTSHDDDVSGLWSFAPCGUSPTL LOQLPHGRVLFTLNLQLGAKVSFVCDGFFL KGSSVSICVLVGMRSLWNNSVPVCEHIFCZN PPALNGRITGTFSGDIPYGKESYTCDPHPDR GMTPALIGSSTRICTSDPHONGVWSSPAPRCE LSVRAGHCKTPEGFFASSTIFINDFEFFVGTS LYRCGPYGFKMFSISCLEALLWSSVEDNC RKRSCGPPFPFNGMVHINTDTQFGSTVNYSC NGGFRLIGSSTTCLVSGNNYTVDKKAPLGEI SCEPPTISNGDPYSNNRTSFHNGTVVTYQCH TQPDGGOLFELVGERSIVGTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFSSLTEI RFRCQPFSWMGSTVTOQCTNOR WOPKLPH CSRVCQPPPELHGEHTLSHDQNFSFGGEVFY SCEPSYDLRGAASLACTPQGDWSFGAPRCT KSCDDFLGQLPHGRVLLPLALQLGAKVSFVC DEGFFLKGRSSHCTLVAGMAXSSVEDNC RKSCGPPFPPSDLRGAASLACTPQGDWSFSFSLTEI RFRCQPFFWMGNTNLIGESTIRTSEPHGNGVWY SCEPSYDLRGAASLACTPQGDWSFSFSLTEI RFRCQPFPFMGLMCHTGNAWSSSPVC CBIFCTPPFALLMGRATGTPLAGDIPYGKEVSTT CDPHDRGMTTNLIGESTIRTSEPHGNGVWY SCEPSYDLRGAASLACTPQGWSSPAPRCE UKKRGNAHENPKEVAIHLHSQGGSSVWP RLTQTMEENSRVLQ QLDHYCKEVNCSSPPLFMMGINSCLELLMKXVY YGDYVTLKCEGGYTLLGSFWSQCQADDRWD PLAKCTSRTHDALTVGTLIGTGFFLLIFLISW ILKHRKGNNAHENPKEVAIHLHSQGGSSVWP RTLQTREENSRVLQ VALHERGGNAWARPOLLPGHT VRTVLGSSBRALGVCSDTAAPLAAVDLKWE HRAVYFLGFGCVYAAAPVGRTAAHWRYPLL TAGAPALGFGVKDEYALTTRAGFSYAKLGDI VALHERGLWERGALMLYAYRPGBEHCFF LVGGLFMRVRORANITVDHLEFAEDDLSHTT TAGAPALGFGVKDEYALTTRAGFSYAKLGDI VALHERGLWERGALMLYAYRPGBEHCFF LVGGLFMRVRORANITVDHLEFAEDDLSHTT TAGAPALGFGVKDEYALTTRAGFSYAKLGDI VALHERGLWERGALMLYAYRPGBEHCFF LVGGLFMRVRORANITVDHLEFAEDDLSHTT TAGAPALGFGGVKDEYALTTRAGFSYAKLGDI VALHERGLWERGALMLYAYRPGGBEHCFF LVGGLFMRVRORANITVDHLEFAEDDLSHTT PECDGGONYARGACAMALMYAYPRGGBEHCFF LVGGLFMRVRORANITVDHLEFAEDDLSH] [MVHVITDIQVGSRINYSCITGHRLIGHSSAECI .
PSIYCTSNDDOVGIWSGPAPQCIIPNKCTPPNV BEGIL VSDNRSLISLINEVVERCOCPPTWIGH REVICO,ALINK WEPELPSCSRVCOPPPDVLHA BERTQRDKDNFSPGGEVFYSCEPGYLRGAAS MRCTPQGDWSPAPTCEVKSCDDFHGQLIAN GRVLFPVNLQLGAKVDFYCDEGFQLKGSSAS YCVLAGMESL WINSSVPVCEGFCFSPVIPNG RHTGKPLEVFPGGAVTYTCDHPDRGTSFD- LIGESTIRCTSDPQONGVWSSPAPCGLIGHC QAPDHELFAKLKTQTDASDFJGTSLKYECRP EYYGRFSTICLDIAN WSSPKDVCKKSCKTP PDPVNGMYHVTDIQVGSRNYSCTTGFRLIG HSAECLISONTAHWSTRFPICORIPGOLIFT ANGDEISTNRENHFYGSVVTYRCNLGSRGKK VFELVGEPSIYCTSNDDQVGIWSGAPACGIPTI ANGDEISTNRENHFYGSVVTYRCNLGSRGKK VFELVGEPSIYCTSNDDQVGIWSGAPACGIPTI ANGDEISTNRENHFYGSVVTYRCNLGSRGKK VFELVGEPSIYCTSNDDQVGIWSGAPACGIPTI ANGDEISTNRENHFYGSVVTYRCNLGSRGKK VFELVGEPSIYCTSNDDQVGIWSGAPACGIPTI ANGDEISTNRENHFYGSVVTYRCNLGSRGKK VFELVGEPSIYCTSNDQVGIWSGAPCGIPTI ANGDEISTNRENHFYGSVVTYRCNLGSRGKK VFELVGEPSIYCTSNDQVGIWSGAPCGIPTI ANGDEISTNRENHFYGSVVTYCCHEDGERL KGSSVSICVLVGMSLWNNSVPVCEHIFCYN FPALLNGRHTGTFSGDPYSCESTVCTDPHDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKFPEGPFFASFTIPINDFEFFVGTS LNYECROLYPGKMFSISCLENLVWSSVEDNC RRSCGLOPPEPFNGWWININTOTGPSTVNYSC NGGFRLIGSSTTICLVSGNNVTWDKKAPICELI SCEPPTISNGDFYSNNRTSFHIGTVYTYQCH GROEGLIFLU GERSIYCTSKDDQVGVWSS PPPRCISTNKCTAFEVBARRYFORNSFPSLTEL INFRCQPGTVMYGSHTVYTQCH CSRVCQPPPEILHGEHTLSHQDWSFSGGEVTY SCEPSTYDLRGAASLIACTTQGDWSPEAPRCT VSCEPSTYDLRGAASLIACTTQGDWSFEAPRCT VSCEPSTYDLRGAASLIACTTQGDWSFEAPRCT VSCEPSTYDLRGAASLIACTTQGDWSFEAPRCT VSCEPSTYDLRGAASLIACTTQGDWSFEAPRCT VSCEPSTYDLRGAASLIACTTQGUNSSGGENPART VTPGMTSTYCTOPGTYLLVKGFFETCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELBMKXVTH YGDYVTLKCEBGYTLEGSFWQQCADDRWU PPLAKCTSRTHBALTUGTSGTFLILHILSUG LLHPRILLILRIGSTRITTSPHGNOWY SPAPRCELPYGGACPHPPKIONGHYIGGHVSL YLLGMTISYTCDFYLLVKGFFETCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELBMKXVTH YGDYVTLKCEBGYTLLGFSTRATLEHFINGWI ILKHKKGNNAHENPKEVAHILISGGGSSVHP TLOTINENSRVLU HORMANAHAPACAMFORFRAGSRICLLILLILLINGUN LKHRKGNNAHENPKEVAHILLSGGGGSCHPARRW YGDYVTLACEBGYVTPLLLIRGSTRATLEHFINGUN VALHERLGWERGGAAALITYAPLLLALLAL LLIPPILLLIRGSTRATLEHFINGHLICHLICH LLTGEIFMRKGRVITYGSPAAFTALLALLAL LLLTGLIFFKGGGGGGGGGGGGRAPRRW PEDIGGGONDASRAGAAGUTYAPURDNETULT LTGGLOFFILDF			1 (l .	LSGNAAHWSTKPPICQRIPCGLPPTIANGUFIS
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BETQRDKDNFSPQQEYFYSCEPGYDLRGAAS MRCTPGGWSFAAPTCEVKSCDTRGQLIN GRVLFFVALQLGAKVDFVCDEGFQLKOSAS YQVLAGMESLWANSSVPVCQUFCPSFPVPING RHTGKPLEVFFFGKAVNTTCDFHPDRGTSIL RHTGKPLEVFFFGKAVNTTCDFHPDRGTSIL RHTGKPLEVFFFGKAVNTTCDFHPDRGTSIL RHTGKPLEVFFFGKAVNTTCDFHPDRGTSIL RHTGKPLEVFFFGKAVNTTCDFHPDRGTSIL RHTGKPLEVFFFGKAVNTTCDFHPDRGTSIL PPYVRGMYNTUTDIQVGSRNTVSCTTGHRLIG HSSABCLLSGNTAHWSTKPFICQRFCGLFFT PPYVRGMYNTUTDIQVGSRNTVSCTTGHRLIG HSSABCLLSGNTAHWSTKPFICQRFCGLFGTA ANGDETSTNEENFHYGSVVTTKCTLGSGRGK VFELVGEFSYTCTSNDDQVGIWSGPAPCCILIF HSSABCLLSGNTAHWSTKPFICQRFCAGFGK KCTPPNVENGIL VSDNRSLISLINEVVEFRCQP GFVMKGPRVKCQALNKWEPELFSCSRVQ PPFELHGBHTTSNQDNFSFGQEVFYSCEPGY DLRGAASHCHTPQDWSPSAPKCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFF KGSWSHCVLVGMRSLWANSVYCEHIFCFN PPALLNGRHTGTSDPHONGWSSPAPKCE LSVRAGHCKTFEQPFASFTIPINDEFFYCHE KGSWSHCVLVGMRSLWANSVYCEHIFCFN PPALLNGRHTGTSDPHONGWSSPAPKCE LSVRAGHCKTFEQPFASFTIPINDEFFYCH KGSWSHCVLVGMRSLWANSVYCEHIFCFN RHTGLIGESTRICTSDPHONGWSSPAPKCE LSVRAGHCKTFEQPFASFTIPINDEFFYCH KGSCGPPFEFRIGMVHNITDTQFGSTVAYSC NEGFRLIGSSTTICLVSGNSSPTCVANGKSPTOK RRSCGPPFEFRIGMVHNITDTQFGSTVAYSC NEGFRLIGSSTTICLVSGNSSPTCVANGKSFTSLTEI RFRCQPGFYMVGSHTVQQTNGRWFFSTSLTEI RFRCQPGFYMVGSHTVQQTNGRWFFSTSLTEI RFRCQPGFYMVGSHTVQQTNGRWFFSTSLTEI RFRCQPGFYMVGSHTVQQTNGRWFFSTSLTEI RFRCQPGFYMVGSHTVQQTNGRWFFSTSLTEI RFRCQPGFYMVGSHTVQQTNGRWFFSTSLTEI RFRCQPGFYMLDGHLTGGTHRXTSEFHONGVWS SPAPRCELPVGAACPHPFKQNGHYGGWSPSTAFTC CSRVCQPPFELHGBHTLSNGDAFSVSVT CDPHPRGMTTHLGGSTTRKTSEFHONGVWS SPAPRCELPVGAACPHPFKQNGHYGGWSSVT CDPHPRGMTTHLGGSTTRKTSEFHONGVWS SPAPRCELPVGAACPHPFKQNGHYGGWSPSAFTC VRGMTSTTCDPYLLVCKGFICTDQGINS QLDHYCKEVNCSPPLFAMGISSLELEMKKVYM YCDLYTLKCEDGVTLSGTBPFLLIFILIFILIFILIFILIFILIFILIFILIFILIFIL		1	1.				ENGIL VSDINKSLESLINE V VERKCQLOL VIMICOL
MRCTPQGDWSPAAPTCEVKSCDDPMGQULSSAS YCVLAGMESLWNSSYPVCEQIFCRSPPVING RHTGKPLEVPFPGKAVNTYCDPHPBGTSFD- HIGHEL EVPFPGKAVNTYCDPHPBGTSFD- LIGESTRCTSDPQGNGVWSSPAPRCGILGHO- QAPDHFLFAKLKTQTHASDPF1GTSLYYECRD- YGRFSTICLDHLVWSSPKDVCKKKSCKTP PYDYNGMVHVTIDIQVGSRNYSCTTGHELDH- HSAACLLSGNTAHWSTKPPICQRTCGLPFTI ANGDFISTINENFHYGSVVTYRCNLCSSRGKYCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCQALINKWEPLEFSCSRVCQ GFVMKGPRSVKCALINKWSVEPLEFSCSRVCQ GFVMKGPRSVKCALINKWSVEPLEFSCSRVCQ GFVMKGPRSVKCALINKWSVEPVCDEFFIC KGSVSHCVLVGMRSLWNSVYVCCHIFICRN FALLINGRHTGTFSGDIPVGKEISYTCDPHDR GMTPNLIGESTIRCTSDPHONGVWSSPAPRCE LSVRAGHCKTEPGFPFASPTIENDFEFFVGTS LNYECRPGYFGKMFSISCLENLWWSSVEPNOT RRKSCQPPFPFNGMVHINDTDFGSTVNYSC NEGFRLIGSFSTTCLVSGNNVTWDKKAPICEIL SCPPPPTSINGDFYSNNTSFHINDFFFVGTS SCPPPPTSINGDFYSNNTSFHINDFFFVGTS SCPPPPTSINGDFYSNNTSFHINDFFFVGTS SCPPPTSINGDFYSNNTSFHINDFFFVGTS SCPPPTSINGDFYSNNTSFHINGVTSSPCPQEVPY SCPPSTDLRGGASHLCTTQGDWSFAPRCTIV KSCDDFLGGLFELVGERSIVCTSKDDQVGVWS SPPFRCISTINKCTAPEVENARVPGRSFFSSLTEI RRKCQFGFVMVGSHTVQCOTNGRWOFKFSTSLTEI RRKCQFGFVMVGSHTVQCOTNGRWOFKFSVLTE CREMPTSTATTLONGRWOFTSFTLIELIFLSWI KSCDDFLGGLFELVGAACPHPFKIQNGHYIGGHYGGHVY CREMPTSTTCDFYLLVKKGFFTCTDQGINS SPAPRCELPVGAACPHPFKIQNGHYIGGHYGGHVY CDPFGRMFTSHLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPFKIQNGHYIGGHYGGHYY GDVTILKCEDGYTLLGSSTRFTGLLIFLISWI LIKHRKGNNAHENREVAHLHISQGGSSVHP FILLTHENSSRV.P ROJVTILKCEDGYTLLGSGRWSQCQADDRWW YCTVLGSSENALGVCSDTAAPLAAVDLKWE LIKHRKGNNAHENREVALHLHISQGGSSVHP FILLTHLINGKGGTSTTLLLIFLSWI LIKHRKGNNAHENREVALHLHISQGGSSVHP FILLTHLINGKGGGGGPAPARFTHMLLALISA GLCGEDVYFFHLDIFGGSLQGGQFAPARFTHMLALALISA GLCGEDVYFFHLDIFGGSLQGGQFAPARFTHMLALALISA GLCGEDVYFFHLDIFGGSLQGGGPAPARFTHMLALALISA GLCGEDVYFFHLDIFGGSLQGGQGPAPARFTHMLALALISA GLCGEDVYFFHLDIFGGSLQGGQGPAPARFTHMENPEU LVEGLFMRVDGATMYCSSPDAFTILMLL		1					EDTODDY DNESPGOEVFYSCEPGYDLRGAAS
GRVLFYVILQLGAKVDFVCDEGFQLKSSSAS YCVLAGMESLEWSFYVECGFCFSFPVIPNOR RHTGKPLEVFFFGKAVNTCDPHDPRGTSFD. LIGESTIRCTSDPQONGVWSSPAPRCGILGHC QAPDHFLFAKLKTQTNASDFPIGTISLKYCCRP EYYGRFSITCLDNLWSSPKDVCKKKSCKTP PDPVNOMVHVITDQVGSRNTYSCTTGHRLIG HSSAECILSONTAHWSTKPPICQRIFCGLPTI ANGDFISTINERHYTGSVVTYRCNLGSKGRK VFELVGERSIYCTSNDDQVGIWSGPAPCCUPN KCTPPVERGILVSDNSLFSLNEVVEFRCQP GFVAKGFRRVKCQALANKWEPELPSCSRVCQ PPPELHGEHTPSHQDNFSPQCVFYSCEGFQ DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPIGRVLFFLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNSNSVVCEHFCCPN PPALINGRHTGTPSGDIPYGKEISYTCDPHDR GMTTNLIGESTIRCTSDPHGNOVWSSPAPRCE LSVRAGHCKTFEQFFASPTIPINDEFFYOTS LNYRCGRGFRGKMFSISCLEBLVWSSVEDNC RRKSCGPPEPPRGMAVHNITDTQFGSTVNYSC NEGFRLIGSFSTTCLSVGRNVTVDKKAPICEIL SCEPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELLVGERSIYCTSXDDQVGVWSS PPPRCISTNKCTAPEVENARKYPONRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGFKLPH CSRVQPYPELHGEHTLSHQNNSPQGEVFY SCEPSTDLRGAASLHCTPQGDWSFEAPRCTV KSCDDFIGGJLPGRVLLFUNQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPC DEGFRLKGRSASHCVLAGMKALWNSSVPC CDEGFRLKGRSASHCVLAGMKALLVCARPDLLFLGUNG CLARLTTRICAGNALAGMCARPDLLFLAGL LLAFLTMFKKGNAAAFPGAFTALMLLLALA HRAGMAALAGVCARPDLLFOWT VATLIJLEGERAMGPGFAGSNALLDLINTT RLLEFTLERKGRVYNCSSPDAFRTLMLALLAG LLEPFLLLLLRGGRKGVYNCSSPDAFRTLMLALLAG LLEPFLLLLLRGGRKGVYNCSSPDAFRTLMLALLAG LLEPFLLLLLGGGSLGGGGGAPRAPPU PAGGGGNVARGAPGALGTATHALALLAG LLEPFLLLLLGGGSLGGGGGAPRAFT RLLETTMFKCGRATHATHAGT LLETTMFKCGRATHATTCDGARPTARLGGLG		[ARCTROGRUSPAAPTCEVKSCDDFMGOLLN
YCVLAGMESLWNSSVPVCEQRICESPYVING RHTGKPLEVFPFGKAVNTTCDPHPDRGTSFD- LIGESTIRCTSDPQGNGWSSPAPRCGILGHC QAPDHFLFAKLKTQTNASDFJGTSLKYECRP EYYGRFSTTCLDNLVWSSPKDVCKRKSCKTP PDFVNGMYHVITDIQVGSRNYSCTTGHRLIG HSSAECLISONTAHWSTKPHCQRIFCGLPFTI ANGDISTINRENFHYGSVVTYRCNLGSRGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVVFERQDP GFVMKGPRVKCQALAKWEPELPSCSRVCQ PPPELLIGEHTPSHQDNFSPQGEVFYSCEPGY DLRGAASLHCTPQGDWSEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSPVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHFCNN PALLNGRHTGPSGDPYGKEISYTCDPHDDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEOPFASPTIDFEPFVGTS LNYSCRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPEFFNGMVHNTDDTGPGSTVNYSC NEGFRLIGSSTTCLVSGNNVTWDKKAPICEIL SCEPPTISNGDFYSNNRTSHNGTVVYYQCH TGPDGEQLFELVGERSIYCTSDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFSLTEI RFRCQPGFVMVGSHTVQCGTNGRWGPKLPF CSRVCQPPPELLYGERSITCLTSDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFSLTEI RFRCQPGFVMVGSHTVQCGTNGRWGPKLPF CSRVCQPPPELLYGGRSTTCLTSDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFSLTEI RFRCQPGFVMVGSHTVQCGTNGRWGPKLPF CSRVCQPPPELLYGGRSTTCLTSDDQVGWWSS PPPRCISTNKCTAPEVENARVPGNRSFSLTEI RFRCQPGFVMMGSHTVGCDTNGRWGPKLPF CSRVCQPPPELLYGGRSTTCTSDDQVGWWSS PPPRCISTNKCTAPEVENARVPGNRSFSLTEI RFRCQPGFVMMGSHTVGCDTNGRWGPKLPF CSRVCQPPELLYGGRSTTCTSDDQVGWWSS PPPRCISTNKCTAPEAVAGNRYGCTNGRWGPKLPF CSRVCQPPELLYGGAACHPPKLNQHYGGWYS SPAPRCELPVGAACHPRYLNQHYGGWYS SPAPRCELPVGAACHPRYLNQHYGGWYS CDPFTDRAGMTFNLGGSTRRTSEPHGGWWS SPAPRCELPVGAACHPRYLNQHYGGWYS CDPFTDRAGMTFNLGGSTRRTSEPHGGWWS SPAPRCELPVGAACHPRYLNQHYGGWYS CDPFTDRAGMTFNLGGSTRRTSEPHGGWWS SPAPRCELPVGAACHPRYLNQHYGGWYS PPLAKCTSRTHDALIVGTLSGTTFTLLHLFLSWI LKHRKGNNAHENFREVAHLHSQGGSSVHP PLAKCTSRTHDALIVGTLSGTTFTLLHFLSWI LKHRKGNNAHENFREVAHLHSQGGSSVHP PLAKCTSRTHDALIVGTLSGTTFTLLTLFLSWI LKHRKGNNAHENFREVAHLHSQGGSSVHP PLAKCTSRTHDALIVGTLSGTTFTLLTLFLSWI LLEPLLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARRYGAVELALAQVXARPOLLTPGTV VRTVLGSSEBALAQVCSTAAPVAGRTTAHWVPLL TAGAPALGFGCVYAAPVGRFTATWAVPLL TAGAPALGFGCVYAAPVGRFTATWAVPLL TAGAPALGFGCVYAAPVGRFTATWAVPLL TAGAPALGFGCVYAAPVGRFTATWAVPLL TAGAPALGFGCVYAAPVGRFTATWAVPLL TAGAPALGFGCVYAAPVGRFTATWAVPLL TAGAPALGFGCVYAAPVGR							GRVI FRVNI OLGAKVDFVCDEGFOLKGSSAS
RHTGKPLEYFFGEA VNYTCDPHPDRG ISID- LIGESTIRCTSDPQORGWYSSPARCGILGHC QAPDHFLPAKLKTQTNASDPHGTSLKYFCRP EYYGRFFSITCLDNLVWSSPKDVCKRKSCKYP PDPVNOMVHVTDIQVGSRINYSCTTGHRLIG HSSAECILSGNTAHWSTKPPICQRIFCGLPTI ANGDFISTNRENFHYGSVVYTQRNLGSRGRK VFELVGEPSIYCTSNDDQVGIWSGPAYCLIPN KCTPPVVENGILVSDNRSJFSLNEVVEFRCQP GFVMKGPRRVKCQALNKWEPELPSCSRVCQ PPPELHGEHTPSHQDNFSPGQEVFYSCEPGY DLRGAASHLHTCPQGDWSEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHFCFN PALNGRHTGTPSGDBPYGKEISYTCDPHDR GMTPNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFFFASPTIPINDFEFFYGTS LNYECRFGYFFASPTIPINDFEFFYGTS LNYECRFGYFFASPTIPINDFEFFYGTS LNYECRFGYFFASPTIPINDFEFFYGTS LNYECRFGYFFNGMYHTDTQFGSTVNYSC REGSCLIGSPSTTCLVSGNNYTVDKKAPICELI SCEPPFTISNGDFYSNNRTSHNGTVVTYCYCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRISTNKCTAPEVENARVPGNRSFFSLTEI RFRCQPGFVMVGSHTVQCCTNGRWGPKLPH CSRVCQPPPELHGEHTLSHQDNISPGGVFY SCEPSTDLRGAASALICTFGGWSFGAPRCTV KSCDDFI GQLPHGRVLLPLNLQLGAKVSFVC EQIFCNPPALINGRHTGTPLODPYGKEVSYT CDPHPDRGMTTNLIGESTRTSEPHORGVWS SPAPRCELPVGAASHLCTTLODDFYGKEVSYT CDPHPDRGMTTNLIGESTRTSEPHORGWS SPAPRCELPVGAACHPPKYQNGHYIGGHVSL LYPGMTISYTCDPGYLLVGKGFFCTDQGWS QLDHYCKEVNCSPPLFMIGGTSTLFLIFLSWI LKHRKGNNAHENFKEVAHLHBSQGGSSVHP YGDYYTLKCEDGYTLEGSPWSQQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIFLSWI LKHRKGNNAHENFKEVAHLHBSGGGSSVHP YGDYYTLKCEDGYTLEGSPWSQQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIFLSWI LKHRKGNNAHENFKEVAHLHBSGGGSSVHP YGDYYTLKCEDGYTLEGSPWSQQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIFLSWI LKHRKGNNAHENFKEVAHLHBSGGSSVHP RTLOTNENSRVLP YGDSYSPLARAGVSDTAAAPLAAVDLKWE HPPAYFLGPGCVYAAAPVGRFTAHWRYLL TAGAPALGFGYKDEYALTTRAGPSYAKLGDD VAALHRRLGWERQALMLYAYRPGDEBEICFF LVEGLFMRVRIDRITTVDHLEFAEDDLSHYT RLLETMFRKGRVYTYCSSPDAFRTILMLALIBA GLCGBDYYFFHLDIFGQSLQGGQGPARRPW BERGGGDVSARGAYCHARRYPLL TAGAPALGFGYKDEYALTTRAGPSYAKLGDD VAALHRRLGWRYVICSPDAFRTIMLALLBA GLCGBDYYFFHLDIFGQSLQGGQGPARRPW BERGGGDNSARGAYGAARAGTYTCXDPDAFRTIMLALLBA GLCGBDYYFFHLDIFGQSLQGGQGPARRPW			İ			ļ	VCVI AGMESI WNSSVPVCEOIFCPSPPVIPNG
LIGESTIRCTSDPQGNGWSSPAPRGGLIGHE QAPDHELFAKLKTOTNASDPIGTSLKYECRP EYYGRPFSITCLDNLWSSPKDVCKRKSCKTP PDPVNOMVHVITDIQVGSRNYSCTTGHRLIG HSSAECLSONTARWSTKPICQRIPCGLPPTI ANGDFISTNRENHYGSVYTYRCNLGSRGKK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVVFRQD GFVMKGPRAVKCQALMKWFPLPSCSRVCQ GFVMKGPRAVKCQALMKWFPLPSCSRVCQ PPPEILHGEHTSHQDNRSLFSLNEVVFRQD GFVMKGPRAVKCQALMKWFPLPSCSRVCQ PPPEILHGEHTSHQDNRSLFGSRVCV PPPEILHGEHTSHQDNRSLFSCSRVCVQ PPPEILHGEHTSHQDNRSLFSCSRVCVQ PPPEILHGEHTSHQDNRSLFSCSRVCVQ PPPEILHGEHTSHQDNGVWSSPAPRCE LSVRAGHCKTPFSOFFFASPIPINDFEPFVGTS LNYECRPGYFRGMFISSCLENLYWSSVENNC RRKSCGPPPEPNGMVHINTDTQFGSTVNYSC NEGFRLIGSFSTTCLVGGNNVTWDKKAPICEIL SCEPPTISNGDFYSNNRTSHNGTVYTYQCH GREENLOGGSTVAPSC NEGFRLIGSFSTTCLVGGNNVTWDKKAPICEIL SCEPPTISNGDFYSNNRTSHNGTVYTYQCH GREENLOGGSTVAPSC NEGFRLIGSFSTCLVGGNNVTWDKKAPICEIL RRRCOPGFWWGSHTVQCOTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNRSPGGEVFY SCEPSTDLRGAASHCTLAGGAKWFVC BCGFCTNPPALHOGGTNGKWGFKLPH CSRVCQPPPEILHGEHTLSHQDNRSPGGEVFY SCEPSTDLRGAASHCTLAGGKWGFKLPH CSRVCQPPPEILHGEHTLSHQDNRSPGGEVFY SCEPSTDLRGAASHCTLAGGKWGFKLPH CSRVCQPPPEILHGESTBRTSEPHGNGWWS SPAPRCLEPVGAACHPPKJQNGHYIGHVSU VECHTANGARTHAGHTGTHGTGWWS SPAPRCLEPVGAACHPPKJQNGHYIGHVSU VLPGMTISYTCDFGYLLVGKGFFCTDQGIWS QLDHYCKEVNCSTPLFMNGISKELEMKKVYH YGDYYTLKCEDGYTLEGSFWSQCQADDRWT VRTNCKEVNCSTPLFMNGISKELEMKKVYH YGDYYTLKCEDGYTLEGSFWSQCQADDRWT PPLAKCTSRTHDALIVGTLSGTHFILLHLSWI LLFRKGNNAHENFREVAHLHSQGGSSVHP RTLQTNEENSRVLP HPAVFLGPGCVYAAAPVGRFTAHWVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDU VAALHRRLGWERQALMLYAYRFGDEEHCFF LVEGLFMKVRDRNITVDHLEFABDDLSHYT RLLETMPRKRGNVTYCSSPDAFRTILMLALLB GLCGBDYYFFHLDIFGQSLQGGQCPARRPW BERGGGDVSARGAYGARGAYGARPGARPRPW BERGGGDVSARGAYGARGAYGARPGARPRPW BERGGGDVSARGAYGARGAYGARPGARPRPW BERGGGDVSARGAYGARGAYGARPGARPRPW BERGGGDVSARGAYGARGAYGARPGARPRPW BERGGGDVSARGAYGAAGGYGTGAARPPRAFRPRAGGRGAACHPBRANDLLTTALALLB GLCGBDYYFFHLDIFGQSLQGGQCPARRPW BERGGGDVSARGAYGAAGAYGTTAMAVPLL BERGGGDANSARGAYGAAGATTYADPSYAKLGD		1	ì				PHTGKPLEVFPFGKAVNYTCDPHPDRGTSFD
QAPDHFLFAKLKTQTHASSPERISKYEURY BYYGRPSTICLDINLVWSSPKDVCKRKSCKTP PDPVNGMYHVITIDIQVGSRNYSCTTGHRLIG HSSAECILSGNTAHWSTKPPICORIPCGLPTI ANGDFISTNRENHTGSVVTYRCNLGSRGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVVERCQP GFVMKGPRRVKCQALNKWFELEJSCSRVCQ PPPEILHGEHTPSHQDNFSPQEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCEBFGV WOMEN GRANGHTGTPSGDIPYGKEISYTCDFHDR GMTPALIGESTRCTSDPHORGVWSSPAPRCE LSVRAGHCKTPEQPFASSPIPINDFEPYOTS LNYECRPGYPGKMFSISCLENLVWSSVSDNC RRKSCGPPPSPPNGMYHNINTDTQFGSTVNYSC NEGFRLIGSSTCLVSGNNYTWDKAPICEIL SCEPPTISNGDFYSNNESFHNGTVVTYQCH TOPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPVENARVPGNSFSFSLTEI RRRCQFGFVMVGSHTVQCQTNGRWGPKLFH CSRVCQPPPELHGEHTLSHQDNTSPQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFTLKGRSASHCVLAGMKALWNSSYPVC EQIFCNPPAILNGRHTGTPLODIPYGKEVSTT CDPHDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPYGAACPHPRIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFFCTDQGIWS QLDHYCKEVNCSFPLFMGISKELEMKKVYM YCDYVTLKCEDGYTLEGSPWSQCQADDRW PPLAKCTSRTHDALIVOTLSGTFFTLLIIFLSWI LKHEKGNAHENNEVAHILHSQGGSSVIP RTLQTNEENSRVLP HGRSASHCVLAGMKALWNSYPVC HOPAVFLGGCVYAAAPVGRTTAHWRVPLL TAGAPALGFGVKDEYALTRAGFSYAKLGDI VAALHRRLGWERQALMI YAYRPGBEHCFF LVEGLFMRVDRINITVDHLEFAEDDLSHYT RLLRTMPRRGNTYNTCSSDAARTILMLALEA GLCGEDYVFFHLIDIFGQSLQGGQGPARRPW RTLQREDVSRDAAKUTVDPNEVIL			1]		ì	LIGESTIRCTSDPOGNGVWSSPAPRCGILGHC
### PPPYNGMYNTIDIQVGSRNYSCTTOHRLIG HSSAECILSGNTAHWSTKPPICORIPCGLPPTI ANGDPISTNKENFHYGSVYTYRCNLGSRGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVPERCQP GFVMKGPRVKCQALNKWEPELPSCSRVCQ PPPEILHGEHTPSHQDNFSPQGEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHFCCPN PPALINGRHTGTPSGDIPYGKEISYTCDPHPDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEGPFASPTIPINDFEFFVGTS LNYECRPGYFGKMSISCLENLVWSSVEDNC RRKSGGPPPEPFNGMYHINTDTQGSTVNYSC NEGFELIGSFSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTINKCTAPEVENAIRVPGNRSFFSLTEI RFRCQPGFVMVGSHTVQCQTNGRWCHLPH CSRVCOPPPEILHGEHTLSHQDNFSPGGEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFFLKGRSASHCVLAGMKALWNSSVPVC BGIFCFNPPAILNGRHTGTPLGDIPYGKEVSTT CDPHEDRGMTFNLIGESTIRRTSEPHONGVWS SPAPRCELPVGAACPHPPKIQNGHVIGGHVSL YLPGMTISYTICDFQYLLVGKGFFCTDQGIWS QLDHYCKEVNCSPFLFMMGISKELEMKKVTH YGDVYTLKCEDGYTLEGSPWSQCADDRWD PPLAKCTSRTIDALIVGTLSGTIFFLLIIFLSWI LKHRKGNNAHENPKEVAHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGFRRPAGSRLRLLLL LLLPHLLLLRGSHAGALTVAVPLLANTSY PWSWARVGPAVELALAQVKARPDLLFGWT VXTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRTTAHWRVPLL TAGAPALGGVKDEYALTTRAGPSYAKLGDI VAALHRRLGWERQALMLYAVRPGDEBHCFF LVEGIFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVYTCSSPDARRTIMLALEA GLCGEDYVFFHLDIFGQSLQGGQDPARRPW FRONGODVSROAFAGAKIITYKOPDNNPEVL RTLLRTMPRKGRVYTCSSPDARRTIMLALEA						ļ	OAPDHFLFAKLKTOTNASDFPIGTSLKYECRP
PDPYNGMYHVITIOIQVGSRINYSCTIGHRLIG HSSAECLLSGNTAHWSTREPICQRIPCGLPTI ANGDPISTNRENFHYGSVVTYRCNLGSGRGK VFELVGEPSIYCTSNDDQVGIWSGPAQCIIPN KCTPPNVENGGLVSDNRSLYSLNEVVEFRCQP GFVMKGPRRVKCQALNKWEPELFSCSRVCQ PPPEILHGEHTPSHQDNFSPGQEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCEBGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHFCPN PPAILNGRHTGTPSGDPYGKEISYTCDFHDR GMTPHLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFPFASSTIPINDFEFFVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPEPFNGMYHINDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPERCISTNKCTAPEVENAIRVFGNSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGGEVFY SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSFAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSPAPRCTV SCEPSYDLRGAASLHCTPQGDWSGAPRCTV SCEPSYDLRGAASLHCTPQGDWSGAPRCTV SCEPSYDLRGAASLHCTPQGDWSGAPRCTV SCEPSYDLRGAASLHCTPQGDWSGAPRCTV SCEPSYDLRGAASLHCTPQGDWSGAPRCTV SCHORT SCHO	1		1	1			EYYGRPFSITCLDNLVWSSPKDVCKRKSCKTP
ANGDFISTNRENHYGSVUTYRCNLGSRRRK VPELVGEPSIYCTSNDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVVEPRCQP GFVMKGPRRVKCQALNKWPELPSCSRVCQ PPPELLIGBEITPSHQDNFSPGQEVFYSCEPGY DLRGAASLHCTPGDWSPEAPRCAVXSCODF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPALLNGRHTGTPSGDDPYGKESTYCDPHEND GMTPNLIGESTIRCTSDPHONGVWSSPAPRCE LSVRAGHCKTPEQFPFASPTIPDDFEFPVGTS LNYECRPGYFGKMFISICELNLVWSSVEDNC RRSCGPPPEFFNGMVHINTDTQFGSTVNYSC NEGFRLIGSSPSTTCLVSGNNVTYDKKAPICEII SCEPPPTISNGPPYSNNTISFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI RFRCQPGFWMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGGEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPINLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVYVC EQIFCPNPPALINGRHTGTPLDDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SFAPRCELPVGAACHPPRLIQNGHYIGGHVSL YLFGMTSYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSPFLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLLGSPWSQCQADDRWT PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI LIKHRKGNNAHENPKEVAHILHSQGGSSVHP RTQTTCHENSRVLJP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPFLLLLLRGISHAGNLTVAVVLPLANTSY VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNRAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDI VAALHRRLGWERQALMLYAYPGDEBHCFF LVEGLFMRVRGRVIYICSSPDAFRTLMLLALEA GLCGEDYYFFHLDIFGQSLGGGGAPRAPW RULTTMFRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYYFFHLDIFGQSLGGGGAPRAPRW RULTTMFRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYYFFHLDIFGGSGGGGGAPRAPRW		1		1	ļ	Ì	PDPVNGMVHVITDIQVGSRINYSCTTGHRLIG
VFELVGERSIYCTSNDDQVGIWSGPAPCLING GFVMKGPRRVKCQALNKWEPELPSCSRVCQ GFVMKGPRRVKCQALNKWEPELPSCSRVCQ PPFELLHGEHTISHQDNFSPGGGVTYSCEDGY DLRGAASLHCTTQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPALINGHTGTPSGDPYGKEISYTCDPHPDR GMTFNLIGESTIRCTSDPHORGWVSSPAPRCE LSVRAGHCKTPEQFFPASPTIPNDFEFPVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFFNGMVHINTDTGGSTVNYSC NEGFRLIGESPTTCLVSGNVTVWKKAPICEII SCEPPFTISNGDFYSNNRTSFENGTVVTVQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARRYPGNRSFFSLTEI IRFRCQPGFVMYGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLIALQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKAVSSVPVC DEGFRLKGRSASHCVLAGMKALWSSVPVC DEGFRLKGRSASHCVLAGMKAVSSVPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVSPVC DEGFRLKGRSASHCVLAGMKAVAVLPLANTSY VLRCHGVC VLRCHGRSASHCVLAGMCALMALAVCLAMP VRTVLGSSENALGVCSDTAAPLAVDLLWE HNPAVFLIGGSCHALAQVKARPDLLFOUT VRTVLGSSENALGVCSDTAAPLAVDLKWE HNPAVFLIGGGGGAPARPW VRLTMFRLIGWERQALMITYMDHLEFAEDDLSHYT TAGAPALGFGVMDENLTTVDHLEFAEDDLSHYT TAGAPALGFGVMDENLTTVDHLEFAEDDLSHYT RLLKTMFRKGRVTYCSSPDAFRTLMLLALEA GLCGEDYYFFHLDIFGQGLGGGGAPARPW BEDGGODMVSROAFOAAKUTYNDDNPEYL		1		1	<u> </u>	i	HSSAECILSGNTAHWSTKPPICQRIPCGLPP11
KCTPPNVENGILVSDNRSLESHEVVEPKUCQ GFVMKGPRVKCQALINK WEPELPSCSRVCQ PPFELLHGEHTPSHQDNFSPGQEVFYSCEPGY DLRGAASLHCITQGDWSPSPARCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHFGFPN PABLNGRHTGTPSGDIPYGKEISYTCDPHDN GMTFNLIGESTRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEOFFFASPITPIDFEFPVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDNC RRSCGPPPEFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEI SCEPPPTISNGDPYSNARTSFHNGTVVTVQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARTVPGNRSFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPELHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHTPGDBWSPSPAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQFCFPPPALINGRHTGTPLODIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKQNGHYIGGHVSL YLPGMTSYTCDPGYLLVGKGFFCTDQGIWS QLDHYCKEVNCSPFLFMNGISSLEMKKVYH YGDYVTLKCEDGYTLGSSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTFFLLIIFLSWI LKHRKGNNAHENPKEVAHLHSQGGSSVHP RTLQTHEENSRVLP RTLQTHEENSRVLP STANDART SEPHGNGVARAPDLLFGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLIGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDI VAALHRRLGWERQALMLYAYRPGDEBHCFF LVEGLFMRVRDRLINTVDHLEFABDLSHYT RLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYYFFHLDIFGQSGGGGAPRAPRW BEDGDGDWSARGAFGAAKUTYKDDNPFYLL FERDGDGDWSARGAFGAAKUTYKDDNPFYL	ļ				Į		ANGDFISTNRENFHYGSVVI YRCNLGSRGRA
GFYMKGPRAVKCQALNKWEPELPSISKYCQ PPPEILHGEHTPSHODNESPOGEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PAILNGRHTGTPSGDDPYGKEISYTCDPHPDR GMTFNLIGESTIRCTSDPHONGVWSSPAPRCE LSVRAGHCKTFEQPFPASPTIPINDFEFFVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRISPHOGTVVTYQCH TGPDGEQLFELVGERSIYCTSXDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFWMVGSHTVQCINGRWGPKLPH CSRVCQPPPELLHGEHTLSHQDNFSFGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLODIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKQNCHYJGGHVSL YLPGMTISYTCDPGYLLVGKGFICTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYM YGDVYTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTFFILLIILSWI LKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTINEENSRVLP HGRSARLAAVPAEAMPGPRFAGSSRLRLLLL LLPPLLLLLRGSHAAGNLTVAVVLPLANTSY PWSWARVQPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWSVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDI VAALHRRLGWERQALMU AYKRGDEBEHCFF LVEGLFMRVRDRDINITVOHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGQGGPAPRPW	l		i	ļ.		1	VFELVGEPSIYCISNDDQVGIWSGFAFQCIIIN
PPPELLHGEHTPSHQDNYSPGQEVPYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWMNSVPVCEHIFCPN PPAILNGRHTGTFSGDPYGKEISYTCDPHPDR GMTTNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTFEQFPFASPTVTDPHFDR GMTNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTFEQFPFASPTVTDPHFDR RRSCGPPPEFNGMVHINIDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEI SCEPPTISNGDFYSNNRTSFHNGTVVTVQCV TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI RFRCQPGFVMVGAASLHCTTPGGWSPEAPRCTV KSCDDFLGQLPHGENTLSHQDMYSPGQEVFY SCEPSYDLRGAASLHCTTPGGWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC EQIFCPNPPAILNGRHTGTFLQDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDFGYLLVGKFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTFFLLIIFLSWI LKHRKGNNAHENPKEVAHLHSQGGSSVHP TLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALATRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRGDEBEICFF LVEGLFMRVRGRNLNITVDHLEFAEDDLSSIYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGFARPPW			1	ļ			KCIPPNVENGILVSDINGEFSENEVVOI
DLRGAASLHCTPQGDWSFEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKYSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPALLNGRITGTTSGDIPYGKEISYTCDPHDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFFFASPTIPINDFEFPVGTS LNYECRPGYFGKMFSISCLENLWSSVEDNC RRKSCGPPPFFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTVDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGGLJFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVQOPPEILHGEHTLSHQDNFSSFGGEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCRNPPALINGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKLQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYYTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVOTLSGTTFFLLIIFLSWI ILKHRKGNNAHENPKEVAHLHSQGGSSVHP RTLQTINEENSRVLP BLLPPLLLLLRGSIRAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLFGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAADTAAPLAAVDLKWE HNPAVFLGPGCVYAADTAAPLAAVDLKWE HNPAVFLGPGCVAADTAAPLAAVDLKWE HNPAVFLGPGCVAADTAAPLAAVDLKWE HNPAVFLGPGCVAADTAAPLAAVDLKWE HNPAVFLGPGCVAADTAAPLAAVDLKWE HNPAVFLGPGCVAADTAAPLAAVDLKWE HNPAVFLGPGCVAADTAAPLARTAHWSVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDB VAALHRRLGWERQALML VAYRGDEBEHCFF LVEGLFMRVRGRRLNITVOPHLEFEADDLSSITY RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFIFHLDIFGGSLQGGQGPAPRPW		ì	1	ŀ			PROPERT HIGHTPSHODNESPGOEVFYSCEPGY
LGQLPHGRVLFPLNLQLGAKVSFVCEBIFRCFN KGSSVSHCVLVGMRSLWNNSVPVCEHIFCFN PPALLNGRHTGTFSGDIPYGKEISYTCDPHPDR GMTFNLIGESTIRCTSDPHORGVWSSPARRCE LSVRAGHCKTPEQFPFASPIPINDFEFFVGTS LNYECRGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFFNGMYINDTOFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIVCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMYOSHTVQCQTNGRWGPKLPH CSRVCQPPPELHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQQDWSPEAPRCTV KSCDDFLGQLPHGRVLLPINLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHEPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPFKIQNGHYIGGHVSL YLPGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPFKIQNGHYIGGHVSL YLPGMTSYTCDGYLLVGKGFFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDVYTLKCEDGYTLLGSFWSQCQADDRWD PPLAKCTSRTHDALIVGTLGSTHFILLIELSWI LKHRKGNNAHENFKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLIRGISHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDD VAALHRRLGWERQALMLYAYRPGDEEHCFF RUGGLFMRVRORINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FEGDGODVSARQAFQOAKUTYKDPDNPEYL		1	1	İ	.	į	DI PGAASI HCTPOGDWSPEAPRCAVKSCDDF
KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPALLNGRHTGTPSGDIPYGKEISYTCDFIPDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEOFPFASFTIPINDEFEFFVGTS LNYECRGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFFNGMYHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEOLFELVGERSIVCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMYOSHTVQCTINGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGGEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRASSHCVLAGMKALWNSSVPVC EQIFCTNPPALLNGRHTGTPLGDIPYGKEVSYT CDPHEDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIILSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWANRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGFGCVYAAAPVGFTAHWRVPLL TAGAPALGFGVKDEVALTTRAGPSYAKLGGB VAALHRRLGWERQALMLYAVRPGDEEHCFF LVEGLFMVKRORNINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLALEA GLCGEDYVFFHLDIFGQSLQGGQGPARRWF FEGDGODVSARQAFQOSLOGGGPARRWF				Ì	1	· ·	LGOLPHGRVLFPLNLQLGAKVSFVCDEGFRL
PPALLNGRHTGTPSGDIPYGKEISYTCDPHPNG GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFPFASPTIPINDFEFPVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTINKCTAPEVENARRVPGNRSFFSLTEI RFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSFEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFFLKGRSASHCVLAGMKALWNSSVPVC DEGFFLKGRSASHCVLAGMKALWNSSVPVC DOBGFRLKGRSASHCVLAGMKALWNSSVPVC DIPPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPKLQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLLGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTFFILLIFLISWI ILKHRKGNNAHENPKEVAHLHSQGGSSVHP RTLQTNEENSRVLP BROADLAGVCSSTAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRTHAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLPMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIPIGQSLQGGQPAPRRPW FREGRGDDVSARQAATOAAKHTYKDPDNPEYL	1	1		1			KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN
GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFPFASPTIPINDFEFPVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDNC RRKSCGPPPFSNGWVHINTDTQFGSTVNYSC NEGFRLIGSPSTTICLVSGNNVTWDKKAPICEII SCEPPPTSNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSFEAPRCTV KSCDDFLGQLPHGVLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFFCTDQGIWS QLDHYCKEVNCSPPLFMNGISKELEMKKVYH YGDVVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVOTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HRRSARLAAVPAEAMPGPRRFAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMILALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FREGRGDDVSAROAAKUTTYKDPDNPEYL		j			}	}	PPAILNGRHTGTPSGDIPYGKEISYTCDPHPDR
LNYECRPGYFGKMYSISCLENLVWSSVEDNC RRKSCGPPPEFFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFINGTVVTYQCH TGPDGEQLFELVGRERIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARRVPGNRSFFSLTEII RRFCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPELLHGEHTLSHQDNYSPGQEVFY SCEPSYDLRGAASHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPALINGHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFLLIIFLSWI ILKHRKGNNAHENFKEVAIHLHSQGGSSVHP RTILQTNEENSVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDI VAALHRRLGWERQALMLYAYRPGDEEHCFF LVGGLFMVRDRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMILALEA GLCGEDYVFHLDIFQGSLQGGQFAPRRPW ERGDGGODVSARGAFOAAKIITYKDPDNPESLT	i		1		1	i	GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE
RRKSCGPPPEPRIGMYHINTDTCJEGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISINGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPHLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTTFILLIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRPAGSRLRLLLL LLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDB VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVTYICSSPDAFRTIMILALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSAROAFOAAKIITYKDPDNFEYL	ì			1			LSVRAGHCKTPEQFPFASPTIPINDFEFFVGTS
NEGFRLIGSPSTTCLVSGNNYTWDKKAPICEII SCEPPPTISNIGDFYSNNRTSFHNGTVYTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPERCISTNIKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTINGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILINGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHONGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFELLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRFGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVYIYCSSPDAFRTIMLLALEA GLCGEDYVFFHLDIFGGSLQGGQGPAPRRPW ERGDGODVSAROAFOAAKIITYKDPDNPEYL		· ·	ł				LNYECRPGYFGKMFSISCLENLVWSSVEDNC
SCEPPTISNGDFYSNNRTSFHNGTVTTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DGGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVM YGDYVTLKCDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGISHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW BERDGGODVSARQAFQALKUTYKDPDNPEYL	1		1	1			RRKSCGPPPEPFNGMVHINTDTQFGSTVNTSC
TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTINKCTAPEVENARRVPGNRSFSLTEI IRFRCQPGFVMVGSHTVQCQTINGRWGPKLPH CSRVCQPPPELHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVILPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILINGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENFKEVAIHLHSQGGSSVHP RTLQTINEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEBHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGGQAPRRPW			-	Į			NEGFRLIGSPSTTCLVSGNNVIWDRAAFICEH
PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVQSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLLGSFWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRILLL LLLPPLLILLRGSSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRILMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FERDDGODVSAROAFOAAKIITYKDPDNPEYL				[l l	SCEPPPIISNGDF YSNNKISFRINGT V TI QCII
IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL Y1LPGMTISYTCDPGY1LLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HTLQTNEENSRVLP WSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVULKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTRAGPSYAKLGDI VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FPRDGGODVSAROAFQAAKIITYKDPDNPEYL		Y					TGPDGEQLFELVGERSTTCTSRDDQVGVVVS
CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASHCTLPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCRPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRGISHAGNLTVAVVLPLANTSY PWSWANVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW EPRGDGODVSAROAFQAAKIITYKDPDNPEYL	1	*		1]		THE COP GEV MY GSHT VOCOTNOR W GPKLPH
SCEPSYDLRGAASLHCTPQGDWSPEAPRCIV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFLLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSAROAFOAAKIITYKDPDNPEYL	Į.	\		i			CSRVCOPPPEILHGEHTLSHODNFSPGQEVFY
KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTYLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	'		1	l l	}		SCEPSYDLRGAASLHCTPOGDWSPEAPRCTV
DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	1	1					KSCDDFLGOLPHGRVLLPLNLQLGAKVSFVC
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CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL		1	1				POIECPNPPAILNGRHTGTPLGDIPYGKEVSYT
SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDE VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL		1		1			CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS
QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVOTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	1	1	1	1		1	SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL
803 2153 A 6574 2 3233 HGSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	1		1 .	1		1	YLPGMTISYTCDPGYLLVGKGFIFCIDQGIWS
PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHILHSQGGSSVHP RTLQTNEENSRVLP 803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRFGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	ļ. ·		}		1	1	QLDHYCKEVNCSFFLIMNUISKELEMAN III
ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP 803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	1		-	1			YGDYVILKCEDG I ILEGSPWSQCQADDKWD
RTLQTNEENSRVLP 803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL	1	1	1			1	T PUDP CONTACT OF THE HEADER TO WE
803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSARQAFQAAKIITYKDPDNPEYL]			1	1	1	DAI OTMEENGPAI D
803 2153 A 6374 2 LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGGPAPRRPW ERGDGDDVSARQAFQAAKUTYKDPDNPEYL	1						LICOSADI A AVDAFAMPGPRRPAGSRLRILLIL
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TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGDDVSARQAFQAAKIITYKDPDNPEYL			- [1	1		HNPAVELGPGCVYAAAPVGRFTAHWRVPLL
VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSAROAFOAAKIITYKDPDNPEYL			1	-			TAGAPALGFGVKDEYALTTRAGPSYAKLGDF
LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSAROAFOAAKIITYKDPDNPEYL			-				VAALHRRLGWEROALMLYAYRPGDEEHCFF
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GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGODVSAROAFOAAKIITYKDPDNPEYL	1.	1]	J	}		RITRTMPRKGRVIYICSSPDAFRTLMLLALEA
	1				1		GLCGEDYVFFHLDIFGOSLOGGQGPAPRRPW
EFLKQLKHLAYEQFNFTMEDGLVNTIPASFH	i		1	1			FRODGODVSAROAFOAAKIITYKDPDNPEYL
	1	-				1	EFLKQLKHLAYEQFNFTMEDGLVNTIPASFH

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	ì	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
) }		residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide	1	nucleotide insertion
				sequence		DGLLLYIQAVTETLAHGGTVTDGENITQRMW
					ŀ	NRSFQGVTGYLKIDSSGDRETDFSLWDMDPE
1	1					NGAFRVVLNYNGTSQELVAVSGRKLNWPLG
	ł]				YPPPDIPKCGFDNEDPACNQDHLSTLEVLALV
]	1	1		ł	l	GSLSLLGILIVSFFIYRKMQLEKELASELWRVR
1	1	1	1	ļ		WEDVEPSSLERHLRSAGSRLTLSGRGSNYGSL
		1				L.TTEGOFOVFAKTAYYKGNLVAVKRVNRKR
ļ	1		ł	Ì		IELTRKVLFELKHMRDVQNEHLTRFVGACID
	1	ì	1	'		PPNICILTEYCPRGSLODILENESITLDWMFRY
	1	1				ST.TNDIVKGMLFLHNGAICSHGNLKSSNCVV
		1		l		DGREVLKITDYGLESFRDLDPEQGHTVYAKK
	ł	ļ	}	ļ	1	LWTAPELLRMASPPVRGSQAGDVYSFGIILQE
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i		1	ì	1	1	QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE
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1		1	1			LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGV
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		1				KVRTYWLLGERGSSTRG
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804	2154	A	6383	12	1.5037	MSERVSGLAGSTYREFERLIVRYDEEVVKELIP
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1	1	1	1	}	1	QLITQYEREKALRKHAEEKFIEFEDSQEQEKK
1	i		1	1	1	DLQTRVESLESQTRQLELKAKNYADQISILEE
		1	1		i	REAELKKEYNALHQRHTEMIHNYMEHLERT
		}		1 '	1	KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP
1		1	1			AGDGLLTPDAQKGGETPGSEQWKFQELSQPR
	ł	1	1	ı		SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV
				1		QVAQETRNVSTGSAENEEKSEVQAIIESTPEL
-	İ				1	DMDKDLSGYKGSSTPTKGIENKAFDRNTESL
ł	ì	1			1	FEELSSAGSGLIGDVDEGADLLGMGREVENLI
	1		ĺ		1	LENTQLLETKNALNIVKNDLIAKVDELTCEK
		1	Ì	•	j	DVLOGELEAVKOAKLKLEEKNRELEEELKKA
		1	[I	i	RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE
1	-	1			1	MARVI MERNOYKERLMELQEAVRWIEMIK
	1	-	1		1	ASPENDAMOEKKRSSIWOFFSRLFSSSSNITK
		{	1			K PEPPVNI KYNAPTSHVTPSVKKRSSTLSQLP
1				1		GDKSK AFDFLSEETEASLASRREOKREQYRQ
1]		1	}		VKAHVQKEDGRVQAFGWSLPQKYKQVTNG
	1	1	1			QGENKMKNLPVPVYLRPLDEKDTSMKLWCA
Ì	ļ	1		1	1	VGVNLSGGKTRDGGSVVGASVFYKDVAGLD
		1		Į		TEGSKQRSASQSSLDKLDQELKEQQKELKNQ
	1	1		1		EELSSLVWICTSTHSATKVLIIDAVQPGNILDS
	1	-				FTVCNSHVLCIASVPGARETDYPAGEDLSESG
1	- 10)	1	1 .	1	QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN
		1	1	1	1	SEVDENVPTAEE\ATEATEGNAGSAEDTVDIS
	1	j	1	1	ì	QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND
	1	1	1		1	QTGVYTEHVFTDPLGVQIPEDLSFVTQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT
	}		1	1		SDAYKDQISVLPNEQDLVREEAQXWSSEEL I MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD
	- [1		1	SILSIVHVKGIVLVALADGTLAIFHRGVDGQW
1	i	-	1	ł	1	DI SNVHI I DI GRPHHSIRCMTVVHDKVWCU
	-	1		1.	-	YRNKTYVVOPKAMKIEKSFDAHPRKESQVRQ
1	- 1	(1		1	I AWVGDGVWVSIRLDSTLRLYHAHTYQHLQ
						DVDIEPYVSKMLGTGKLGFSFVRITALMVSC
1	1 .	- 1		l		

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	}	ļ	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i	ļ		amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		1	ì	residue of	Sequence	/-possible nucleotide deletion, \-possible
	1		ł	peptide	1	nucleotide insertion
				sequence	ļ	NRLWVGTGNGVIISIPLTETVILHQGRLLGLR
						ANKTSGVPGNRPGSVIRVYGDENSDKVTPGT
1	ļ			1		FIPYCSMAHAQLCFHGHRDAVKFFVAVPGQV
	1			I		ISPOSSSSGTDLTGDKGRGHLHRSLVVRRP
	1	i			<u> </u>	FGRLLWGTAFKSWKMKAPIPHLILLYATFTQ
805	2155	A	6605	469	2602	SLKVVTKRGSADGCTDWSIDIKKYQVLVGEP
1 003	1					VRIKCALFYGYIRTNYSLAQSAGLSLMWYKS
	1		1	1		VRIKCALFYGYIKINYSLAQSAGLSLIVIV IKS
	1	1	1	Ì	1	SGPGDFEEPIAFDGSRMSKEEDSIWFRPTLLQ
1	ļ	1	1	}	ł	DSGLYACVIRNSTYCMKVSISLTVGENDTGL
1	1				1	CYNSKMKYFEKAELSKSKEISCRDIEDFLLPT
1	1	ł				REPEILWYKECRTKTWRPSIVFKRDTLLIREV
i	ŀ		1			REDDIGNYTCELKYGGFVVRRTTELTVTAPL
	4			1		TDKPPKLLYPMESKLTIQETQLGDSANLTCRA
	1		j			FFGYSGDVSPLIYWMKGEKFIEDLDENRVWE
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ļ		1			ł	LGAILLLLVCLVTIYKCYKIEIMLFYRNHFGA
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\	}	1	1			EERFALEILPDMLEKHYGYKLFIPDRDLIPTGT
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806	2156	A	0014	13	1.50	HSPAHRPPGFSVAOKPFGATYVWSSIINTLUT
		1		i	ł	OVEVKKRRHRIKRHNDCFVGSEAVDVIFSHL
	1		ł	ì	i	LONKYEGDYDIPRAKVVRVCOALMDYKVFE
	1 .	- 1	l		ľ	AVPTKVFGKDKKPTFEDSSCSLYRFTIPNQD
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		1		1	}	CPORVOKKVSCOVLGLLOVPSVLPPDIEILD
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	İ	- 1		1	1	LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS
1	1		1	1		NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD
1	1	1	1	1		FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT
1	1	- 1	-			FSLQQLRVLDLSCNSIEAFQTASIQFQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR
1	1	l		1		WLDLRENKLLHFPULAALFKLII LINLSINALIK
I	1.	1	i			LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS
	1					GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL
		1		ŀ		NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE
		l		ŀ	1	TLELGARALG\SLRTLLLQGNALRDLPPYTFA
		- 1				NLASLQRLNLQGNRVSPCGGPDEPGP\SGCV\
- 1	- {		1	- 1		AFSGITSLRSLSLVDNEIELLRAGAFLHTPLTE

				ore I	Prodicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
		SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
		NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
		peptide	1	in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
е	otide	seq-	ŀ	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
s	eq-	uence	\	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ι	ience		ł	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
}	}		- 1		amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
l	1	Ì			residue of	sequence	/=possible nucleotide deletion, \=possible
l	ľ				peptide	į	nucleotide insertion
١	1				sequence	<u> </u>	LDLSSNPGLEVATGALGGLEASLEVLALQGN
Г					•	1	GLMVLQVDLPCFICLKRLNLAENRLSHLPAW
ì	į				•	1	TOAVSLEVLDLRNNSFSLLPGSAMGGLETSLR
١	į		. '	1			RLYLQGNPLSCCGNGWLAAQLHQGRVDVDA
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L	1					<u> </u>	YKA FKALSQYIYTNTHLEREAAFEVAILLRRMEEG
۲	808	2158	A	6619	153	1852	ARHRNNTEKKHPGGGESDASPEAGSGGGGV
1					ł		ALKKEIGLVSACGIIVGNIIGSGIFVSPKGVLEN
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1	•		1		1		PKSGGDYFYVKDIFGGLAGFLRLWIAVLVIYP
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1	-1		1]	1	1	AICLLLLTWVNCSSVRWATRVQDIFTAGKLL
			1	1	}	1	ALALIIMGIVQICKGEYFWLEPKNAFENFQEP
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		1	1	1			DP\YKNL\PRAIFISIP\LVTFVYVFANV/ALYVT
1		}	ł	1 .			AMSPQEL\LAS\NAVAVTFGEKLLGVMAWIM
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Ţ			1	1	i .		SVLAMIHVKRCTPIPALLFTCISTLLMLVTSD
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١		ļ	!				CGIGLAIMLTGVPVYFLGVYWQHKPKCFSDFI
١		}	1		ì		ELLTLVSQKMCVVVYPEVERGSGTEEANED
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١			l l	İ			VLLSIWLCVSTIGFGFVLDMGFFETIKLLLWV
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							GAIEIFLVYIVPRAAIFHSDDALKESAAMLNN MRVYGTAFLVLMVLVVFIGVRYVNKFASLFL ACVIVSILAIYAGAIKSSFAPPHFPVCMLGNRT LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS OFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGDLKD AOK SIPIGTILAILTTSFVYLSNVVLFGACIEGV
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residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop cod /=possible nucleotide deletion, \=possible nucleotide insertion FGHSKANGEPTWALLLTAAIAELC VAPILSMFFLMCYLFVNLACALQT RPFFRYYHWALSFMGMSICLALM IVAMVIAGMIYKYEYQGAEKEW LSAARFALLRLEEGPPHTKNWRPC DEDLHVKHPRLLTFASQLKAGKG GNFLENYGEALAAEQTIKHLMEAILVVAAKLREGISHLIQSCGLGGMK GWPNGWRQSEDARAWKTFIGTVU ALLVAKNISFFPSNVEQFSEGNIDU GMLLPFLLK\QHKVWRKCSIRI DNSIQMKKDLATFLYHLRIEAEVE DISAYTYERTLMMEQRSQMLRHM	GILIASLDL TLLRTPNW FISSWYYA GDGIRGLS QLLVLLKL LTIVGSVIV EKVKGFCQ CHNTVVM
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KLVLLNMPGPPRNPEGDENYMEF	LEVLTEGL
ERVLLVRGGGSEVITIYS	
640 AVCIMSEMAELSELYEESSDLQM	DVMPGEG
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MEEEEAQPMAAPEGKRSLANGPN	IAGEOPGO
VAGADFESEDEGEEFDDWEDDYI	YPEEEOLS
GAGYRVSAALEEADKMFLRTREF	PALDGGEO
MHYEKTPFDQLAFIEELF\SLMVV	NRI TEELG
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813 2163 A 6630 708 1355 AKMGAYKYIQELWRKKQSDVMI	CLLKAKC
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ATYGKPVHHGVNQLKFARSLQSV	/AEERAGR
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PLTKESIRQKEMESKRLRLLQEET	
GFNASSMLRKSQLGFLNVTNYCH	ILAHELKES
CMERKKVQIRSMDPSALASDRFN	ILILADINS
	LKTPILKVF
MHENT YETNEK VINSVCWASLNI	HLDSHILLC
I I MGLAETPGCATLLPASLFVNSH	PAGIDRPG\
	ICFSTGLSR
RVLLTNVVTGHRQSFGTNSDVLA	OOFALMA
PLLFNGCRSGEIFAIDLRCGNQGK	GWKATRIF
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HDSAVTSVRILQDEQYLMASDM	
LRTTKCVRQYEGHVNEYAYLPLI	TAUECEGIF
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			ano I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i.				peptide		/-possible nucleotide deletion, \-possible
}				sequence		nucleotide insertion
		<u> </u>				RVFETLKDLKVLNLAYNKINKIADEAFYGLD
ł					1	NLQVLNLSYNLLGELYSSNFYGLPKVAYIDL
Ì						QKNHIAIIQDQTFKFLEKLQTLDLRDNALTTIH
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ł	1					EGLSHLQVLYLNHNYLNSLPPGVFSHLTALR
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1	1	1	\ ·	İ	i	KONNIPI OTVATIS
1				<u> </u>	3811	PDRAGVRPAGKOHAAAAFYDVGGDRPWDS
816 -	2166	Α	6646	1	3011	CNTO PPRNPVKANAMFGAGDEDDIDILSPS
		1	1	1		GGARLASLFGLDOAAAGHGNEFFQYTAPKQP
	-	1			1	KKGOGTAATGNOATPKTAPATMSTPTILVAT
		ł	1	1	ì	AVHAYRYTNGQYVKQGKFGAAVLGNHTTR
1	Ì				ļ	EYRILLYISQQQPVTVARIHVNFELMVRPNNY
1					1	STFYDDQRQNWSIMFESEKAAVEFNKQVCIA
ì		1	 		1	KCNSTSSLDAVLSQDLIVADGPAVEVGDSLE
1		1				VAYTGWLFQNHVLGQVFDSTANKDKLLRLK LGSGKVIKGWEDGMLGMKKGGKRLLIVPPA
ł	1	1	ì	1		CAVGSEGVIGWTQATDSILVFEVEVRRVKIA
1	-	1	1	1	1	KDSGSDGHSVSSRDSAAPSPIPGADNLSADPV
1	'			ļ.	Į.	VSPPTSIPFKSGEPALRTKSNSLSEQLAINTSPD
1	}					AVKAKLISRMAKMGOPMLPILPPQLDSNDSEL
8		1	1	ì		EDVNTLOGGGOPVVTPSVQPSLQPAHPALPQ
	'	1	1			MTSOAPOPSVTGLOAPSAALMQVSSLDSHSA
	1	1	1	1		VSGNAOSFOPYAGMOAYAYPQASAVTSQLQ
	i	1		1		PURPLYPAPLSOPPHFQGSGDMASFLMTEAK
)	1	1	1	1	İ	QHNTEIRMAVSKVADKMDHLMTKVEELQKH
1					ļ	SAGNSMLIPSMSVTMETSMIMSNIQRIIQENER
			1		ļ	LKQEILEKSNRIEEQNDKISELIERNQRYVEQS
1	Į.		1			NLMMEKRNNSLQTATENTQARVLHAEQEKA
1		1				KVTEELAAATAQVSHLQLKMTAHQKKETEL
	1	1				QMQLTESLKETDLLRGQLTKVQAKLSELQET SEQAQSKFKSEKQNRKQLELKVTSLEEELTDL
		1	1	1		RVEKESLEKNLSERKKKSAQERSQAEEEIDEI
	-	1 .		ŀ	1	RVEKESLEKNLSERAKASAQEASQALELIDER RKSYQEELDKLRQLLKKTRVSTDQAAAEQLS
1]	1		1	LVQAELQTQWEAKCEHLLASAKDEHLQQYQ
1		1				EVCAORDAYOOKI.VOLOEKSVCFA\CLALQA
	1	-		1	1.	OITAI TKONFOHIKELEKNKSOMSGVEAAAS
	1	1		1		DPSFKVKKIMNOVFOSLRREFELEESYNGKII
	1	1	1		}	I CTIMNTIKMVTLOLLNOOEOEKEESSSEEEE
1	1	1	1	1	1	LEK AFFRPRRPSOFOSASASSGOPQAPLNRERP
	-	1	1	1		PSPANDSROVVERAVPLPPOALTTSQDGHRK
	1			1		KGDSEAEAL SEIKDGSLPPELSCIPSHKVLGPP
	1		1	1		TSIPPEPL GPVSMDSECEESLAASPMAAK VPDN
1	1	1	1	ı		DOCK VCVRRVAPDGPLOESSTRLSLTS VDPEE
			1	1	1	GDPLALGPESPGEPQPPQLKKDDVTSSTGPHK
			1		`(·	ODLIVEOU FOR OW 61. 6
					1	FI 99TE A GSTV A GA AL RPSHHSUKSSLSUDEE
						ELSSTEAGSTVAGAALRPSHHSQKSSLSGDEE DELFKGATLKALRPKAQPEEEDEDEVSMKGR
						ELSSTEAGSTVAGAALRPSHHSQKSSLSQDEE DELFKGATLKALRPKAQPEEEDEDEVSMKGR
817	2167	A	6649	63	1073	ELSSTEAGSTVAGAALRPSHHSQKSSLSGDEE DELFKGATLKALRPKAQPEEEDEDEVSMKGR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	Ì	1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
	1		1	peptide		nucleotide insertion
	<u> </u>		<u> </u>	sequence		KS/ARNSQLRIVLVGKTGAGKSATGNSILGRK
						VFHSGTAAKSITKKCEKRSSSWKETELVVVD
		1	- 0		Į.	TPGIFDTEVPNAETSKEURCILLTSPGPHALLL
						VVPLGRYTEEEHKATEKILKMFGERARSFMIL
	1	1				IFTRKDDLGDTNLHDYLREAPEDIQDLMDIFG
	ì	}	1			DRYCALNNKATGAEQEAQRAQLLGLIQRVV
	1	1				RENKEGCYTNRMYORAEEEIQKQTQAMQEL
	1		1		ì	HRVELEREKARIREEYEEKIRKLEDKVEQEKR
		1	1		1	KKQMEKKLAEQEAHYAVRQQRARTEVESKD
}	1			Ì		GILELIMTALQIASFILLRLFAED
010	2168	A	6660	357	1890	APSGSWTRVVLTLDPCSLRSRSPRSLLDPGMP
818	2100	^	3000	1		GISARGLSHEGRKQLAVNLTRVLALYRSILDA
1		1)	1	1	YHEFFYTDNLWDTLPCSWQEALDGLKPPQLA
1		i	}	1		TMLLGMPGEGEVVRYRSVWPLTLLALKSTA
. '	ł	1		1	1	CALAFTRMPGFQTPSEFLENPSQSSRLTAPFR
l	1	1	Ì	{		KHVRPKKQHEIRRLGELVKKLSDFT/GLHPGC RRGLRPG\HLSRFMALGLGLMVKSIEGDQRL
	1	1		1	i	VERAQRLDQELLQALEKEEKRNPQVVQTSPR
ł	1		ļ			HSPHHVVRWVDPTALCEELLLPLENPCQGRA
]	1	1	1	Į		RLLLTGLHACG\DLSVALLRHFSCCPEVVALA
ļ	İ	1	ì	1		SVGCCYMKLSDPGGYPLSQWVAGLPGYELP
İ		1	Į	ļ	i	YRLREGACHALEEYAERLQKAGPGLRTHCY
		1		1	1	RAALETVIRRARPELRRPGVQGIPRVHELKIEE
1	1 .	Ì	İ	Ĭ	ì	VVORGLORVGLDPOLPLNLAALQAHLAQEN
	,	1	1	ł		DAVVAFESI ALLI APLVETLILLDRLLYLQEQA
		1				LSP\GFHAELLPIFSPELSPRNLVLVATKMPLG
1	ļ		1	1		OALSVLETEDS
	2169	A	6661	65	2686	SGSGHCLAEAASMGPWGWKLRWTVALLLA
819	2103	^	10001	"		AAGTAVGDRCERNEFQCQDGKCISYKWVCD
1	1		1.		Ì	GSAECQDGSDESQETCLSVTCKSGDFSCGGR
}		1	1	i	[VNRCIPQFWRCDGQVDCDNGSDEQGCPPKTC
1	İ	1	1	į	,	SQDEFRCHDGKCISRQFVCDSDRDCLDGSDE
1		- [-	İ		ASCPVLTCGPASFQCNSSTCIPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH
ł		Ì	}		1	CEDGSDEWPQRCRGLTYFQGDSSTCBALLTT
1				1	1	TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS
		ı	i	l		DEVGCVNVTLCEGPNKFKCHSGECITLDKVC
1 '		1	1		1	NMARDCRDWSDEPIKECGTNECLDNNGGCS
				(Í	HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE
}	1			1	i	CODEDICSOLCVNLEGGYKCOCEEGFQLDPH
		1			I	TY ACK AVGSTAYL FFTNRHEVRKMILDRSEY
1			}	1)	TSLIPNI.RNVVALDTEVASNRIYWSDLSQRMI
ı		1	1	ı		COTOL DRAHGVSSYDTVISRDIOAPDGLAVD
1	1			1		WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR
		1		1	1	ENGSKPRATVVDPVHGFMYWTDWGTPAKIK
	1	- 1		1	1	KGGI NGVDIYSLVTENIOWPNGITLDLLSGRU
		-				VWVDSKLHSISSIDVNGGNRKTILEDEKRLAH
1 .	1	1	ļ	1	Į.	PEST AVEEDKVEWTDIINEAIFSANRLTGSDV
	1				}	NI LAENI LSPEDMVLFHNLTQPRGVNWCERT
1	- 1	1		1	1	TI SNGGCOYLCLPAPOINPHSPKFTCACPDGM
1		1		1	1	I I AR\DMRSCLTEG\EAAVATQETSTVRLKVS
1				1		STAVRTOHTTTRPVPDTSRLPGATPGLTTVEI
	j	J	1	ļ	1	VTMSHOALGDVAG\RGN\EKKPSSVRALSIVL
1		1	1	1	1	PIVALLYFLCLGVFLLWKNWRLKNINSINFDNY
		1				VYQKTTEDEVHICHNQDGYSYPSRQMVSLED
1		1				DVA
820	2170	-	6666	17	4146	ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA
020	21/0		3000	"		LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI
		1		1	1	EGYLHILLISKAEDYRSYRFPKLTVITEYLLLF
1		- 1		-		RVAGLESLGDLFPNLTVIRGWKLFYNYALVIF
L						

	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of		1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		•	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			}		sequence	/=possible nucleotide deletion, \=possible
1		1		peptide		nucleotide insertion
				sequence		EMTNLKDIGLYNLRNITRGVAIRIEKNADLCYL
						STVDWSLILDAVSNNYIVGNKPPKECGDLCP
					}	GTMEEKPMCEKTTINNEYNYRCWTTNRCQK
		1				MCPSTCGKRACTENNECCHPECLGSCSAPDN
			1		1	MCPSICGRACIENNECCHPECLOSCOAI DIN
		ļ		į		DTACVACRHYYYAGVCVPACPPNTYRFEGW
		i	Ï	0.0	[RCVDRDFCANILSAESSDSEGFVIHDGECMQE
		ŀ	Į.	}	i	CPSGFIRNGSQSMYCIPCEGPCPKVCEEEKKT
1		1	1	}		KTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIA
		1	1			SELENFMGLIEVVTGYVKIRHSHALVSLSFLK
'		}				NLRLILGEEQLEGNYSFYVLDNQNLQQLWD
		j]	j	ļ	WDHRNLTIKAGKMYFAFNPKLCVSEIYRMEE
1		1	{	Į.		VTGTKGRQSKGDINTRNNGERASCESDVLHF
		1	1	Ĺ		TSTTTSKNRIIITWHRYRPPDYRDLISFTVYYK
	į.	1	ļ	1		EAPFKNVTEYDGQDACGSNSWNMVDVDLPP
			1			NKDVEPGILLHGLKPWTQYAVYVKAVTLTM
ļ.	1	1				VENDHIRGAKSEILYIRTNASVPSIPLDVLSAS
}		1			ł	NSSSQLIVKWNPPSLPNGNLSYYIVRWQRQP
l		1			ļ	QDGYLYRHNYCSKDKIPIRKYADGTIDIEEVT
		1				ENPKTEVCGGEKGPCCACPKTEAEKQAEKEE
	i	l				AEYRKVFENFLHNSIFVPRPERKRRDVMQVA
		1	İ]	1	NTTMSSRSRNTTAADTYNITDPEELETEYPFF
1	ĺ	i		1		ESRVDNKERTVISNLRPFTLYRIDIHSCNHEAE
		1	1	1		KLGCSASNFVFARTMPAEGADDIPGPVTWEP
		1		1	1 .	RPENSIFLKWPEPENPNGLILMYEIKYGSQVE
	1		1	1		DQRECVSRQEYRKYGGAKLNRLNPGNYTARI
ļ.						QATSLSGNGSWTDPVFFYVQAKRYENFIHLII
i	1	1	j	}	ļ	ALPVAVLLIVGGLVIMLYVFHRKRNNSRLGN
			1	1		GVLYASVNPEYFSAADVYVPDEWEVAREKIT
1 .		1	1	ļ	ļ	MSRELGQGSFGMVYEGVAKGVVKDEPETRV
1.	ļ	j	Į	l	1	AIKTVNEAASMRERIEFLNEASVMKEFNCHH
1	1	1	1	į.	j	VVRLLGVVSQGQPTLVIMELMTRGDLKSYLR
		1		1	ì	SLRPEMENNPVLAPPSLSKMIQMAGEIADGM
1	į	1	1		1	AYLNANKFVHRDLAARNCMVAEDFTVKIGD
}	i .	ŀ	1	1		FGMTRDIYETDYYRKGGKGLLPVRWMSPESL
ł				1		KDGVFTTYSDVWSFGVVLWEIATLAEQPYQ
1	1	1			1	GLSNEOVLRFV\MEGGLLDKPDNCPDMLFEL
1	ļ	}	1	1		MRMCWQYNPKMRPSFLEIISSIKEEMEPGFRE
1	Ì	1	ł	1	1	VSFYYSEENKLPEPEELDLEPENMESVPLDPS
1	1	1			İ	ASSSSLPLPDRHSGHKAENGPGPGVLVLRASF
]	1	1	1	1	1	DEROPYAHMNGGRKNERALPLPQSSTC
100:	2141	HA-	6691	106	825	GRVLFRGCGVGHKGOVLMGTFILAQDWLSE
821	2171	A	1 0071	1.00		SNHVFCVSSMLRLOKRLASSVLRCGKKKVW
	1 .	1	1	1	1	LDPNETNEIANANSROOIRKLIKDGLIIRKPVT
	1		1	1		VHSRARCRKNTLARRKGRHMGIGKRKGTAN
		1		1		ARMPEK VTWMRRMRILRRLLRRYRES/KRYR
	1	1	1	1	1	ESKKIDRHMYHSLYLKVKGNVFKNKRILMEH
]	Į.	1		1	1	IHKLKADKARKKLLADQAEARRSKTKEARK
		1	1	1	1	RREERLQAKKEEIKTLSKEEETKK
L			<u> </u>	 	1	DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI
822	2172	Α	6715	772	21	SGAKSSSS/RFTDSKRYEK/DFQ/SCFGLHETR/
		1			1	SGAKSSSSKFIDSKRIBNDFQSCFGLIDIKI SGDI\CNA\CVLL\LKRWKKLPAGSKK\NWNH
1		!	1			VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST
			1	1		A ANAKARLOMEL TIPLEVA VET POPULE
		ļ	1		İ	QISKLQKEFKR\HNSDAHSTTS\SASP\AQSPLF
	1		1	1		TVNQFRWTGSDTGVGFPGSNRNHPVFSFLDL\
	J	1	1		1	TYWKRQKICCGNIYKGRFGEVLIDTHLFKPCC
[1		1			SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM
823	2173	A	6727	3	4063	PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG
المتا	1	1.:	1			NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA
1					1	SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS
	[1			VGGQNPSTGGISADRTQGNIGCGGDTDPGQS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			'	residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
				sequence		SSQPSQDGQESNVPSVGSLADPDYLNTPQMN
		Γ		1	1	TPVTLNSAAPASNSGAGVLPSPATPRFSVPTP
				ł		RTPRTPRTPRGGGTASGQGSVKYDSTDQGSP
	Į.	İ			ļ	ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLIL
			1			SDSVMNIFKDRNFDSCCICACNMNIKGADVG
	1	1	l		1	1.YIPDSSNEDOYRCTCGFSAIMNRKLGYNSGL
		i	1			FI EDEL DIEGKNSDIGOAAERRLMMCQSTFL
		1	1		}	POVEGTKKPOEPPISLLLLLONOHTQPFASLN
	1	1	1	l	1	FLDYISSNNROTLPCVSWSYDRVQADNNDY
	1	l .	ļ		ľ	WTECENALEOGROYVDNPTGGKVDEALVKS
	1	i				ATVHSWPHSNVLDISMLSSODVVRMLLSLQP
	[1			1	FI OD A JOKKRTGRTWENIOHVQGPLTWQQFH
	1	1]	J	1	YMAGRGTYGSEESPEPLPIPTLLVGYDKDFL1
	1		1	i		ISPFSLPFWERLLLDPYGGHRDVAYIVVCPEN
	1	1		1		EALLEGAKTFFRDLSAVYEMCRLGQHKPICK
ļ		}]	}	}	VLRDGIMRVGKTVAQKLTDELVSEWFNQPW SGEENDNHSRLKLYAQVCRHHLAPYLATLQL
İ	1	1				DSSLLIPPKYQTPPAAAQGQATPGNAGPLAPN
		1				GSAAPPAGSAFNPTSNSSSTNPAASSSASGSSV
				l		PPVSSSASAPGISQISTTSSSGFSGSVGGQNPST
1			1	1.	1	GGISADRTOGNIGCGGDTDPGQSSSQPSQDG
ł	ł	1	1			ORSVTERERIGIPTEPDSADSHAHPPAVVIYM
	1			İ		VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD
ì	1				Ì	AT DELIMPNISHI OTVPCOYMLOTMKDEQVEY
		1	1			IOVI KSMAFSVYCOCRRPLPTQIHIKSLTGFGP
		ł	1			AASIEMTLKNPERPSPIQLYSPPFILAPIKUKUI
1		1	1	1		ELGETFGEASQKYNVLFVGYCLSHDQRWLL
		1	,	1		ASCTDLHGELLETCVVNIALPNRSRRSKVSAR
		1	ļ			KIGLQKLWEWCIGIVQMTSLPWRVVIGRLGR
	}	1	ĺ			LGHGELKDWSILLGECSLQTISKKLKDVCRM CGISAADSPSILSACLVAMEPQGSFVVMPDAV
1		1		1		TMGSVFGRSTALNMQSSQLNTPQDASCTHIL
1		1	1	1	i	VFPTSSTIQVAPANYPNEDGFSPNNDDMFVDL
	,	1	1	1		PFPDDMDNDIGILMTGNLHSSPNSSPVPSPGSP
1		1			j	SGIGVGSHFOHSRSOGERLLSREAPEELKQQP
	1	1				I ALGVEVSTAKAENLPOWEWSSCPUAUNIQU
		ł		ļ		DI FI KASI HHHISVAOTDELLPARNSQRVPHP
1	•	Ì	1	İ	j	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD
1	Í	1				RTSCLPVHFVVLTOLYNAIMNIL
<u> </u>	10154	A	6732	2440	365	VEEGLGRRRTPPGGRRGPVTPARPGPDSVKK
824	2174	^	10/32	1		PI I PPSSA A A FSSHRHNLLCSRRRGGGGGGGG
				1	1	GGGGGTIKRPGITGPTAATSPSGEPGNAASAP
1	1	1		1	ł	LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC
1		ì				ASLVFGRLQHRGGDRKRGLLGRSSGDAASD
		1		Į.	1	QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG
j		1	}	1		GLAAREGNVKVLRKLLKKURSVDVADING WMPIHEAAYHNSVECLQMLINADSSENYIKM
		1		1		KTFEGFCALHLAASQGHWKIVQILLEAGADP
1			1		1	NATTLEETTPLFLAVENGQIDVLRLLLQHGAN
	1	1	1	1	1	VNGSHSMCGWNSLHQASFQENAEIIKLLLRK
1				1	}	GANKECODDEGITPLEVAAOYG\KLESL\SILIS
1				1		COLANDATOR ATPLFIAAOEGHTKCVELL
1			1		1	T CCCADPDLYCNEDSWOLPHAAAQMGHINI
1	- [-			1	I DI I IDI TNIR ACDTGI NKVSPVYSAVEGUHE
1	1					DOT ETT I RNGYSPDAOACLVFGFSSPVCMAFQ
.		1	1	1		L NDCEEECIVNII I KYGAOINELHLAYULKIEN
1				1		POTED VET DICCOL GPWNHIYEFVNHALKAQA
				l		KAKEMI BHI TAYAGEDEFITTCURMING A2ID I
					- {	I IETI EETNWKTI APAVERMLSAKASNAWIL
		- [{	1		QQHIATVPSLTHLCRLEIRSSLKSERLRSDSYIS
(1					

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seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
401100	ļ	ì		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
	}	1	1	peptide	ł	nucleotide insertion
1 .	ļ	l		sequence		QLPLPRSLHNYLLYEDVLRMYEVPELAAIQD
						(-
ĺ		l	l			G RIMGLFDRGVQMLLTTVGAFAAFSLMTIAVG
825	2175	A	6735	277	1252	TDYWLYSRGVCKTKSVSENETSKKNEEVMT
		1		1	1	HSGLWRTCCLEGNFKGLCKQIDHFPEDADYE
1	İ		i			ADTAEYFLRAVRASSIFPILSVILLFMGGLCIA
	Į.			ł		ASEFYKTRHNIILSAGIFFVSAGLSNIIGIIVYIS
		ļ			ļ	ANAGDPSKSDSKKNSYSYGWSFYFGALSFIIA
į		1		1	j	FMVGVLAVHMFIDRHKOLRATARA\TDYLQ
1	1	l		1.		ASAITRIPSYRYRYORRSRSSSRSTEPSHSRDA
1	1	1	1	i	,	SPVGIKGFNTLPSTEISMYTLSRDPLKAATTPT
1	1		1			ATYNSDRDNSFLQVHNCIQKENKDSLHSNTA
ì	ł		1	1		NRRTTPV
00.5	2176	A	6744	3	5177	SDDLRTGLFODVODAESLKLPGVYEVLFYNE
826	21/0	^	0/44	1		TEDCPGMMLWRYPEPRGLTLVRITPVPFNTT
Ì	1	1		1	1	EDPDISTADLGDVLQDPCSLEYWDELQKVFV
		1		i		AFREFNLSESKVCELQLPDINLVNDQKKLVSS
		1	1	1		DLWRIVLNSSQNGADDQSSASESGSQSTCDPL
1		1				VTPTALAACTRVDSCFTPWFVPSLCVSFQFAH
	ļ	ļ	ł	1		LEFHLCHHLDQLGTAAPQYLQPFVSDRNMPS
i	Ì	l	1	ļ		ELEYMIVSFREPHMYLRQWNNGSVCQEIQFL AQADCKLLECRNVTMQSVVKPFSIFGQMAVS
1	ŀ			ì		SDVVEKLLDCTVIVDSVFVNLGQHVVHSLNT
1			1	ł	1	AIQAWQQNKCPEVEELVFSHFVICNDTQETL
i		1				RFGQVDTDENILLASLHSHQYSWRSHKSPQL
		1]	}	1	LHICIEGWGNWRWSEPFSVDHAGTFIRTIQYR
· ['	-	1			GRTASLIIKVQQLNGVQKQIIICGRQIICSYLSQ
		1	1			STELK V V OHYIGODGO AV V REHFD CLTAK QK
	1	l		i	1	LPSYILENNELTELCVKAKGDEDWSRDVCLE
Ì		ļ	Ì	i	1	SKAPEYSIVIOVPSSNSSIIYVWCTVLTLEPNS
}		1	-	1	1	OVOORMIVESPLEIMRSHLPDPIIIHLEKRSLGL
	1		1		ļ	SETOTIPGKGOEKPLONIEPDLVHHLTFQAREE
1	1		1		ì	VDPSDCAVPISTSLIKOIATKVHPGGTVNQILD
-				Ì		FEVGPEKSLOPIWPYNKKDSDRNEQLSQWDS
	1	1		1		PMRVKLSIWKPYVRTLLIELLPWALLINESKW
	1	1	1	ĺ		DLWLFEGEKIVLQVPAGKIIIPPNFQEAFQIGIY
	1	1		1		WANTNTVHKSVAIKLVHNLTSPKWKDGGNG
1		Į.	-			EVVTLDEEAFVDTEIRLGAFPGHQKLCQFCIS
		Ì	1	İ		SMVQQGIQIIQIEDKTTIINNTPYQIFYKPQLSV CNPHSGKEYFRVPDSATFSICPGGEQPAMKSS
		İ	ļ	1		SLPCWDLMPDISQSVLDASLLQKQIMLGFSPA
			ł		l l	PGADSSQCWSLPAIVRPEFPRQSVAVPLGNFR
}	1	1	1	1		ENGFCTRAIVLTYQEHLGVTYLTLSEDPSPRV
		1		1	4	THINR CPVKMLIKENIKDIPKFEVYCKKIPSECS
				1	1	THHELYHOISSYPDCKTKDLLPSLLLRVEPLDE
1				1		VTTEWSDAIDINSOGTOVVFLTGFGYVYVDV
		ł	1	1	1	VHOCGTVFITVAPEGKAGPILTNTNRAPEKIV
		1		1	1	TEIKMEITOLSLAVEDDLTHHKASAELLRLTL
1		ì				DNIFL CVAPGAGPLPGEEPVAALFELYCVEIC
		-	-	1	1	CGDLOLDNOLYNKSNFHFAVLVCQGEKAEPI
	ì	1		1	1	OCSKMOSLLISNKELEEYKEKCFIKLCITLNEG
		-	1	1		KSILCDINEFSFELKPARLYVEDTFVYYIKTLF
1	ĺ	1		1	1	DTYLPNSRLAGHSTHLSGGKQVLPMQVTQH
	1		1	1		ARALVNPVKLRKLVIOPVNLLVSIHASLKLYI
1	1		1	1		ASDHTPL SESVEERGPIFTTAROLVHALAMHY
-	1	- 1	1	Į.		A AGAI FRAGWVVGSLDILGSPASLVRSIGNG
				1	1	VADFFRLPYEGLTRGPGAFVSGVSRGTTSFVK
1		- [1		1	HISK GTI TSITNI ATSLARNMDRLSLDEEHYN
						ROFEWRROLPESLGEGLROGLSRLGISLLGAI
		ı		1		AGIVDQPMQNFQKTSEAQASAGHKAKGVISG
1	- 1	1	1			

					Deadlesed and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ.	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1	ĺ		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
1		1	}	residue of	sequence	Y=1yrosine, X=Unknown, Y=Stop codon,
l	1	1]	peptide		/=possible nucleotide deletion, \=possible
İ		1	ì	sequence		nucleotide insertion
	+					VGKGIMGVFTKPIGGAAELVSQTGYGILHGA
1		1	ł	1	ŀ	GLSQLPKQRHQPSD\VHADQAPNSHVKYVW
		j		j		KMLQSLGRPEVHMALDVVLVRGSGQEHEGC
	{	1		i]	LLLTSEVLFVVSVSEDTQQQAFPVTEIDCAQD
	1	1		ļ		SKQNNLLTVQLKQPRVACDVEVDGVRERLSE
1	l	i]		OOYNRI.VDYITKTSCHLAPSCSSMQIPCPVVA
į.			1	ì	,	AEPPPSTVKTYHYLVDPHFAQVFLSKFTMVK
1	1	İ			}	NKALRKGFP
·				<u> </u>	1662	FVGAPRRGNPFGSPGNPGRHQGPCHRPRGTK
827	2177	Α	6748	2	1002	ASGVSPTLWRPQAAATGLEMPSSGRALLDSP
	1	1	1		1	LDSGSLTSLDSSVFCSEGEGEPLALGDCFTVN
1		1		1	1	VGGSRFVLSQQALSCFPHTRLGKLAVVVASY
1		1	1	1		RRPGALAAVPSPLELCDDANPVDNEYFFDRS
1			1	}	1	SQAFRYVLHYYRTGRLHVMEQLCALSFLQEI
1 .			1	i	1	SAME ATUI I KIOKTUANTA COLORDA ANTONIO
		1	1	1	i	QYWGIDELSIDSCCRDRYFRRKELSETLDFKK
1		1	1	1	1	DTEDQESQHESEQDFSQGPCPTVRQKLWNIL
1	1	1		1		EKPGSSTAARIFGVISIIFVGVSIINMALMSAEL
1	1	Į.	Ì	l	[SWLDLQLLEILEYVCISWFTGEFVLRFLCVRD
1	1	ĺ	1	1	1	RCRFLRKVPNIIDLLAILPFYITLLVESLSG\SQT
1			1	1		TQEL\ENVGAHCPGCLRLLRAL\RMLKAWGR
		1	1	ł		HSTGLRSLGMTITQCYEEVGLLLLFLSVGISIF
		1		k		STVEYFAEQSIPDTTFTSVPCAWWWATTSMT
1	1	1	1			TVGYGDIRPDTTTGKIVAFMCILSGILVLALPI
ļ			1			AINTORESACYFTLKLKEAAVROREALKKLIK
1	Ì	1		1		NIATDSYISVNLRDVYARSIMEMLRLKGRER
1		1	1	ì] .	ASTRSSGGDDFWF
	1	+	(700	5672	1360	GTHPASSGPVPLPPAAVSAATREELGEPVPFV
828	2178	A	6786	3072	.500	TASSGFOSMHSSNPKVRSSPSGNTQSSPKSKQ
1	1				1	FVMVRPPTVMSPSGNPOLDSKFSNQGKQGGS
		1		1	i .	ASOSOPSPCDSKSGGHTPKALPGPGGSMGLK
1		ì			}	NGAGNGAKGKGKRERSISADSFDQRDPGTPN
-	1			140		DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT
				ļ	1	APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS
		})	j		TEMANKAAEAVLKGQVETIVSFHIQNISNNK
				1		TERSTAPLNTQISALRNDPKPLPQQPPAPANQ
1	1	1		1	1	DONSSONTRLOPTPPIPAPAPKPAAPPRPLDRE
	1			ĺ	1	SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN
	1	J		1	1	NRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPT
Ì	1		1]		LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP
-	.1			1	1	PARABAC Y OCCUDONIDATA DEPORTABLES
}	}	1		1		DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI
1	1	1		1	1	QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR
		1		1		DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP
		1		1		EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ
1		1)	1	ŀ	DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP
		-		1		GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ
1	1	1 '	l	1		MRI.PGFAGMINSEMEGPNVPNPASRPGLSGV
	- 1	1		1	1	SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP
	1	1		1	1	NPOGL SEEMFOOOLAEKOLGLPPGMAMEGIK
		1		1		PSMEMNRMIPGSORHMEPGNNPIFPRIPVEGP
	1			1 .	1	1 SPSRGDFPKGIPPOMGPGRELEFGMVPSGM
1				J	1	K CDVNI NVNMGSNSOMIPOKMREAGAGPEE
1		{	[1	1	MI KI PPGGSDMLPAOOKMVPLPFGEHPQQE
-		- 1			1	YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDQ
		-	}	1.	}	RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG
1	1	1	1	l l		KINSKLSHWIFFLINGSSWF1SCWIMI VQKO
ì			1	1		LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ
		- 1		1	1	SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA
		1	1	1		SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS
	Ì	Ì	i	1		PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG
	-			1		GPPPPTASOPASYNIPG\SLPSSTPYTMPPEPIL
1		1			1	SQNPLSIMMSR\MSKFAM\PS\SNPGYNHDAI
1	- 1	- 1	1	I	I	

			T	N	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A enertic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	ļ	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ.	1			residue of	sequence	/=possible nucleotide deletion, \=possible
	l	1		peptide		nucleotide insertion
		l	· .	sequence		KTVASSDDDSPPARSPNLPSMNNMPGMGINT
		 				KTVASSDDDSPPARSPNLPSWINNWFGWGWY
	l	ŀ				QNPRISGPNPVVPMPTLSPMGMTQPLSHSNQ
		ĺ				MPSPNAVGPNIPPHGVPMGPGLMSHNPIMGH
		1				GSQEPPMVPQGRMGFPQGFPPVQSPPQQVPFP
ļ		1		İ		HNGPSGGQGSFPGGMGFPGEGPLGRPSNLPQ
ļ.	1	j	1			SSADAALCKPGGPGGPDSFTVLGNSMPSVFT
	1	1	ľ	ł		DPDLQEVIRPGATGIPEFDLSRIPSEKPSQTLQ
1	l l	1	1	1		VERR GEVEGRKOPOGPGPGFSHMQGMMGEQ
	ĺ	l	1	1		APRINGLALPGMGGPGPVGTPDIPLGTAPSMP
	1	1	l			GHNPMRPPAFLOOGMMGPHHRMMSPAQST
İ	1	İ	1			MPGQPTLMSNPAAAVGMIPGKDRGPAGLYT
	ì	1	1	İ	Į	HPGPVGSPGMMMSMQGMMGP\NRTS
	ŀ	}			<u> </u>	ASFFNFSICICKIILEVGPPVGHPAHDDVGGRH
829	2179	A	6797	433	3	GPGGR/GSRSPRSLQCAPGGGRRSGCPAGSSP
1				1	l	ASTCPPSPGGSGADRFGPSPPPPSREAAPTAG
1	İ	ì			1	AAASSTSSGASCPPVPASSRWGVRSRTRSGSG
	1	1			Ì	AAASSISSUASCITVIASSKWUVIOKINGGG
1	1	1		l .		GEREPRORPSERPRLV
830	2180	A	6800	3	1911	LPERAFGPRTPRAPRRRRRLLLSPPPRPPPPL
830	2160	1.	1			DREPRAPGPWLCPSRAGTAQDPARIRERRGR
	1	ľ				VAGGAAGPAMELRARGWWLLCAAAALVAC
	1	1	1	1		ARGDPASKSRSCGEVRQIYGAKGFSSS\DVPQ
			ļ	Į.	1	AEISGEHLRICPQGYTCCTSEMEENLANRSHA
	i	1		1		ELETALRDSSRVLQAMLATQLRSFDDHFQHL
	1	1				I NIDSERTI OATFPGAFGELYTQNARAFRULY
1	i	1		i		SELRLYYRGANLHLEETLAEFWARLLEKLFK
	1	1				OLHPOLLLPDDYLDCLGKQAEALRPF\GEAP\
1	Į.	l				DET DI RATIRAIFVAARISFVOGLGVASIDVVR
1	ŀ	1	ļ	1		KVAOVPLG\PEC\SRAVIEAGSYC/ALHCVGYP
	1				1	GARPCPDYCRNVLKGCLANQADLDAEWKNL
ľ			1	i i	,	LDSMVLITDKFWGTSGVESVIGSVHTWLAEA
1						INALQDNRDTLTAKVIQGCGNPKVNPQGPGP
						EEKRRRGKLAPRERPPSGTLEKLVSEAKAQL
1	1	1	1		1	RDVQDFWISLPGTLCSEKMALSTASDDRCWN
1		l l	ł			GMARGRYLPEVMGDGLANQINNPEVEVDIT
		1	ĺ	1		KPDMTIRQQIMQLKIMTNRLRSAYNGNDVDF
		l l		1	1	QDASDDGSGSGSGDGCLDDLCGRKVSRKSSS
}		1	ì	1		QDASDDGSGSGSGSGDGCCDDCCGCCVGCVGGCSGS
		1			1	SRTPLTHALPGLSEQEGQKTSAASCPQPPTFL
		1		1	1	LPLLLFLALTVARPRWR
921	2181	A	6808	2	1522	ASRHGMTPGALLMLLGALGPPLAPGVRGSEA
831	2101	1 ~	5550		İ	EGRLREKLFSGYDSSVRPAREVGDRVRVSVG
-	1	1				LILAQLISLNEKDEEMSTKVYLDLEWTDYRLS
	1	1				WDPAEHDGIDSLRITAESVWLPDVVLLNNND
1						CNEDVALDISVVVSSDGSVRWOPPGIYKSSCS
1	1	l	-	1		IOVTVEPEDWONCTMVFSSYSYDSSEVSLQT
			Ì		,	GI GPDGOGHOFIHIHEGTFIENGOWENIHKPS
			- 1			RI TOPPGOPROGREGOROEVIFYLIIKKKPLFY
			1			I MAINTAPCII ITI LAIFVFYLPPDAGEKMGLSIF
		1	}	1		ALL THE TWELL LLADK VPETSLS VPIIKYLMET
		1	1			LAND VITESTII SVVVI NLHHRSPHTHOMPLWV
		1			1	POTEITIKI PLYLRI KRPKPERDLMPEPPHCSSP
1		-		1		CONCRETEFIER KPPSDFLFPKPNKFQPEL
1	1	1			1	SAPDLRRFIDGPNRAVALLPELREVVSSISYIA
1	1			1	1	RQLQEQEDHDALKEDWQFVAMVVDRLFLW
1	1	1		1		KOLOEGEDUNALVED MALAVIA A PROPER
1		}		i		TFIIFTSVGTL\VIFLDATYHLPPPDPFP
020	2102	HA-	6824	71	1079	ETMAKNPPENCEDCHILNAEAFKSKKICKSLK
832	2182	1^	0024	1.2		ICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
1	1	1		1	1	DMEHTEVSNGEKKKTYMEIDPVTRTEIFRSGN
	l		1	1	1	CTDETI EVHDEKNGYTGIYFVGLOKCFIKIQI
-		1	1	- 1	1	LANDERSEPEREIDENEEITTIFFEOSVIW VPAL
4	1	1			1	KPIENRDFLKNSKILEICDNVTMYW\INPTL\IS
1		ı	1			

SEQ ID Mot bod b							La lun add namer as /A-Alanina C-Custaina
NO. of mucle of the sequence o	SEO ID	SEQ ID	Met		Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
uence wilde sequence whether the corresponding overspondi			hod				D=Aspartic Acid, r=Glucine H=Hictidine
uence 1914 of	nucl-	peptide	l				r=rnenylalanine, o=olycine, n=ristianie,
uence 1914 1914 2 2 2 2 2 2 2 2 2	eotide	seq-	[-			M-Methionine N=Acorporine P=Proline
mino acid residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per company to the peptide sequence per company to the period sequence per company to the per company to the period sequence per company to the period sequ	seq-	uence					O-Glutamine R=Arginine S=Serine
residue of peptide sequence peptide sequence peptide sequence sequ	uence		1	914			T-Throning V-Veline W-Trystophen
Popsible muleotide delation, Possible muleotide insertion mu	1		1	Ì		of pepude	V-Typeoine Y=Inknown *=Ston codon
			1			sequence	/
	1	İ	l	1			numbertide insertion
ANEKKĞIEONEOWYPOYXVEKTRHARQAS SEELPINYTHONEEPPM_DERGYCCYCYCRR GRYCYRYCEPLLGYYPYPYCYQGGRYICRV MPCDYWYARM.LGRV		<u> </u>	<u> </u>		sequence		CTEANOLUDIEARIU VERI ODEEERGEDI HEP
BEELPRIDTYTENGIEFDPM.DERGYCCTVCRR GRYCRYCEPLLGYPYPYPYCYCGGRYICRY MPCNWWYARM.GRY			ļ	1		1	ANTERCONTENTAL ILLA OLLO DE LA DECLA DELLA
B33 2183 A 6846 116 602 GRYCKTRIVCEPLLGYYPTYPYCYGGGRVICRY MPCNWYARMLGRY		}	1				CEET PINIDYTENGIFFOPMI DERGYCCIYCRR
BMPCNWWARMLGRY		1	i	i	Í	[CARRYCERI I GVVPVPVCYOGGRVICRV
833 2183 A 6846 116 602 EAEGEQVOGAKCGDAPHVENREETARICS GVAENCERAL INLIVENVIQUENDEKDEKE QVANKGEPLAL PLINVSEVCYPRORNERSPR QPLQYRWDIMHELGEPQARMERIGE EVRQLMEKLREKQLSHSLRAVSTDPPHHDHH DEFOLMP			l		1		IMPCHWWVARMI GRV
33 2183 A 6851 3 2024 PROVINCIEUD RENDER Q'ANAKGEPLALPIN'SECVPREGRIRRERUR Q'ANAKGEPLALPIN'SECVPREGRIRRERUR Q'PILOYEWOIMHELGEPQARMEEN MERIGE EVRQUMEKLREKQLSHSLRAVSTOPPHHONDER PRIGVALLILIFGAAVIPNTNYMFQDALGGRSR GREESPAPSRAPASASLWERLVVVAAKMAA HAAAAAQAAAAAQAAHAAAADSWYLALLGF AHFTSSPPKIRLCYVELQAVPFPROREA RTHILQLGSVLYHHTIKNSEQARSHILEKAWLIS QIPPOFEDWEFBAASLISELYQCHSVDAAKP LIVAAQAAQAAHAAAAASUNGASHILEKAWLIS QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAASLISELYQCHAQUHTHLISL QIPPOFEDWEFBAALHISLISK QIPPOFEDWEFBALFIRLISL QIPPOFEDWEFBALFIRLISL QIPPOFEDWEFBALFIRLISL QIPPOFEDWEFBALFIRLISL QIPPOFEDWEFBAASLISELYQCHAQUHSCHISL QIPPOFEDWEFBAASLISELYQCHAQUHSCHISL QIPPOFEDWEFBAASLISELYQCHAQUHSCHISL QIPPOFEDWEFBAASLISELYQCHAQUHSCHISL QIPPOFEDWEFBAASLISELYQCHAQUHSCHISL QIPPOFEDWEFBAASTUR QIPPOFENDER PRESEPSWEMEKVOFEDWEFBAASTUR QIPPOFENDER PRESEPSWEMEKVOFEDWEFBAASTUR QIPPOFENDER PRESEPSWEMEKVOFEDWEFBAASTUR QIPPOFENDER PRESEPSWEMEKVOFEDWEFBAASTUR QIPPOFENDER PRESEPSWEMEKVOFEDWEFBAASTUR QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER QIPPOFENDER		<u> </u>				602	FARGEOVCGAKCCGDAPHVENREEETARIGP
QVANKGEPLALPILNYSEYCVPRGNRRRRIGE QPILQYWWDIMHELGEPQARMERIGE QPILQYWWDIMHELGEPQARMERIGE PYRQLMEKLREKQLSHSLRAVSTDPPHHDHH DEFCLUM BIFCLUM PRIGVALLHILPGAAVIPNTNYMFQDALGGRSR GSREESPAPSRAPASASLWRRLVVVEAKMAH AAAAAQAAAQAHARAADSWYLALLIGF AEHFFTSSPKIRLCYHCLQAVPFPKPPQRE RTHILQLGSVLYHHTKNSEQARSHLEKAWLIS QQIPQFEDWKFRAASLISLLYCQENSVDAAK RHALQLGSVLYHHTKNSEQARSHLEKAWLIS QQIPQFEDWKFRAASLISLYCQENSVDAAK LYACACHILLEKO LYACACHILL	833	2183	A	6846	110	002	GYMESKEER AL NNLIVENVNOENDEKDEKE
			İ		Í		OVANKGEPLALPLNVSEYCVPRGNRRRFRVR
834 2184 A 6851 3 2024 PINGVALLHLPGAAVIPNTNYMFODALGERS GSREESPAPSRAPASASLWRRLVVVVEAKMAA HAAAAAQAAAAAQAAHABADSWYLALLGF AEHFRTSSPKIRLCVHCLQAVPFKPPQREA RTHLQLGSVLYHHTKNSEQARSHLEKAWLIS QQPQFGEDVKFEAASLLSELVQENSVDAKP LIKRKAJQISQOTPYWHCRLIFOLAQLHTLEKD LVSACDLLGVGAEYARVVGSEYTRAKFLISK GMLLLMFRKLQEVPHLTLCGQIVENWQGM PIQKESLRVPFLVLQVTHYLDAGQVKSVKPC LKQLQQCIQTISTLHDDELPSNPADLFHWLP KEHMCVLVYLVTVMHSMQAYLEKAQKYT DKALMQLEKLKMILDCSPILSSFQVILLEHIM CRLVTGHKATALQEISVCLQCQSPRIFSN HAQLHTLIGLYCVSVNCMDNAEAGFTTAL RLTNHQELWAFIVTNLASVYLGCHQASVKPC LKQLQCTLCQSPRIFSN HAAQLHTLIGLYCVSVNCMDNAEAGFTTAL RLTNHQELWAFIVTNLASVYLGHMSATALQEISVCLQCQSPRIFSN GRIVTGHKATALQEISVCLQCQSPRIFSN HAQQLHTLIGLYCVSVNCMDNAEAGFTTAL RLTNHQELWAFIVTNLASVYLGHMSAKFLRETIKMSNAEDLINKITA CSLVLLGHFFVLGNHEESINNMVVPAMQLAS KIPDMSVQLWSSALLRDLNKACGNAMDAHE AQAMHQNFSQQLLQDHIERGRHGEVV LYSLLERINFQDLLQTHACASTSE LYSLULGHFFVLGNHEESINNMVVPAMQLAS KIPDMSVQLWSSALLRDLNKACGNAMDAHE AQAMHQNFSQQLLQDHIERGHRHGEV SAVYPCQTQDRDAIRLTLEQIDLIRMACSTSE LELVTSAKALNDTQKLACLIQVEGGHSLDNS LSLRTTYMG.GVRVLTLTHTCNTFWASSAK GVHSFYNNISGLTPFGGKVYAEMNRLGMMV DLSHYSDAVARRALEVSQAVIFSISAARGV CNSARNVPDDLQLLEEERWAFMVSLFHGE LQWQPRPMCSTVADHFDHKAVIGSKFGG GGDVDGAGKYRKKTCAPWRTSSMARGV CNSARNVPDDLQLLEEERWAFMVSLFHGE LQWQPRPMCSTVADHFDHKAVIGSKFGG GGDVDGAGKYRKKTCAPWRTSSMARGM CNSARNVPCQTGPGGGRPP VLRGQRGGGAGKYRKKVVPGGRSWWGGTGPFGQ RPEIRLLPLPMTGACGAVAASRTGSSGGGSSL PNGGGGGGSLDAGLAGNPGHLGLGSSFGT LYRQGGGGGAGKYGLAGHAGNPGHLGLGSSFGT LYRQGGGGGAGKYGLAGHAGNPGHLGLGSSFGT LYRQGGGGGAGKTGLAGNPGHLGLGSSFGT LYRQGGGGGAGAGAGAAGARAFTAGGAMA AKDRINGTMA AKDNELWTPLHAAATCGHANVA AKDNELWTPLHAAATGHAAAFWGQMAB LLUSHGANWA					1		OPIL OVEWDIMHELGEPOARMREENMERIGE
DEFCLMP		1	}	1			EVROI MEKI REKOLSHSLRAVSTDPPHHDHH
834 2184 A 6851 3 2024 PNGVALIHLPGAAVPINTNYMFODALGGRSR GSRESPAPSAPASASLINERILVVCEAKMAA HAAAAAQAAAAQAHABAADSWYLALLGF AEHFRTSSPEKIRLVVCHAGKAYPFKPPQRIBA RTIHLQLGGVITYHHKNISEQARSHLEKAWLIS QQPQFEDVKFEAASLLSELVCQENSVDAAKP LIRKAQISQOTTYWHKCHLCAQVEPWQGA QQPQFEDVKFEAASLLSELVCQENSVDAAKP LIRKAQISQOTTYWHKCHLCAQVEPWQGA PLACQIVTYWHCHLACQIVEPWQGA PLACQIVTYWHCHLACQIVEPWQGA PLACQIVTYHTYLDAGQWSSVAPC LKQLQQQTISTILDDELPSNPADLFHWL KEHMCVLVYLVTVMHSMQAGYLEKAQKYT DKAALMQLEKLKMLDCSPLSSFQVILLEHIM CRLVTGHKATALQEISQVCQLQQSPRLFSN HAQLHTLIGLVCVSVNCMDNABAQFTTAL RLTNHQELWAFIVTILASYVALCHIM CRLVTGHKATALQEISQVCQLCQQSPRLFSN CRLTGHWYTYLAGAFYVAGLF SFFQGRYNBAKRFLRETLKMSNAGDLNRLTA CSLVLLGHIFYVLGNHRESSNNMVYPAMQLAS KIPDMSVQLWSSALLRDLNRACGNAMDAHE AQMHQNFSQQLLQDHIBEAGRHGEVY LYSLLERINPDHSFPVSHCLRAAAFYVRGLF SFFQGRYNBAKRFLRETLKMSNAGDLNRLTA CSLVLLGHIFYVLGNHRESSNNMVYPAMQLAS KIPDMSVQLWSSALLRDLNRACGNAMDAHE AQMHQNFSQQLLQDHIBEAGSLFERNLTIVTT DGPPPVQFQAONGPNTSLASLL TRIPPPLPLTSRAISVSPPLQGKQHTLVKSCL SVSGIGGFLVSLSSRMKLQTLAVSVTALKFWS AYVPCQTQDRDALRLTLEQIDLIRRAMCASYSE LELVTSAKALNDTQKLACLIQVEGGHSLDNS LSLRTTYMG.GVRTLLTHTCNTFWABSSAK GVHSFYNNISGLTDFGEKVAZHNRIGMMV DLSHVSDAVARRALEVSQAVIFSISAARGV CNSARNVPDDLQLEEERKAVASHARGV CNSARNVPDDLQLLEEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPDDLQLLEERKAVASHARGV CNSARNVPSDLDLQLLEERKAVASHARGV CNSARNVPSDLDLQLLEERKAVASHARGV CNSARNVPSDLQLLLLEHLAAATGV CNASNTGSSCOFGSL PNGHGGGGGLANGLAGNPGHLGLGSSFGT GPGGRPP VLRGQRGGAGAVAAASRTGSSGCFGSSL PNGHGGGGGALAGLARGRAPGHURIDATG QDLAVNSDGMPYDLCEDEPTLDVIETCMAY QGTTQEKNTEMRVAPPGQAMADHCMAAAG QLALAVARTSMDEMPDLCEEERKALLLDH GVRVDVKDWDGWPHAAAAFWASHQAMABHLIDH GVRVDVKDWDGWASHLASSLSGRTIRQA SVGKVVRRTAAAFWASHCAMARTSMDEMPDLCEEEREFKALLLDH GVRVDVKDWDGARATLLARAAFWGGAMAA LLVSHGANUAMARTSMDEMPDLCEEERFKAL LLLDH GVRVDVKDWDGARHKSSLSRATSHRQA SVGKVVRRTAGARGVARAAFKGG	l						
GSREESPAPSRAPASASLWRRLVVVEAKMAA HAAAAQAAAAAQASHAPADSWYLALLGF AEHFRTSSPPKIRLCVHCLQAVPFFKPPORIEA RTHLQLGSVLYHHTKNSEQARSHLEKAWLIS QOPOFEDVKFEAASLLSELVCQENSVDAAKP LIRKAQISQQTYYWHCRLLFQLAQLHTLEKD LVSACDLLGVGAEYARVVGSSYTRALFLLSK GMLLLMBRKLQEVHPLLTLCGQIVENWGN PIQKESLRVFFLVQVTHYLDAGQVKSVKPC LKQLQCQGTISTLHDDEILPSNPADLFHWLP KEHMCVLVYLVTVMSMQAGYJEKAAQKYT DKAALMQLEKLKMLDCSPILSSFQVILLEHIM CRILVTGHKATALQEISQVCQLCQQSPRLFSN HAAQLHTLGLVCVSVNCMDAAQFTTAL RTNHQELWAFIVTHLASVVIREGRRHQEVV LYSLLERINDHSFPVSSHCLRAAAFYVRGLF SFFQGRYNEAKFFLRETLKNSNAEDLINGLTA CSLVLLGHIFYVLGNHFESNNMVVPAMQLAS KIPDMSVQLWSSALIRDLNACGNAMDAHE AQMHQNFSQQLLQDHIBACSLPEHNLITWT DGPPPVQFQAQNGPNTSLASLL SVSGIGGFLVSLSSRNKLQTLAVSVTALKTWS AYVPCOTORDAIATLTEQIDLRRMCASYSE LELVTSAKALNDTOKLACLIGVEGGHSLDNS LSLRTFYMLGVRYLLTHITTPWAESSAK GVHSFYNNISGLTDFGEKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAVIFSHSAARGV CNSARNVPDDIOLQLEEERKWAFVMVSLFHGE GGDVDGAGKYKKKTCKAPWTSSRMSS GVHSFYNNISGLTDFGEKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAVIFSHSAARGV CNSARNVPDDIOLQLEEERKWAFVMVSLFHGE LIQWQPRPMCSTVADHFDHIKAVUGSKFIGI GGDVDGAGKYKKKTTCKAPWTSSRMSS GVHSFYNNISGLTDFGEKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAVIFSHSAARGV CNSARNVPDDIOLQLEEERKWAFVMVSLFHGE GGDVDGAGKYKKKTTCKAPWTSSRMSS THE PRESENCE AND THE PROPERSON OF TH					ļ	2024	PNGVALLHI PGAAVIPNTNYMFODALGGRSR
HAAAAAQAAAAQAAHABAADSWYLALLGF AEHFRTSSPEKIR.CYVICLQAVFPFKPPORIEA RTHLQLGSVLYHHTKNSEQARSHLEKAWLIS QQIPQFEDVKFEAASLLSELYQQENSVDAAKP LLKRAIQISQQTPYWHCKLIPQLAQLHTLEKD LVSACDLLGVGAYYARVVGSEYTFALFLISK GMLLLMERLQEVIPELIT.CGQVPSNWQGN PIQKESLRVFFLVLQVTHYLDAGQVKSVKPC LKQLQQCIQTISTH.DDELLPSIN PALDFHWLIP KEHMCVLYYLVTVMISMQAGYLEKAQKYT DKALMQLEKLKMLDCSPILSSFQVLQLCQOSPLISHIN CRILYTGHKATALQEISQVCQLCQOSPLISHIN CRILYTGHKATALQEISQVCQLCQOSPLISHIN HAAQLHTLLGLYCVSVNCMDMAEAGFTTAL RITNHQELWAFIVTNLASVYIRGINRIQEVVA LYSLLERINPDHSPPYSSHCIRAAAFYYRGLF SFFQGRYNEAKRFLRETLKMSNAEDLNRLTA CSLVLLGHIPYVLGHRIESDNAVYPAMQLAS KIPDMSVQLWSSALLRDINKTACANAMDAHE AAQMIQNFSQQLLQDHEACSLPEHNLITWT CSLVLLGHIPYVLGHRIESDNAVYPAMQLAS KIPDMSVQLWSSALLRDINKACGNAMDAHE AAQMIQNFSQQLLQDHEACSLPEHNLITWT CSLVLLGHIPYVLGHRIESDNAVYPAMQLAS KIPDMSVQLWSSALLRDINKACGNAMDAHE AAQMIQNFSQQLLDHEACSLPEHNLITWT CSLVLLGHIPYVLGHRIESDNAVYPAMQLAS KIPDMSVQLWSSALLRDINKACGNAMDAHE AAQMIQNFSQQLLDHEACSLPEHNLITWT CSLVLLGHIPYVLGHRIESDLINKACSONAMDAHE AAQMIQNFSQQLLDHEACSLPEHNLITWT CSLVLLGHIPYVLGHRIESDNAVYPAMQLAS KIPDMSVQLWSSALLRDINKACSONAMDAHE AAQMIQNFSQQLLDHEACSLPEHNLITWT CSLVLLGHIPYVLGHRIESDLINKACSVTALKFWS AYVPCQTQDRDALRLTLEQUILRRMCASYSE LELVTSAKALNDTQKLACLIGVEGGHSLDNS SYSGIGGFLYSLSSRMKLUTLAVSVTALKFWS AYVPCQTQDRDALRLTLEQUILRRMCASYSE LELVTSAKALNDTQKLACCLIGVEGGHSLDNS SUSGIGGFLYADHFDHIKAVIGSKFIGI GGDYDGAGKYRKTTCKAPWRTSSRMSS GYHSFYNNISGLTDFGEKVVAEMNVSLFHGE LIQWQFIRMCSTVADHFDHIKAVIGSKFIGI GGDYDGAGKYRKTTCKAPWRTSSRMSS RYGFEVURDLPHTGACGAVASRTGSSGFGSSL PNGHGGKGSGLANGLAGNPGHLGLGSSFGT GPGSGRPP WILLIPLMFAGAGAVASRTGSSGFGSSL PNGHGGKGSGLANGLAGNPGHLGLGSSFGT GPGSGRPP VIRGGGGPAGGLAEERRGRNEWRHDVTT APFGLJVGRNSRLLIVSQVYFIKLKVSPDLC NEDGLTALHQCCIDNFEDVYLLISHGANVN AKDNELWYPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMFYDLCEDEFILVELUSHGANVN AKDNELWYPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMFYDLCEDEFITVLUSHCMAY QCITQEKINGMYAPAGQMADAL LLYSHGANNLNARTSNDEQMADHICMMAAGQ DLDWIDAQGATLLHLAGANGYLRAAGLLLDH GVRVDVKDWGWEPHAAAAFWGQMMAE LLYSHGANNLNARTSNDEQMAD	834	2184	A	0821	3	2024	GSREESPAPSRAPASASLWRRLVVVEAKMAA
AEHFRTSSPKILCVHCUQAVFPKPQREAR RTHI, QLGSV, YHHTKNSEQARSHLEKAWLIS QQPQFEDVKFEAASLLSELYCQENSVDAAKP LLRKAIQISQQTPYWHCRLLFQLAQHTLEKD LVSACDLLGVGAEYARVVGSEYTRALFILLSK GMLLLMERKLQEVHPLLTLCGQTVSPWQGN PIQKESLRYFFLVLQVTYLDAGQVKSVKPC LKQLQQCIQTISTLHDDELPSNPADLFHWLP KEHMCVLYYLVTVMHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPLSSFQVILLEHIM CRLVTGHKATALQEISQVCQLCQQSPRLFSN HAAQLHTLLGLYCVSVNCMDMAEAQFTTAL RITHHQELWARTVTNLASVYIREGNRHQEVVA LYSLLERINPDHSFPVSSHCLRAAAFVRGLF SFFCQRYNEAKRFLRETIKMSNAEDLNRLTA CSLVLLGHIFYVLGHRESNNMVYPAMQLAS KIPDMSVQLWSSALLRDLNKACGNAMDAHE AAQMHQNFSQQLLQDHEACSLPENNLITWT DGPPPVQFQAQNGPNTSLASIL SVSGIGGFLVSLSSRMKLQTLAVSYTALKFWS AYVPCQTQDRDALRUTLEQDLIRRACASYSE LELVTSKAKALNDTQKLACLIGVEGGHSLDNS LSILRTFYMLGVRYLTLTHTCNTFWASSAK GVHSFYNNISGLTPGFGEKAVSLERHMACHSVSFAG UNGVPRIFMCSTVADHFDHKAVUSERHGI LIQWQPIRFMCSTVADHFDHKAVUSERHGI LIQWQPIRFMCSTVADHFDHKAVUSERHGI GGDYDGAGKYRKKTTCKAPWRTSSRMSS PNGHGKGSGLANGLAGNPGHLGLGSSFGT GPGSGRPP 836 2186 A 6862 315 11 PPRSRFSCWRKKVGPGRPWWASHFIGS LIQWQPRFMCSTVADHFDHKAVUSERHGI GGDYDGAGKYRKKTTCKAPWRTSSRMSS PNGHGKGSGLANGLAGNPGHLGLGSSFGT GPGSGRPP 837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRRGRNEWRIHDVTT APFFGLVQRRSRLLIVSQVRYFLKNYSPLC BEGLTALHQCCIDNFEEDVILLISHGANVN AKDNELWTPLHAAATCGHINLVKLVQYGA DLLAVNSDGNMPYDLCEDEFIVLULISHGANVN AKDNELWTPLHAAATCGHINLVKLVQYGA DLLAVNSDGNMPYDLCEDEFIVLULISHGANVN AKDNELWTPLHAAATCGHINLVKLVQYGA DLLAVNSDGNMPYDLCEDEFIVLULISHGANVN AKDNELWTPLHAAATCGHINLVKLVQYGA DLLAVNSDGNMPYDLCEDEFIVLULISHGANVN AKDNELWTPLHAAATCGHINLVKRYSPLC GGTQEKRMRVAPPQQMMADHCMTAAAQ QLDWDAQQATLIHAGANGYLRAAABLLDH GVRVDVKDWDGWEPLHAAAFWQQMMAB LLVSHGANNLNARTSMDEMPIDLCEEEFKVL LLELKVHKHDVMKSQLRHKSSISRTSHRQA SKYGKVVRTDVPGTOPNLLYKREYYEGERAI	1		1		1		HAAAAAQAAAAQAAHAEAADSWYLALLGF
RTHLQLGSVLYHHTKNSEQARSHLEKAWLIS QQPQFEDVKFRAASLLSELYCQENSVDAAKP LLRRAQISQQTPYWHCRLLFQLAQLHTLEKD LVSACDLLGYGAEYARVVGSEYTRALFLLSK GMLLIMERKLQEVIPELITLGGQIVENWQGN PIQKESLRVFELVLQVTHYLDAGQVKSVKPC LKQLQQCIQTISTH.HDDELSPRADLFHWLP KEHMCVLYYLVTVMHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPLSSFQVULLEHIM CRLVTGHKATALQEISQVQLCQQSPRLFSN HAAQLHTLLGLYCVSVNCMDNAAGQFTTAL RLTHHQELWAFIVTNLASYVIREGNRHQEVVA LYSLLERNPDHSFPVSSHCLRAAAFYVRGLF SFFQGRYNEAKRELRETLKMSNAEDLINLTA CSLVLLGHIFYVLGHRIESNMVVYPAMQLAS KIPDMSVQLWSSALLRDINKACGNAMDAHE AAQMHQNFSQQLLQDHESNSMXLSCLFEINLITWT DGPPPVQFQAQNGPNTSLASLL 835 2185 A 6855 334 1268 PTRRPILPLTSPKAISVPSPLQGKGHTVKSCL SVGLIGGFLYSLSSRMKLQTLAVSYTALKFWS AYVPCQTQDRDALRLTLEQDLIRRACASYSE LELVTSAKALNDTOKLACLIGVEGGHSLDNS LSLRTFYMLGVRYLTLTHTCNTPWAESSAK GVHSFYNNISGLTDFGEKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAFVIFSHSAARGV CNSARNVPDDLQLLEERRWAFVMVSLFHGE LIQWQPIRPMCSTVADHFDHKAVUGSKFIGI GGDYDGAGKYRIKKTTCKAPWRTSSRMSS PREBILLPLPMTGACGAVASRTGSSOPGSSL PNGHGGKGSGLANGLAGNFGHLGLGSSFGT GPGSGRPP VLRGGGRGPAGGLAEERRRGRNEWRHDVTT APFGLJVGRASKLILVSQVRYFLKKNVSPDLC NEDGLTALHJAGANGYLRAAGLLDH GVRVDVKDWDGWEPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMFYDLCEDEFILDVIETCMAY QCITQEKINEMRVAFPGQMIADHHCMIAAGQ DLDWIDAQGATLLHLAGANGYLRAAGLLLDH GVRVDVKDWDGWEPLHAAATWGCHNAAGG DLDWIDAQGATLLHLAGANGYLRAAGLLLDH GVRVDVKDWDGWEPHLYKEYFGERAI					1		AEHFRTSSPPKIRLCVHCLQAVFPFKPPQRIEA
QQIPGFEDVKFEAASILISELYQENSDAAKP LIRKAIQISQITYPWHCRILFQLAQLITIEKD LVSACDLLGVGAEYARVVGSEYTRALFILISK GMLLLMERKLQEVHPILTICQIYENWQGN PIQKESIRVFFLVQVTHYTJDAGQVKSVKPC LKQLQQCIQTISTLHDDELFSPADLFHWILF KEHMCVLVYLVTVMHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPILSSFQVILLEHIIM CRLVTGHKATALQEISQVCQLCQSPRLFSN HAQLHTILGILVCSVNCMDNAEAQFTTAL RITNHQELWAFIVTNLASVYIREGNRIQEVV LYSLLERIPDHSFPVSSHCLRAAAFYVRGLF SFFQGRYNEAKFLRETILKMSNAEDLINLITA CSLVLLGHIFYVLGNHRESNNMVYPAMQLAS KIPDMSVQLWSSALLDIKAGGNAMDAHE AAQMHQNFSQQLLQDHEACSLPEHNLITWT DCPPPVQFQAQNCPNTSLASLI. SIGNIFYMGYDLASSRMKLQTLAVSVTALKFWS AYVPCQTQDRDALRLTLEQDILRRMCASYSE LELVTSAKALNDTQKLACLIGVEGGHSLDNS LSILRTFYMLGVRYLTILTHICTNIPWAESSAK GYHSFYNNISGLTDFGEKVVAEMRILGMMV DLSHVSDAVARRALEVSQAPVIFSHSAARGV CNSARNVPDDILQLLEEERWAFVMVSLFHGE LIQWQPIPMCSTVADHPDHIKAVIGSKFIGI GGDYDGAGKYKKKTTCKAPWRTSSRMSS CNSARNVPDDILQLLEEERWAFVMVSLFHGE LIQWQPRMCSTVADHPDHIKAVIGSKFIGI GGDYDGAGKYRKKTTCKAPWRTSSRMSS PPRSFSCWRKKVGPGRPWWWGGTGPFQGG GFGSGPPP 836 2186 A 6862 315 11 PPRSRFSCWRKKVGPGRPWWWGGTGPFQGG GFGSGPPP 837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRRGNEWRIHDVTT AFFFGLVQRRSRLLINSQVRYFIKNKVSPDL NEGGLTALHQCCIDNFEITYKLLSSRGANNN AKDNELWTPLHAAATCGHNILVKILVQYGA DLLAVNSDGNMPYDLCEDEPTILDVIETCMAY QGITQEKNEMRVAPEQQMIADHCMIAAGQ DLDWIDAQGATLHHAGANGYTRAABLLDH GVVDVVDWDWGGWGTHAAAFWGQMMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELKYHKHDVIMKSQLRHKSSSRRTSSRROSSRSSSRSTSRRSCS		·	ł		ì		RTHLOLGSVLYHHTKNSEOARSHLEKAWLIS
LILRKAIQISQQITPYWHCRLIFQLAQHITLESK UVSCDLLGVGAGYARVVGSEYTRALFILLSK GMLLMERKLQEVHPLLTLCGQIVENWQGN PIQKESLRVFFLVLQVTHYLDAQVKSVKRO LKQLQQCQITSITLHDEILPSNPADLFHWLP KEHMCVLVYLVTVMHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPILSSPQVILLEHIIM CRLVTGHKATALQEISGVCQLCQSPRIFSN HAAQLHTLIGLYCVSVNCMDNAEAQFTTAL RLTNHQELWAFIVTNLASVYIRGGNRIGOEVVA LYSLLERNPDHSFFVSSHCLRAAAFYVRGLF SFFQGRYNEAKRFLRETIKMSNAADLNRLTAL CSLVLLGHIFYVLGHHESNNMVVPAMQLAS KIPDMSVQLWSSALLRDLNKACGNAMDAHE AAQMHQNFSQQLLQDHBACSLPEHNLITVT DGPPVQPQAQNGPNTSLASLL 835 2185 A 6855 334 1268 PTRRPILFITSFKAISVPSPLQGKQHTLVKSCL SVSGIGGFLVSLSSRNKLQTLAVSVTALKFWS AYVPCQTQDRALRILBQIDLIRRMCASVSE LELVTSAKALNDTQKLACLIGVGGHSLDNS LSILRTFYMLGVRYLTLTHTCNTPWAESSAK GVHSFYNNISGLTDFGKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAPVIFSHSAARGV CNSARNVPDDILQLEEREWAFVMVSLFHGE LIQWQPIRPMCSTVADHFDHKAVIGSKFIGI GGDYDGAGKYKKTTCKAPWRTSSRMSS PPRSRPSSCWRKKVFGRFWWWGGTGPFGQG RPEIRLPLPMTGACGAVAASRTGSSGPGSBG 10 VURGGRGGAGGLARGLAGNSPGHLGLGSSFGT GGSGCPPP 878FSSFSCWRKKVFGRFWWWGGTGPFGQG RPEIRLPLPMTGACGAVAASRTGSSGPGSBG 10 VURGQRGPAGGLAEERRGRBWRHDDVTT APFPGLVQRRSRLILVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEIVKLLSHGANNN AKDNELWTPLHAAATCGHNLVKILVQVGA DLLAVNSDGMMPYDLCEEDFTILDVIETCMAY QGITQEKNEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLHHAAATCGHNLVKILVQVGA DLLAVNSDGMMPYDLCEEDFTILDVIETCMAY QGITQEKNEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLHHAAAFWGQMMAE LLVSHGANLNARTSMDEMPIDLCEEEFKUL LSELKYHKHDVIMKSQLRHKSSSRRTSSIRG		}	i				OOIPOFEDYKFEAASLLSELYCQENSVDAAKP
LVSACDLLGVGAEYARVVGSETTRALFILISK GMLLLMERKLGEVPALVTATVHQGN GMLLLMERKLGEVPHLITLCGQIVENWQGN PIQKESLRVFFLVLQVTHYLDAGQVKSVKPC LKQLQQCIQTISTLHEDELLPSNPADLFHWIL KEHMCVLVYLVTWHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPILSSFQVILLEHIM CRIVTGHKATALQEISQVCQLCQQSPRLFSN HAQLHTLIGJVCVSVNCMDNAEAQFTTAL RITNHQELWAFIVTHLASVYIRGBRRIQEVV\		}	1			į	LLRKAIOISOOTPYWHCRLLFQLAQLHTLEKD
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NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DILLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DILDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI	837	2187	A	6863	2	1012	APEDGL VORRSRI LIVSOVR VELKNKVSPDLC
AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI			1		100		NEDGI TAL HOCCIDNFEEIVKI LLSHGANVN
DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA SSVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI		}		1	}		AKDNELWTPLHAAATCGHINI VKILVOYGA
QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA SSVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI				1	1	1	DI I AVNSDGNMPYDI CEDEPTI DVIRTCMAY
DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA SSVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI			1		1		OCTOEKINEMRVAPEOOMIADIHCMIAAGO
GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI	}	1	1		1		DI DWIDA OGATI LHIAGANGVI RAAFI I LDH
LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI			1		1		GVDVDVKDWDGWEPI HA A FWGOMOMAE
LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI	1				1		I I VOUGANI NARTSMOEMPIOI CEFFFEKVI.
S/SVGKVVRRTOPVGTGPNL\YRKEYE/GEEAI	1	1		1	1	l	THE KARKHDAIMK SOI BRKSSI ZB B LZHBUY
LWQRSA\AEDQRTSTYNGDIRET\RTDQENKD	1		1	1	1	1 .	C/CV/GK-VV/RRTOPV/GTGPNI_\YRKEYF/GERAI
LWQNAMEDQRIST MODIFICIALIZATION	1		1	1	1		LWORSA\AFDORTSTVNGDIRFT\RTDOFNKD
	L	<u> </u>		1		J	LANGUSA MELOGICA THOUSING THE STATES

Cono III	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	nence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uence		l	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1	ł		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
1		1		peptide sequence	1	nucleotide insertion
				Sequence		PNPRLEK\PVLLSEFPTKIPRGELDMPVENGLR
	ì	1	1		•	APVSAYOYALANGDVWKVHEVPDYSMAYG
1		ł				NPGVADATPPWSSYKEQSPQTLLELKRQRAA
1	1			İ		AKLLSHPFLSTHLGSSMARTGESSSEGKAPLI
İ	Ì			}	1	GGRTSPYSSNGTSVYYTVTSGDPPLLKFKAPI
1			1			EEMEEKVHGCCRIS
838	2188	A	6865	6291	739	AGPLEPRVQGAMALQLWALTLLGLLGAGAS LRPRKLDFFRSEKELNHLAVDEASGVVYLGA
1		-	1		-	VNALYQLDAKLQLEQQVATGPVLDNKKCTP
		1	1		1	PIEASQCHEAEMTDNVNQLLLVDPPRKRLVE
	}					CGQLLKGI\CALRALSNISLRLFYEDGSGEKSF
	1	ļ	1		ł	VASNDEGVATVGLVSSTGPGGDRVLFVGKG
Į.	Į.	i	}	}	:	NGPHONGITVSTRLLDRTDSREAFEAYTDHAT
		1				YKAGYLSTNTQQFVAAFEDGPYVFFVFNQQD
1					1	KHPARNRTLLARMCREDPNYYSYLEMDLQC
	1	1		ł	1	RDPDIHAAAFGTCLAASVAAPGSGRVLYAVF SRDSRSSGGPGAGLCLFPLDEVHAKMEANRN
	1	1	1		ļ	ACYTGTREARDIFYKPFHGDIQCGGHAPGSSK
ļ		i i		İ		SFPCGSEHLPYPLGSRDGLRGTAVLQRGGLN
	1				1	I TAVTVAAENNHTVAFLGTSDGRILKVYLTP
ì	1	1	1			DGTSSEYDSILVEINKRVKRDLVLSGDLGSLY
	1	1	1		1	AMTODKVFRLPVOECLSYPTCTQCRDSQDPY
		1	1	1	1	CGWCVVEGRCTRKAECPRAEEASHWLWSRS
	i	Į.			ļ	KSCVAVTSAQPQNMSRRAQGEVQLTVSPLPA
	1			1		LSEEDELLCLFGESPPHPARVEGEAVICNSPSS IPVTPPGQDHVAVTIQLLLRRGNIFLTSYQYPF
			1			YDCRQAMSLEENLPCISCVSNRWTCQWDLR
j		1	1	1		YHECREASPNPEDGIVRAHMEDSCPQFLGPSP
1			1			LVIPMNHETDVNFQGKNLDTVKGSSLHVGSD
		1		ļ	ļ	LLKFMEPVTMOESGTFAFRTPKLSHDANETL
		İ	1]		PLHLYVKSYGKNIDSKLHVTLYDCSFGRSDC
		i			1	SLCRAANPDYRCAWCGGQSRCVYEALCNTT
	Į		1	İ	•	SECPPPVITRIQPETGPLGGGIRITILGSNLGVQ AGDIQRISVAGRNCSFQPERYSVSTRIVCVIEA
	1			1	}	AGDIQKISVAGKICSPQFEKTSVSTRAVOTALINA AGDIQKISVAGKISVAGKICSPQFEKTSVSTRAVOTALINA AGDIQKISVAGK
		1		}	•	KPLSVEPQQGPQAGGTTLTIHGTHLDTGSQED
			-	1		VRVTLNGVPCKVTKFGAQLQCVTGPQATKG
		İ	1	1	j	OMLLEVSYGGSPVPNPGIFFTYRENPVLRAFE
1				1	1	PLRSFASGGRSINVTGOGFSLIQRFAMVVIALP
		1				I OSWOPPREAESLOPMTVVGTDYVFHNDTK
	1	1			1	VVFLSPAVPEEPEAYNLTVLIEMDGHKALLKI
		ľ				EAGAFEYVPDPTFENFTGGVKKQVNKLIRAR GTNLNKAMTLQEAEAFVGAERCTMKTLTET
			}	l	1	DLYCEPPEVQPPPKRRQKRDTTHNLPEFIVKF
			}		1	GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM
						VVVIAVSVYCYWRKSOOAEREYEKIKSQLEG
-			1	1		LEESVRDRCKKEFTDLMIEMEDQTNDVHEAG
	1		1	1	[IPVI DYKTYTDRVFFLPSKDGDKDVMITGKL
		1			I	DIPERREVVEOALYOFSNLLNSKSFLINFIHT
-		-				LENOPEFSARAKVYFASLLTVALHGKLEYYT
		-			1	DIMHTLFLELLEQYVVAKNPKLMLRRSETVV
	-				1 .	ERMLSNWMSICLYQYLKDSAGEPLYKLFKAI KHQVEKGPVDAVQKKAKYTLNDTGLLGDD
	1	-				VEYAPLTVSVIVQDEGVDAIPVKVLNCDTISQ
		1				L VERKITO OVYR GOPCSCWPRPDSVVLEWKPG
				1		CTAOTI SDI DI TSOREGRWKRVNTLMHYNVK
						DGATLELSKVGVSOOPEDSOODLPGERHALL
		1			ļ	FEENR VWHI. VRPTDEVDEGKSKRGSVALAL
		-	ĺ	1 '		PTK ATTERVI TRI L SVKGTLOOFVDNFFQSVL
1			1].	APGHAVPPAVKYFFDFLDEQAEKHNIQDEDTI
L						

	•					Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-]	USSN	location	corresponding	J=Isoleucine, K=Lysine, L=Deucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	l			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	i '	İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide		/=possible nucleotide deletion, \=possible
}		1 1	١.			nucleotide insertion
				sequence		HIWKTNSLPLRFWVNILKNPHFIFDVHVHEVV
		İ			1	DASLSVIAQTFMDACTRTEHKLSRDSPSNKLL
l	1	1		l .	}	YAKEISTYKKMVEDYYKGIRQMVQVSDQDM
ł	l	Į.	1	[ļ	YAKEISI YKKIMVEDI I KUIKQIMVQ VSDQDIM
1		1		1		NTHLAEISRAHTDSLNTLVALHQLYQYTQKY
1	1		l			YDEINALEEDPAAQKMQLAFRLQQIAAALE
ì	1	l .	ļ	1		NKVIDL
		 	6872	1	1485	RARRLALQCHVCVCALTPGEQSGRRLPGQT
839	2189	A	00/2	1 1	1705	WI_MFSCFCFSLODNSFSSTTVTECDEDPVSLH
			1	į	1	EDQTDCSSLRDENNKENYPDAGALVEEHAPP
			1		j	SWEPQQQNVEATVLVDSVLRPSMGNFKSRKP
İ	1	ĺ	1	,		KSIFKAESGRSHGESQETEHVVSSQSECQVRA
1		ļ	1			KSIFKAESOKSHOLSQLILLIT V 55QCDCQ VIAT
İ	1	1	1			GTPAHESPQNNAFKCQET\VRL\QPRIDQRTAT
1	1	1		1]	SPKDAFETR\QDLNEEEAAQVHGVKDPAPAS
1 .		1				TQSVLA\DGTDSADPSPVHKDGQNEADSAPE
1						DLHSVGTSRLLL/YHITDGDNPTAVRHGCSL/F
		1	1		1	SGOSORFNLDPESAPSPPSTQQFMMPRSSSRC
		1	1	!		SCGDGKEPOTITOLTKHIQSLKRKIRKFEEKFE
1	ļ	ŀ	į	1	-	QEKKYRPSHGDKTSNPEVLKWMNDLAKGRK
J	}	1		{	1	OLKELKLKLSEEQGSAPKGPPRNLLCEQPTVP
	ļ	1		ļ.		RENGKPEAAGPEPSSSGEETPDAALTCLKERR
Ì]	1		}		EQLPPQEDSKVTKQDKNLIKPLYDRYRIIKQIL
	i		1	}	1	STPSLIPTIVSQDTCMLLLCTDV
1				ł		STPSLIPTIVSQDTCMLLECTDV
840	2190	A	6873	2	2054	FFRFYFSFIRLFAMSLADLTKTNIDEHFFGVAL
040	2170	1	1			ENNRRSAACKRSPGTGDFSRNSNASNKSVDY
1	1	1	l	1		SRSQCSCGSLSSQYDYSEDFLCDCSEKAINRN
ł	Į	1	ì	Ĭ	1	YLKQPVVKEKEKKKYNVSKISQSKGQKEISV
1	l .	1	1	i .		EKKHTWNASLFNSQIHMIAQRRDAMAHRILS
i		1	1	1		ARLHKIKGLKNELADMHHKLEAILTENQFLK
1		1		ı		QLQLRHLKAIGKYENSQNNLPQIMAKHQNEV
1	1	1		1		KNLRQLLRKSQEKERTLSRKLRETDSQLLKT
ł		1	i	1		KDILQALQKLSEDKNLAEREELTHKLSIITTK
	1	1		1		MDANDKKIQSLEKQLRLNCRAFSRQLAIETR
1						MDANDARIQUERQUERCICAT SICQUERT
1	1			[KTLAAQTATKTLQVEVKHLQQKLKEKDREL
ì	1					EIKNIYSHRILKNLHDTEDYPKVSSTKSVQAD
1			1			RKILPFTSMRHQGTQKSDVPPL/TTKGKKATG
1	1		1	l .		NIDHKEKSTEINHEIPHCVNKLPKQEDSKRKY
1	ł	1	1	1	I	EDLSGEEKHLEVQILLENTGRQKDKKEDQEK
1 .			1			KNIFVKEEOELPPKIIEVIHPERESNQEDVLVR
	1	1		1		EKFKRSMQRNGVDDT\LGKGTAPYTKGPLRQ
1		1	1		1	RRHYSFTEATENLHHGLPASGGPANAGNMR
1		1	1	1		YSHSTGKHLSNREEMELEHS\DSGYEPSFGKS
1	}		1	1		SRIKVKDTTFRDKKSSLMEELFGSGYVLKTD
1				1		QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA
1	1	1	1	1		Q55FGVAKG5EEFLQ5KE5HFLFF5QA515HA
}	1.		1	1		FGDSKVTVVNSIKPSSPTEGKRKIII
041	2191	1 _A -	6874	3	2867	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG
841	2191	\ \frac{1}{2}	1 00/7	1		NAPAPGTPAASGWOPPTYHSGRAFSARYPRP
1	1		1	1	1	SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA
1	1	1	1	1		DHAVRPI.HGARGGOPPVPOOHVLERQVQLS
1	1	ŀ	1	1	1	QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE
1	1			i	1	DTPWSDQRPREGEGEPPRGQLQPSRPTRARG
1	i			1	1	TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP
1		1	1	1	1	1C2AEDLFFA COMPLAYER VOLGO A 1 DDD LCATAT C
1	1	1	ł	1	1	REPRRTVSESVIAVKASFPSSALPPRTGVALG
1	1	1		1	l	RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP
1	1	1	1	1	1	SGSVGGPARPASGPROAREASLVVTCRTNKF
		1	ĺ	1	1	RKNNYKWVAASSKSPRVARRALSPRVAAEN
1	1	1	1 .	1	1	VCKASAGMANKVEKPOLIADPEPKPRKPATS
	i		1	1		SKPGSAPSKYKWKASSPSASSSSFRWQSEAG
	1	1		1	1	SKPGSAPSK I KWAASSI SASSSOSI KWQGSI IS SKDHASQLSPVLSRSPSGD\RPALAHSGLKPLS
i		1		1	1	SKUMASQUSI YESKSI SUUVITALARISULATES
		1	1	1	1	GETPLSAYKVKTRTKIIRRRGSTSLPGDKKSG
					ŀ	TSPAATAKSHLSLRRRQALRGKSSPVLKKTPN
1	1	I	1	J		

						7) No. 3 O Oustring
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	Sequence	/=possible nucleotide deletion, \=possible
	ł			peptide		nucleotide insertion
				sequence	 	KGLVOVTKHRLCRLPPSRAHLPTKEASSLHA
		1			1	VRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLS
		1]	}	I PSWRARRISLSRSLVLNRLRPVASGGGKAQ
		1	1	1	ļ.	PGSPWWRSKGYRCIGGVLYKVSANKLSKTSG
	1	i	1	[İ	OPSDAGSRPLLRTGRLDPAGSCSRSLASKAVQ
	1	1	1			RSI AIIROARORREKRKEYCMYYNRFGRUNK
	1	1	1		Ì	GERCPYTHDPEKVAVCTRFVRGTCKKTDGTC
	ł	1	1	ì	1	PECHHUSKEKMPVCSYFLKGICSNSNCPYSHV
	1	1		ļ	j	VVSRKAEVCSDFLKGYCPLGAKCKKKHTLLC
	1	1				POPARRGACPRGAOCOLLHRTQKRHSRRAAT
	i	1		ì		SPARGESDATARSRVSASHGPRKPSASQRPIK
	1	1	}			OTPOGA ALTA A AVA APPHOPGGS ASPSSSKAS
	1		1	1	,	CCCCCCCCPDACLDHE\APSLOEAALAAACSNK
			1].	LCKLPSFISLQSSPSPGAQPRVRAPRAPLIKDS
		1	1	1		CKDI HIKPRI
	2192	HA-	6898	506	2071	WPDLVHTWSSEEAMGSCCSCPDKDTVPDNH
842	2192	^	0070	1 500		RNKFKVINVDDDGNELGSGIMELTDTELILYT
	İ	.1		i	1	RKRDSVKWHYLCLRRYGYDSNLFSFESGRRC
		1	İ	ł		QTGQGIFAFKCARAEELFNMLQEIMQNNSIN
		1.	1	1		VVEEPVVERNNHQTELEVPRTPRTPTTPGFAA
	1	l	1	1		QNLPNGYPRYPSFGDASSHPSSRHPSVGSARL
		1	1		1	PSVGEESTHPLLVAEEQVHTYVNTTGVQEER
			İ	1		KNRTSVHVPLEARVSNAESSTPKEEPSSIEDR
	1	1				DPQILLEPEGVKFVLGPTPVQKQLMEKEKLE QLGRDQVSGSGANNTEWDTGYDSDERRDAP
	1	Į.				SVNKLVYENINGLSIPSASGVRGRLTSTSTSD
İ	1	1	1			TONINNSAORRTALLNYENLPSLPPVWEARK
		1		1	1	LSRDEDDNLGPKTPSLNGYHNNLDPMHNYV
			1	1	1	NTENVTVPASAHKIEYSRRRDCTPTVFNFDIR
	i	1		1	{	RPSLEHRQLNYIQVDLEGGSDSDNPQTPKTPT
		1	J	j ·	1	TPLPQTPTRRTELYAVIDIERTAAMSNLQKAL
		1	1	1		DDDDGTSR/KTRHNST\DLPL
						ACRECTHASCKMAYOSLRLEYLQIPPYSKA
843	2193	A	6919	2	663	VTTACVITTAAVOLELITPFQLYFNPELIFKHF
.]		1	1	.]	1	OUND I ITNEI FEGPVGFNFLFNMIFLYRYCRM
1	})		Ì		I FEGSERGRTADEVEMELEGGELMTLEGLEVS
l .		1.				I WEI GPGI VNN/GSSMCGAE/EPLCPHELLRP
	- }	1	1			SOI PGPLSALGAHGIFLVVGELNHCGPFGYCS
1		1				WITHIEF GROSOSTWWNKNSENTLYFESYF
			- 6000	1002	366	TIRE CMPIOGACGERME/FSLLLPGLEUNGVIL
844	2194	A	6928	902	1 300	AUCNI RI PGSSNSPASASOVAGITUVCHHAK
				1	1	I TEVESVETGELHAGOAGLELLTSGDPPASAS
1	1			1	1	QSAGITGKSQHTRPGYEFIIPYSAAQEDALKA
	ľ			1	_	1 T.M.
		 -	6939	1660	317	I VDENI GESI FPILL LPPPWPDGGRPCCVEMS
845	2195	A	ענעס	1000	1	TD A KKI D DIWDII EEKESVAGAVOTLLIKSQE
1		1		j		CCUATO A A ACTI SEPPRETOESETETRALGLES
1	- [- 1				I I DAKEKI A ASTEPOGPRPVLGRESVQVPUDQD
					ì	FROSER SECENTRY GWNLTYSKAGVSVWVQAV
	1		1			EMORTI HKIKCRMECCDVPAETLYDVLHDLE
		-	- 1		1	YKKWDSNVIETFDIARLTVNADVGYYSWR
				i		YRKKWDSNVIETI DIRECTION
						CDK DI KNR DVITT. RSWLPMGADYIIMNYSVK
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT VLAOVDPKGSLPKWVVNKSSOFLAPKAMKK
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT YLAQVDPKGSLPKWVVNKSQFLAPKAMKK MYKACLKYPEWKQKHLPHFKPWLHPEQSP
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK MYKACLKYPEWKQKHLYPHFKPWL\HPEQSP LPSLAS\ELSVQHADS\LENIDESAV\AESREE
						CPKPLKNRDVITLRSWLPMGADYIIMNYSVK HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK

		32. 1	OFO.	Dendistad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	M=vietnionine, N-Asparagine, r-rionine,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
i				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide	•	/=possible nucleotide deletion, \=possible
1	ļ			sequence	1	nucleotide insertion
			2044		2672	RRKMAGCRGSLCCCCRWCCCCGERETRTPE
846	2196	Α	6944	42	2012	ELTILGETQEEEDEILPRKDYESLDYDRCINDP
						YLEVLETMONKKGRRYEAVKWMVVFAIGV
1	1					I TEACH INDIVIDUAL DESCRIPTION OF THE CO.
1	j				ŀ	CTGLVGLFVDFFVRLFTQLKFGVVQTSVEECS
	1					QKGCLALSLLELLGFNLTFVFLESLLGLIEPVE
	1	İ		,	j	AGSGITEGKCYLYARQVPGLVRLPTLLWKAL
1	İ	ĺ·]	GVLLTVAAMLLI\GLGSPMIHSGSVVGAGLPQ
ł		1			ļ	FQSISLRKIQFNFPYFRSDRYGK\DKRDFVSAG
]	1	!	1	ł	i	AAAGVAAAFGAPIGGTLFSLEEGSSFWNQGL
1	i	1	 	1		TWKVLFCSMSATFTLNFFRSGIQFGSWGSFQL
1	1	İ	ļ.	1		PGLLNFGEFKCSDSDKKCHLWTAMDLGFFV
1	ĺ	l	l	1	İ	VMGVIGGLLGATFNCLNKRLAKYRMRNVHP
1		1	1		1	AMICA ICOT FOR THE INTERVENT OF UNITED AND OF U
1		l	1	!	1	KPKLVRVLESLLVSLVTTVVVFVASMVLGEC
				1		RQMSSSSQIGNDSFQLQVTEDVNSSIKTFFCP
}	1	1		I	1	NDTYNDMATLFFNPQESAILQLFHQDGTFSPV
1.		1	1	I		TLALFFVLYFLLACWTYGISVPSGLFVPSLLC
}	1	1	1	1.	J	GAAFGRLVANVLKSYIGLGHIYSGTFALIGAA
1	ľ	ĺ		1	1	AFLGGVVRMTISLTVILIEST\NEITYGLPIMVT
1	1					LMVGKWTGDFFNKGI\YDIHVGLRGVPLLEW
1	I	l	1		ļ	ETEVEMDKLRASDIMEPNLTYVYPHTRIQSLV
1	}	ł	İ			SILRTTVHHAFPVVTENRGNEKEFMKGNQLIS
ŀ		j	ļ			NNIKFKKSSILTRAGEQRKRSQSMKSYPSSEL
1	i	1		Į		RNMCDEHIASEEPAEKEDLLQQMLERRYTPY
1	ļ	1	1			PNLYPDQSPSEDWTMEERFRPLTFHGLILRSQ
	ł	ł	l	1	[PNL YPDQSYSED W INIEER REDERIEN A EMAED
1		1	1		1	LVTLLVRGVCYSESQSSASQPRLSYAEMAED
)	j	ļ		l	YPRYPDIHDLDLTLLNPRMIVDVTPYMNPSPF
1		1	Ì		1	TVSPNTHVSQVFNLFRTMGLRHLPVVNAVGE
'		1 .	ļ)	IVGIITRHNLTYEFLQARLRQHYQTI
047	2197	A	6951	3	1994	NTNSSSVTNSAAGVEDLNIVQVTVPDNEKER
847	2197	^	10931	-	***	LSSIEKIKQLREQVNDLFSRKFGEAIGVDFPVK
ļ	1	ł			1	VPYRKITFNPGCVVIDGMPPGVVFKAPGYLEI
١.		1			ł	SSMRRILEAAEFIKFTVIRPLPGLELSNGEYST
1	1			ł	1	VGKRKIDQEGRVFQEKWERAYFFVEVQNIST
1	1			i		CLICKRSMSVSKEYNLRRHYQTNHSKHYDQY
ł	Į.	1	İ	1		MERMRDEKLHELKKGLRKYLLGLSDTECPE
- }	1	1	ł	1		QKQVFANPSPTQKSPVQPVEDLAGNLWEKLR
1	l .	1	1			QKQVFANPSP1QKSFVQFVEDLAGNEWEREEK
]	1	1	1	1	1	EKIRSFVAYSIAIDEITDINNTTQLAIFIRGVDE
	1	1	1	1	1	NFDVSEELLDTVPMTGTKSGNEIFSRVEKSLK
1	1	1		1.	J	NFCINWSKLVSVASTGTPPMVDANNGLVTKL
1	1	1		1		KSRVATFCKGAELKSICCIIHPESLCAQ\KLKM
1	1	1		1	1	DHVMDVVVKSVNWICSRGLNHSEFTTLLYEL
1	1	1		1	i	DSQYGSLLYYTEIKWLSRGLVLKRFFESLEEI
	1	1				DSFMSSRGKPLPQLSSIDWIRDLAFLVDMTM
!	1	1	1	1	1	HLNALNISLQGHSQIVTQMYDLIRAFLAKLCL
1	1	1		1	1	WETHLTRNNLAHFPTLKLVSRNESDGLNYIP
	Į.			1	1	THE PROPERTY OF THE PROPERTY!
ł	}	}	1	1		I KIVELKIERUK KI SORKI ARSELLI PASELAIA
		}		1	ļ	KIAELKTEFOKRLSDFKLYESELTLFSSPFSTKI
						DSVHEELOMEVIDLOCNTVLKTKYDKVGIPE
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT
9/19	2108	A	6985	3	289	DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVOYLPGRPTRTHASTDAPLMLKFTPLPSKTK
848	2198	A	6985	3	289	DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVOCLLLMAATFSPOGLAKPHSGTIPIT\C
848	2198	A	6985	3	289	DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C CFNAINTKIPIORLESYTRITNIQCPKEAVM
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C CFNAINTKIPIORLESYTRITNIQCPKEAVM
848	2198	A	6985	963	289	DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPITVC CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPITVC CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHL\AVVDIAYACNTVPRMLVNLLHP
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPITVC CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHLVAVVDIAYACNTVPRMLVNLLHP AKPISFAGRMMOTFLFSTFAVTECLLLVVMS
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPITVC CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHLVAVVDIAYACNTVPRMLVNLLHP AKPISFAGRMMQTFLFSTFAVTECLLLVVMS YDLYVAICHPLRYLAIMTWRVCITLAVTSWT
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHL\AVVDIAYACNTVPRMLVNILLHP AKPISFAGRMMQTFLFSTFAVTECLLLVVMS YDLYV\AICHPLRYLAIMTWRVCITLAVTSWT TGVLLSLIHLVLLLPLPFCRPOKIYHFFCEILA
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHL\AVVDIAYACNTVPRMLVNLLHP AKPISFAGRMMQTFLFSTFAVTECLLLVVMS YDLYVAICHPLRYLAIMTWRVCITLAVTSWT TGVLLSLIHLVLLLPLPFCRPQKIYHFFCEILA VI.KI.ACADTHINENMVLAGAISGLVGPLSTIV
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPITVC CFNAINTKIPIQRLESYTRITNIQCPKEAVM LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHLVAVVDIAYACNTVPRMLVNLLHP AKPISFAGRMMQTFLFSTFAVTECLLLVVMS YDLYVAICHPLRYLAIMTWRVCITLAVTSWT

CEO ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	peptide	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence .		l	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
					sednence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
				sequence		
						GLFYGTAIIMYVGPRYGNPKEQKKYLLLFHS
				<u> </u>		LFNPMLNPLICSLRNSEVKNTLKRVLGVERAL
850	2200	Α	7001	1	1011	MGNDSVSYEYGDYSDLSDRPVDCLDGACLAI
	ĺ	1				DPLRVAPLPLYAAIFLVGVPGNAMVAWVAG
					}	KVARRRVGATWLLHLAVADLLCCLSLPILAV
		1			ľ	PIARGGHWPYGAVGCRALPSIILLTMYASVLL
ļ	İ	1	1			LAALSADLCFLALGPAW\CLRFS/GACGVQVA
1		i	l	X		CGAAWTLALLLTVPSAIYRRLHQEHFPARLQ
ĺ	ĺ	{				CVVDYGGSSSTENAVTAIRFLFGFLGPLVAVA
		İ				SCHSALLCWAARRCRPLGTAIVVGFFVCWAP
1	1	ł				YHLLGLVLTVAAPNSALLARALRAEPLIVGL
İ		l	l	1		ALAHSCLNPMLFLYFGRAQLRRSLPAACHW
	ļ	ì]	1	ALRESQGQDESVDSKKSTSHDLVSEMEV
-0.51	0001	<u> </u>	7011	1	2310	AAASPLRMSRKGPRAEVCADCSAPDPGWASI
851	2201	A	7011	1 .	2310	SRGVLVCDECCSVHRSLGRHISIVKHLRHSA
1		1	1			WPTTLLQMVHTLASNGANSIWEHSLLDPAQV
	ł	l	Ì	1		QSGPALKQTPKDKV\HPIKSEFIRAKYQMLAF
'	į.		ł		1	VHKLPCRDDDGVTAKDLSKQLHSSVRTGNLE
	ļ		ļ			TCLRLLSLGAQANFFHPEKGTTPLHVAAKAG
	1	1	1			QTLQAELLVVYGADPGSPDVNGRTPIDYARQ
		1			J	CITIZET APPLIATION OF TOPI APVI COPED
ĺ	1	ĺ	1	1	1	AGHHELAERLVECQYELTDRLAFYLCGRKPD
į.						HKNGHYIIPQMADSLDLSELAKAAKKKLQAL
	1	·		l		SNRLFEELAMDVYDEVDRRENDAVWLATQN
						HSTLVTERSAVPFLPVNPEYSATRNQGRQKL
ĺ	}]	j	į	ļ	ARFNAREFATLIIDILSEAKRRQQGKSLSSPTD
	Ì	1	ì	i		NLELSLRSQSDLDDQHDYDSVASDEDTDQEP
		1	İ	1	}	LRSTGATRSNRARSMDSSDLSDGAVTLQEYL
1					ĺ	ELKKALATSEAKVQQLMKVNSSLSDELRRLQ
ĺ	}	1		ļ ·		REIHKLQAENLQLRQPPGPVPTPPLPSERAEH
j	1	1	1	1	1	TPMAPGGSTHRRDRQAFSMYEPGSALKPFGG
Ì		i	1			PPGDELTTRLQPFHSTELEDDAIYSVHVPAGL
1		1		İ		YRIRKGVSASAVPFTPSSPLLSCSQEGSRHTSK
\		1	}	ļ	1	LSRHGSGADSDYENTQSGDPLLGLEGKRFLE
[1				LGKEEDFHPELESLDGDLDPGLPSTEDVILKT
1		1		/	İ	EQVTKNIQELLRAAQEFKHDSFVPCSEKIHLA
ì		1		ł	•	VTEMASLFPKRPALEPVRSSLRLLNASAYRLQ
			1			SECRKTVPPEPGAPVDFQLLTQQVIQCAYDIA
		1	1	}	1	KAAKQLVTITTREKKQ
852	2202	A	7016	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLL
عده ا	2202	\^	1010	107	1	TVKGLLKPSFSPRNYKALSEVQGWKQRMAA
İ	1	1		1		KELARQNMDLGFKLLKKLAFYNPGRNIFLSP
	Į.	1				LSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP
l	1	1	1	l		EKDLHEGFHYIHELTQKTQDLKLSIGNTLFID
1	I					ORLOPORKFLEDAKNFYSAETILTNFQNLEM
1	1	1		ł		AQKQINDFI/ESKTHGKINNLIENIDPGTVMLL
		j]	j.		ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS
1 .	1	1		[VKVPMMFRSGIYQVGYDDKLSCTILEIPYQK
'	1			1		ALLA TELL DECOMING THE ENGLOYMETER TON
		1	1	1		NITAIFIL PDEGKLKHLEKGLQVDTFSRWKTL
1		1	1		I	LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVS
1		1	ļ	1		KIFEEHGDLTKIAPHRSLKVGEAVNKAELKM
1		1		ŀ	1	DERGTEGAAGTGAQTLPMETPLVVKIDKPYL
				<u> </u>		LLIYSEKIPSVLFLGKIVNPIGK
853	2203	A	7017	1	3293	MTHACNPSTLGGQGRRITRSHGRRRSSRGPV
		1 -		1		ARHVAAGAGHENKHGGSRRFPAGVAPRRAM
1	1	1	Ì	1	1	ANVSKKVSWSGRDRDDEEAAPLLRRTARPG
	1 .	1	1			GGTPLLNGAGPGAARQSPRSALFRVGHMSSV
		1	1	1	1	ELDDELLEP\DMDPPHPFPKEIPHNEKLLSLKY
1		1	1			ESLDYDNSENQLFLEEERRINHTAFRTVEIKR
	1	1	1	1		WVICALIGILTGLVACFIDIVVENLAGLKYRVI
1	1	1	1	1	1	KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV
1	ī	1	1	J	<u> </u>	

			970	D. Hand	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid; E=Glutamic Acid,
NO: of	NO: of	, hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide		[=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	ĺ	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	
uence		j .	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		[amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		Ī	i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
!			ļ	peptide	•	/=possible nucleotide deletion, \=possible
,			ŀ	sequence		nucleotide insertion
				sequence		LVGSVIVAFIEPVAAGSGIPOIKCFLNGVKIPH
1		ļ		1		VVRLKTLVIKVSGVILSVVGGLAVGKEGPMI
		1	1	<u> </u>		
-	ł	1	ľ	}		HSGSVIAAGISQGRSTSLKRDFKIFEYFRRDTE
1			ł.	ł		KRDFVSAGAAAGVSAAFGAPVGGVLFSLEEG
j	ŀ			l .		ASFWNQFLTWRIFFASMISTFTLNFVLSIYHG
1				!		NMWDLSSPGLINFGRFDSEKMAYTIHEIPVFI
	İ	1		1	l	AMGVVGGVLGAVFNALNYWLTMFRIRYIHR
1 .	[l		1		PCLQVIEAVLVAAVTATVAFVLIYSSRDCQPL
	1	1		i .	•	QGGSMŞYPLQLFCADGEYNSMAAAFFNTPEK
	ì		1	1	<u> </u>	SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT
{			Į.	ļ		YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG
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				1	I	AAIWADPGKYALMGAAAQLGGIVRMTLSLT
		1		1]	VIMMEATSNVTYGFPIMLVLMTAKIVGDVFIE
l .	ĺ		1	1		GLYDMHIQLQSVPFLHWEAPVTSHSLTAREV
'		1	1	1	1	MSTPVTCLRRREKVGVIVDVLSDTASNHNGF
			1		1	PVVEHADDTQPARLQGLILRSQLIVLLKHKVF
1		ł	1	1	1	VERSNLGLVQRRLRLKDFRDAYPRFPPIQSIH
1		ł	ł	i	t	VSQDERECTMDLSEFMNPSPYTVPQEASLPR
				1	İ	VFKLFRALGLRHLVVVDNRNQVVGLVTRKD
	ļ	1	1	ì		LARYRLGKRGLEELSLAQTGPKAQATAEGRV
ł	1	ł	l	ľ	[AGAAQQPCQLRAVTLEDLGLLLAGGLASPEP
				1		LSLEELSERYESSHPTSTASVPEQDTAKHWNQ
		i .		ł	ļ	LEQWVVELQAEVACLREHKQRCERATRSLL
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1		1	í	i	ļ	QEEQGREVACGALQKNQEDSSRRVDLEVAR
	٠.					M
954			7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EOOVAKRRTKRDVYQEPTDPKFPQQWYL\SG
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTO\RDLMYKAAWAQGYTGHGIVVSILDDGI
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TOMNDNRHGTRCAGEVAAVANNGVCGVGV
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHTYSASWGPEDDGKTVDGPARLAEEAFFR
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATOFGNVPWYSEACSSTLA
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNONEKQIVTTDLRQKCTESHTGTSAS
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMYKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS API.AAGIIALTLEANKNLTWRDMQHLVVQTS
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAONWTTVAPORKCIDILTEPKDI
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAONWTTVAPORKCIDILTEPKDI
854	2204	A	7037	139	2604	M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGY AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHTTRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMYKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSOACVVCEEGFSLHQKSCVQHCPP
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYLLSG VTQ\RDLMYKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPOVLDTHYSTENDVETIRASVCAPCHAS
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYLLSG VTQVRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAHILVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEVVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCOGPALTDCLSCPSHASLDPVEQTCSRQS
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS OSSRESPPOOOPPRLPPEVEAGORLRAGLLPS
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGY AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHTTRLEHAQARLT LSYNRRGDLAHILVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HI PEVVAGLSCAFIYLVFYTVFLVLQLRSGFS
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGY AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHTTRLEHAQARLT LSYNRRGDLAHILVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HI PEVVAGLSCAFIYLVFYTVFLVLQLRSGFS
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAHILVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD
854		A				AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL
854	2204	A	7037	139	. 1441	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFYTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL
						AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHTRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFTVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF
						AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMYKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFTVLVFVTVFLVLQLRSGFS FRGVKYYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL
						AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYLISG VTQIRDLMYKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWITVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL EDGNFLKLANNGTVLRASHGTKMMTPEVLA
						AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWYVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMYKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFTVLVFVTVFLVLQLRSGFS FRGVKYYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	<u> </u>		/	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
	\			peptide		
				sequence		nucleotide insertion YFDLPGALLCARVVDYLTKLNNGQKTFDFW
						KDIVAAIQHNYKMSAFKENCGIYFPEIKRDPG
	ļ	i	Ĭ]	RVLHSRPESVKKWLROLKNAGKILLLITSSHS
	Į.	1	l			DYCRLLCA\YILGNDFTDLFDIVITNALKPGFF
		1	ļ		Ì	SHI PSORPERTLENDEEOEALPSLDKPGWYSQ
	1		١		}	GNAVHI VELLKKMTGKPEPKVVYFGDSMHS
	Į.	1	· ·	1		DIFPARHYSNWETVLILEELRGDEGTRSQRPE
		1		1	1	ESEPLEKKGKYEGPKAKPLNTSSKKWGSFFU
].		1	}	DSVLGLENTEDSLVYTWSCKRISTYSTIAIPSI
		ļ		j		EAIAELPLDYKFTRFSSSNSKTAGYYPNPPLV
	1	1		i	1	LSSDETLISK SSPSVFEFEHAVQPVFTMEFLKTCVLRRNACT
856	2206	A	7082	396	1635	AVCFWRSKVVQKPSVRRISTTSPRSTVMPAW
	1					VIDKYGKNEVLRFTONMMMPUHYPNEVIVK
	1	Ì	1	\		VHAASVNPIDVNMRSGYGATALNMKRDPLH
		}]		1 .	VKIKGEEFPLTLGRDVSGVVMECGLDVKYFK
		1	1		1	PGDEVWAAVPPWKOGTLSEFVVVSGNEVSH
		ì		1		KPKSLTHTOAASLPYVALTAWSAINKVGGLN
	ŀ	İ	ŀ			DKNCTGKRVLILGASGGVGTFAIQVMKAWD
	1	1		Ì	1	AHVTAVCSQDASELVRKLGADDVIDYKSGSV
	1	1		ŀ	1	EEQLKSLKPFDFILDNVGGSTETWAPDFLKK
	-	1		l .		WSGATYVTLVTPFLLNMDRLGIADGMLQTG VTVGSKALKHFWKGVHYRWAFFMASGPCL
	ļ	1	1	1		DDIAELVDAGKIRPVIEQTFPFSKVPEAFLKV
		1				ERGHARGKTVINVV
				1000	2417	IRRRKMTPOSLLOTTLFLLSLLFLVQGAHGR
857	2207	A	7088	320	2417	GHREDFRFCSORNOTHRSSLHYKPTPDLRISIE
	ì		1		ł	NSPEALTVHAPFPAAHPASRSFPDPRGLYHFU
	1	İ				I VWNRHAGRLHLLYGKRDFLLSDKASSLLCF
		1		ì	ĺ	QHQEESLAQGPPLLATSVTSWWSPQNISLPSA
1]				ASFTFSFHSPPHTGAHNASVDMCELKRDLQL
İ		1	}			LSQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMGSFEEDRINATVWKLQPTAGLQ
ļ		1		į.	1	DLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKG
		1	1 .	İ		RSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
ļ	Ì	1		ł	İ	KVLGIVVQNTKVANLTEPVVLTFQHQLQPKN
		1		i		VTLOCVEWVEDPTLSSPGHWSSAGCETVKKE
	-1					TOTSCECNHLTYFAVLMVSSVEVDAVHKHY
		1	-	Į.		1 ST I SYVICEVVSALACLYTIAAYLCSRVPLPC
l	ł	- 1	ł	1		PREPRINTIKVHMNLLLAVELLUISELLSERV
		- 1				ALTGSEAGCRASAIFLHFSLLTCLSWMGLEG
	1				1	YNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI
1	1	1	- 1		Į.	FLVTLVALVDVDNYGPIILAVHRTPEGVIYPS
1	1		1		{	MCWIRDSLVSYITNLGLFSLVFLFNMAMLAT MVVQILRLRPHTQKWSHVLTLLCLSLVLG/LP
1	1	-	-	1	1	WALIFFSFASGTFQLVVLYLFSITSFQGFLIFI
			1			WYWSMRLQARGGPSPLKSNSDSARLPISSGS
		1		1		TSSSET
				105	415	DAGAVKSSDTNIWFRGMCDDKKGHRCPS*G
858	2208	A	7091	185	413	QPQHFHVAFHTEAEGAMFYFRLHVIHRVMQS
1					1	OOOI FPSTLFSWLLE
-			7136	 3	302	FFFWROSLALLPRLECSGATGAHCNLHFPGSS
859	2209	A	/130	'	302	DCPTSAS*IAGITGACYHAWLLFVFLAEIGFH
1	l			1		HVGQGGLELLTSSDPSGSASQSAGITGVSHCT
			1			WPI
860	2210	- A	7156	23	591	ALSTETRTPDMRRLLLVTSLVVVLLWEAGAV
000	2210	1	1			PAPKVPIKMQVKHWPSEQDPEKAWGARVVE
1		-				PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGR GPILPGTKAWMETEDTLGRVLSPEPDHDSLY
	1	ı	j.	1	İ	GLITA I LY AMMETED I TOKA FOLEL DI IDOPI

		Met	CEC T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	peptide	HOG	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	denio		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
UCIICC		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	Ì			sequence		nucleotide insertion HPPPEEDQGEERPRLWVMPNHQVLLGPEEDQ
				\		DHIYHPQ*GSRGHHCPRPVPRPRLLGLGPSLP
		1]	1	, -
		(CPS NYVCTIAF*EKKMGF*LSLSCLVLLFVLFLDCI
861	2211	A	7161	1220	1003	LTTTTRIMFHCTYLFASVCLSLLNTLLSPNCL
	1	[İ			KSAMILO .
					947	LKYYHITMGIYKTGKKVIL*KSSMSNRFSVIF
862	2212	Α	7211	665	847	YKNIQKLSFSNYVYHQNYVFSSDWSYDF
		1		-	1273	HGSSCALGDLAPG*LPSGPVLSSPAVRL*RKP
863	2213	A	7212	924	12/3	LVWDSPSCLPATGPT*GLVLVLGGPDCT*WA
)	RGQHEHKRMRAP*SCRVTVNLAKKKKKTDQ
į .		1	1			CIKPNYOSPPKECDYNILANSVA
	100:	4-	7214	845	1619	SDKGGKKADRKNHLRHAFPLLPHRVRERLH
864	2214	Α	1214	7		DPKVPVDADHVOGODPGRAAHDIHGEDVTE
		1	i	i	1	KVSKDPLAPDEVGDTDEGHDRHGHREVGQK
	ı				ì	- HGHDQEEVAYEERACEGGKFATVEVTDKPV
	1	1	1		[DEALREAMPKVAKYAGGTNDKGIGMGMTV
1.		1	ļ			PISFAVFPNEDGSLQKKLKVWFRIPNQFQSDP
1		1	1	1		PAPSDKSVKIEEREGITVYSMQFGGYAKEAD
Į.	1	1		1	•	YVAQATRLRAALEGTATYRGDIYFCTGYDPP
		l	Ì			MKPYGRRNEIWLLKT RRLGAVAHAYTSSTLGGRGGWIT*GQELQTS
865	2215	A	7246	559	682	LANMAKPRLY
		}			1010	TCTYKYLMGWIRGRRSRHSWEMSEFHNYNL
866	2216	A	7257	641	1310	DIKKSDESTRWOKORCPVVKSKCRENASPFF
	Ì	ł		i	1	FCCFIAVAMGIRFIIMVAIWSAVFLNSLFNQEV
1	1	į.	1	A.		OIPLTESYCGPCPKNWICYKNNCYOFFDESKN
}		Į.	ì	1		WYESOASCMSONASLLKVYSKEDQDLLKLV
		1	1			KSYHWMGLVHIPTNGSWOWEDGSILSPNLLT
1	1	}			İ	IIEMQKGDCALYASSFKGYIENCSTPNTYICM
1		1				QRTV
867	2217	+A	7288	151	396	SIKIIEAFGSNGPDFWFFRYWSP*LFRQQVVFI
807	2217	1"	1.200			MPFFQTLWLMNANRFCSIFTTTNVANNCWW
	}	ł	1			TPYHCWLSVVVCRCESHGI
868	2218	I A	7298	3	272	PDTVIGGRGSGGKEFGRWVLW*VFE*RLGTP
		. 1		1		KGSCPAGGSRMVSESD*EGRGC*ASYPCAC*
						AGS*WR*GSRPAGRGTPPRSLSHARPP PRRDAEDRDESCLNPAFPIGLLHPNSVNSMAR
869	2219	A	7332	1223	332 .	PREDAEDROESCLINFAFFIGLEHFINSVINGUAL FLTLCTWLLLLGPGLLATVRAECSQDCATCS
1		ļ			1	YRLVRPADINFLACVMECEGKLPSLKIWETC
1		1		1	1	KELLQLSKPELPQDGTSTLRENSKPEESHLLA
1]			!	KRYGGFMKRYGGFMKKMDELYPMEPEEEA
1	ĺ	1		1	1	NGSEILAKRYGGFMKKDAEEDDSLANSSDLL
1	Ì	1			1	KELLETGDNRERSHHODGSDNEEEVSKRYGG
Ī		- 1		1	1	EMRGI KRSPOLKEKAKELOKRYGGFMRRVG
		ļ		1	}	POKW*MTSPQNRYGGFLKRFAEALPSDEEGE
1	ľ		1	1	1	SVSKEVPEMEKRYGGFMRF
			7202	216	1018	FIHORI.TERTOFLDESKKNPNS*QANLLRGGG
870	2220	A	7382	210	1	AGOGRGREGAESGGSRGEGPGSDGRLPATGD
				1		FWSPRSORRGCCGRRAPRPEAMENGAVYSPT
	1	-		1	1	TEEDPGPARGPRSGLAAYFFMGRLPLLRRVL
		- 1	1	}	}	KGLQLLLSLLAFICEEVVSQCTLCGGLYFFEF
1			- 1	1	1	VSCSAFLLSLLILIVYCTPFYERVDTTKVKSSD
	1	1	- 1	1	1	FYITLGTGCVFLLASIIFVSTHDRTSAEIAAIVF
1		1		1	1	GFIASFMFLLDFITMLYEKRQESQLRKPENTT
1	1		- 1	1		RAEALTEPLNA
871	2221	- A-	7403	3	393	SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSVN
871	2221	A	7403	3	393	SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSVN DPGNMSFVKETVDKLLTGFRCFREREAAPRR ALRGAALPGESEAGDPESLRSSVNADWIQYS

	GEO TO	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Accordic Acid E=Glutamic Acid.
10: of	NO: of peptide	1104 .	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-		ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq- uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	Delice	!	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	i	'	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	i	1	Ì	peptide		/=possible nucleotide deletion, \=possible
	1	}	l	sequence		nucleotide insertion
	 	┼				DLWEAEVSTPRCEAGFCQECFRTPGNQEKDG
	l	1	1			PFIC PFIC
872	2222	A	7413	1061	359	FVDIVSVVEFPHCPEARFPAQHGQDSKRLTLC
012		1				PGGS*PQATLHLDRMRVSASPTKEIQVKKYK CGLIKPCPANYFAFKICSGAANVVGPTMCFED
		1	ì	}		RMIMSPVKNNVGRGLNIALVNGTTGAVLGQ
	1	{	İ	1	1	KAFDMYSGDVMHLVKFLKEIPGGALVLVAS
			İ	1	1	YDDPGTKMNDESRKLFSDLGSSYAKQLGFRD
						SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE
•	1	1	}		i	GWPELLEMEGCMPPKPF
	Ì	1				ILKCAGHGGSCL*SQHFGRLRWEDRLRLGVQ
873	2223	A	7429	2242	2394	DHPGQHCETPSLLKIERKLF
						PCTSCVLWATLHLPASTRKAPQAECGMISITE
874	2224	A	7468	146	894	WOKIGVGITGFGIFFILFGTLLYFDSVLLAFGN
		1			ļ	LLFLTGLSLIIGLRKTFWFFFQRHKLKGTSFLL
		1		1		GGVVIVLLRWPLLGMFLETYGFFSLFKGFFPV
	1		1	ì	1	AFGFLGNVCNIPFLGALFRRLQGTSSMV*KTE
	1	1	-	i		MSSI NI DHWI KGAKREEWEPPPOSPALTHSP
		1	1	-\		TVPGPPOVOKERNGAEOLTSNPQVDSRGCQE
	}	1			1	AEMOTPRRI.GWGWYHTLTLYLWEEK
	34.5		1 100	 	251	GEKPVPTWLQDEAGQWLLGFVAQPWGWPG
875	2225	A	7498	91	231	SERHEP*HGGVLFRLGPSAPPGKL
			1	403	587	VSCI_CFI_FKHITSFKNSVHIWLGTVVHAYNPN
876	2226	Α	7544	403	767	II GGOGGWIA*GOEFKTSLGNTVRPCLYK
			7566	12	940	GCAPOTREEVPEPGGRGAAPWVALVARGGC
877	2227	Α	7360	12	1740	TEKDKVI VA ARRNASAVVLYNEERYGNITLI
	Ì	1	-	1	i	MSHAGTGNIVVIMISYPKGREILELVQKGIPV
	ŀ	1				TMTIGVGTRHVOEFISGOSVVFVAIAFITMMI
	-	1		Į.		SI AWI IFYYIORFLYTGSOIGSQSHRKETKKV
			ì	1	1	GOLLI HTVKHGEKGIDVDAENCAVCIENIKV
ĺ	İ		1		1	KDIIRILPCKHIFHRICIDPWLLDHRTCPMCKL
		1	1			DVIKALGYWGEPGDVQEMPAPESPPGRDPA
<u> </u>		1		ļ		NLSLALPDDDGSDESSPPSASPAESEPQCDPSI
ĺ		-)	1		KGDAGENTALLEAGRSDSRHGGPIS
878	2228	A	7586	315	1232	ERSLLCKVDVRWIYVSEGTKTQRRHRQGSLF
0/0	2220	1.				RGRMQAACWYVLFLLQPTVYLVTCANLTNO
	1			1	ļ	GKSELLKSGSSKSTLKHIWTESSKDLSISRLLS
ŀ	1		İ	1 '	1	QTFRGKENDTDLDLRYDTPEPYSEQDLWDW
		1	Ì		ļ	LRNSTDLQEPRPRAKRRPIVKTGKFKKMFGV
		1	1		İ	GDFHSNIKTVKLNLLITGKIVDHGNGTFSVYI
					}	RHNSTGQGNVSVSLVPPTKIVEFDLAQQTVII
		- (}		AKDSKSFNCRIEYEKVDKATKNTLCNYDPSK
		-	1	· ·	1.	TCYQEQTQSHVSWLCSKPFKVICIYISFYSTD
1	1	- 1			<u> L</u>	YKLVQKVCPDYNYHSDTPYFPSG
879	2229	A	7605	479	391	TESWKLKWWSPTCLDQLNGSAPGNVFIHG
880	2230	A	7612	93	659	DAAVAMTAQGGLVANRGRRFKWAIELSGP
000	1	1				GGSRGRSDRGSGQGDSLYPVGYLDKQVPDT
l		i	1			VQETDRILVEKRCWDIALGPLKQIPMNLFIM
1		1		1	1	MAGNTISIFPTMMVCMMAWRPIQALMAISA FKMLESSSQKFLQGLVYLIGNLMGLALAVY
	l	1		1	1	FKMLESSOUNTLUGEV I LIGHTINGTALAVI
1	1	- 1				COSMGLLPTHASDWLAFIEPPERMEFSGGGI
1		- 1		1		LL COMPANY ATTYON COMPANY SHRWING
881	2231	$-\frac{1}{A}$	7615	291	1452	SPOKTMRSHTITMTTTSVSSWPYSSHRMRFI
601	1 222,	11		1		NHSDQPPQNFSATPNVTTCPMDEKLLSTVLT
		- 1	ļ		İ	SYSVIFIVGLVGNIIALYVFLGIHRKRNSIQIY
1	- 1	1	1	1	1	LNVAIADLLLIFCLPFRIMYHINQNKWILGV
1	1		-			CKVVGTLFYMNMYISIILLGFISLDRYIKINRS QQRKAITTKQSIYVCCIVWMLALGGFLTMIII
1			1	1		L DODK VILLKONIA ACCIA MMPWPORKPIMM
	i	- 1				TLKKGGHNSTMCFHYRDKHNAKGEAIFNFI

	AEG **	14-4	CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1 .	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	ļ	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	İ	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide		nucleotide insertion
	ļ	İ	<u> </u>	sequence	L	VVMFWLIFLLIILSYIKIGKNLLRISKRRSKFPN
						SGKYATTARNSFIVLIFTICFVPYHAFRFIYISS
	1	1		1		QLNVSSCYWKEIVHKTNEIMLVLSSFNSCLDP
	1	-	1	İ		QLNVSSCYWKEIVHKINEIMLVLSSTASCEDI
	1	1		1		VMYFLMSSNIRKIMCQLLFRRFQGEPSRSEST
			1			SEFKPGYSLHDTSVAVKIQSSSKST
882	2232	A	7617	67	379	RQMALLKANKDLISAGLKEFSVLLNQQVFND
002	22.32	1	1,41			PLVSEEDMVTVVEDWMNFYINYYRQQVTGE
Ì	1	1			ļ	PQERDKALQELRQELNTLANPFLAKYRDFLK
					İ	SHELPSHPPPSS
002	2233	A	7622	400	215	KVKTCRYNPKYSAANDTGFVDIPSREKDLAK
883	2233	Ι^	1022	1 400		AVATVGPISVAVGASHVFFQFYKKGKHLSS
-004	10024	 	7638	2640	2861	APVILILOMVKLSIVLTPOFLSHDOGQLTKELQ
884	2234	A	1038	2010		QHVKSVTCPCEYLRKVSECRQMGPGALEQFP
ì	1	1			1	GLSCHTSHSG
					455	PSRGKMELEAMSRYTSPVNPAVFPHLTVVLL
885	2235	A	7642	201	433	AIGMFFTAWFFVYEVTSTKYTRDIYKELLISL
ì	1	ŀ	1	ì	1	VASLFMGFGVLFLLLWVGIYV
					569	APENPFSRQHFNSETKVKLSLKTGTWLGNHA
886	2236	A	7692	61	309	HLGEHFSTHHELGLSGKVVGFLVKNILEVIRN
		1		1	1 .	GGMETRHPGKVSSWFHRWDSRAEQHNHAE
	1	1	1		ľ	HHEDVPQGDEDSKVSEAQQEFPDVVTCAGLP
	Ì	,	1'	1	1	GLLPKALRVLLFQLKVQHRPGIHQQRPEQQD
		1				VSDHRYGRSVRQNRK
						NPGCCLPVAMRTSYLLLFTLCLLLSEMASGG
887	2237	A	7693	85	315	NFLTGLGHRSDHYNCVSSGGQCLYSACPIFTK
				1		NELIGEGRADE INC VSSG GCD I SECTION IN
						IQGTCYRGKAKCCK APSHRRRYLSPSRSAGQLGNMALERLCSVLK
888	2238	A	7702	242	1298	VLLITVLVVEGIAVAQKTQDGQNIGIKHIPAT
		1		1		QCGIWVRTSNGGHFASPNYPDSYPPNKECIYI
1		1	ĺ	[QCGIWVKISNGGHPASPNIPDSITINADOTI
Į.			į.	1		LEAAPRQRIELTFDEHYYIEPSFECRFDHLEVR DGPFGFSPLIDRYCGVKSPPLIRSTGRFMWIKF
						SSDEELEGLGFRAKYSFIPDPDFTYLGGILNPIP
		1				SSDEELEGLGFRAKYSFIPDPDF17LGGGLVFI
1	1	1		· ·		DCQFELSGADGIVRSSQVEQEEKTKPGQAVD
	-		1			CIWTIKATPKAKIYLRFLDYQMEHSNECKRNF
		1	'	1	1	VAVYDGSSSIENLKAKFCSTVANDVMLKTGI
}	1	1	1	ł	1	GVIRMWADEGSRLNRFRMLFTSFGGASPAQA
		1		1		ALSFCHSNMCINNSLVCNGVQNCAYPWDEN
1	1	- 1				HC CE
889	2239	A	7707	185	2911	CHYIMNPSTHHPASAGGSILGLFDFFGLGLGE
609.	2233	^	1 .,,,,	1		MTMDALLARLKLLNPDDLREEIVKAGLKCGP
1		ļ	1	1	Į	ITSTTRFIFEKKLAOALLEQGGRLSSFYHHEA
		l l		1		GVTALSODPORILKPAEGNPTDOAGFSEDRDF
	-					GYSVGLNPPEEEAVTSKTCSVPPSDTDTYRAG
1				1	1	ATASK EPPLYYGVCPVYEDVPARNERIYVYE
1			1		1	NKKEALOAVKMIKGSRFKAFSTREDAEKFAR
	1		1		1	GICDYFPSPSKTSLPLSPVKTAPLFSNDRLKDG
		ļ			1	I CLSESETVNKERANSYKNPRTQDLTAKLRK
1	1	1		J	1	AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIVQ
Ì	1	1		1	1	FGCRYNVMHVAAKENOASICOLTLDVLENP
1	1				1	DFMRLMYPDDDEAMLQKRIRYVVDLYLNTP
1	1	1		1	1	DKMGYDTPLHFACKFGNADVVNVLSSHHLI
	j	- 1	}	1	1	VKNSRNKYDKTPEDVICERSKNKSVELKERIR
		ı				EYLKGHYYVPLLRAEETSSPVIGELWSPDQTA
	1			1	1	EASHVSRYGGSPRDPVLTLRAFAGPLSPAKAE
1		ı	1			DFRKLWKTPPREKAGFLHHVKKSDPERGFER
1		1	ł	1		VGRELAHELGYPWVEYWEFLGCFVDLSSQE
		1	1	1		OF ORI PRINT TOOPICAL VOCETCEDE V CODI
			1	Í		GLORLEEYLTQQEIGKKAQQETGEREASCRD
ı	1	1		1	1	KATTSGSNSISVRAFLDEDDMSLEEIKNRQNA ARNNSPPTVGAFGHTRCSAFPLEQEADLIEAA

			OF O	Dundisted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	İ	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	İ	1		peptide	•	/-possible nucleotide deletion, \-possible
		1		sequence		nucleotide insertion
	 			30400		EPGGPHSSRNGLCHPLNHSRTLAGKRPKAPR
1	ĺ	1	1			GEEAHLPPVSDLTVEFDKLNLQNIGRSVSKTP
1			1	1	·	DESTKTKDQILTSRINAVERDLLEPSPADQLG
1		1	l .	Į	1	NGHRRTESEMSARIAKMSLSPSSPRHEDQLEV
ľ	ĺ		1	\	1	TREPARRLFLFGEEPSKLDQDVLAALECADV
	1	1	ì			DPHQFPAVHRWKSAVLCYSPSDRQSWPSPAV
1.	1	}]	1	1	KGRFKSQLPDLSGPHSYSPGRNSVAGSNPAKP
1	1	1.				GLGSPGRYSPVHGSQLRRMARLAELAAL
890	2240	A	7711	360	269	RHMPVIPALWEAEVGGLLEPRSSRSAWATE
891	2241	Ä	7721	61	1175	KLPWEPSFLIKMQIIRHSEQTLKTALISKNPVL
071	2271	1	1			VSQYEKLDAGEQRLMNEAFQPASDLFGPITL HSPSDWITSHPEAPQDFEQFFSDPYRKTPSPN
1	1	1	1	1		HSPSDWITSHPEAPQUFEQFFSDF TRATTS IN KRSIYIQSIGSLGNTRIISEEYIKWLTGYCKAYF
		1	1	1		YGLRVKLLEPVPVSVTRCSFRVNENTHNLQIH
	1		1	1)	AGDILKFLKKKKPEDAFCVVGITMIDLYPRDS
1	i	1	1	1	Į.	WNFVFGQASLTDGVGIFSFARYGSDFYSMHY
		1	1		1	KGKVKKLKKTSSSDYSIFDNYYIPEITSVLLLR
		1			j	SCKTLTHEIGHIFGLRHCQWLACLMQGSNHL
}	1	İ		· ·		FEADRRI NI CPICLHKLOCAVGFSIVEKYKA
	1	1		}	1	LVRWIDDESSDTPGATPEHSHEDNGNLPKPV
***	1	1	1]		FAFKEWKEWIIKCLAVLOK
			 		1650	SAPTAPARPCRAERGSGGGMLALLAASVALA
892	2242	A	7723	2	1030	VAAGAODSPAPGSRFVCTALPPEAVHAGCPL
		1		1	1	PAMPMOGGAOSPEEELRAAVLULKETVVQV
1			Ì			KETI ASARAIRELTGKLARCEGLAGGKAKGA
ł		l l	Ì		İ	CATCKDTMGDLPRDPGHVVEOLSRSLQTLK
1	1	-	1	}	1	DRI ESI EPI PAMPMOGGAOSPEEELKAAVLQ
1	1	1	ļ	Ì		LRETVVQQKETLASARAIRELTGKLARCEGL
	\ \	1		1		AGGKARGAGATGKDTMGDLPRDPGHVVEQ
j		- 1	1	1	ł	LSRSLQTLKDRLESLEHQLRANVSNAGLPGD
		- 1	į.	1	ì	FREVLOORLGELERQLLRKGABLEDEKSLLH
1	ŀ	1	ļ		1	NETSAHROKTESTLNALLORVTELERGNSAF KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT
}	}	1			1	ICLWLRSSASPGMGTPFSYAVPGQANEIVLE
1	1		l			WGNNPIELLINDKVAQLPLFVSDGKWHHICV
1	1	-	-	j		TWTTRDGMWEAFQDGKKLGTGENLAPWHPI
-		ł	1			KPGGVLILGQEQDTVGGRFDATQAFVGELSQ
		-	ļ		1	FNIWDRVLRAQEIVNIANCSTNMPGNIIPWVD
		[1	Ì	\	NINTVIOVEGGASKWPVETCEERLLDL
					2410	LTAGTAMNYPI TLEMDLENLEDLEWELDKL
893	2243	A	7729	3554	2419	DAIVAIDTSI VENHI CPATEGPLMASPAAVEVE
		1	ŀ	}	1	VAVOLIELI GVIGNVI VI VILERHROLKSSLEL
	- 1	1	1	- {		TELETIAVADILIVEILPEAVAEGSVGWVLGIF
- []		}	1	LICETULAT TIKUNFYCSSLLLACIAVDKYLATY
1		1				UAVHAVRHRRLLSIHITCGTIWLVGFLLALPEI
		1	-	1		I EAR VIOLGHHMNSI PRCTFSOENOAETHAWF
		1	ļ	ŀ	ł	TEDET VHVAGELLPMLVMGWCYVGVVHKLK
		1		1	i	O A ORR DOROK AVRVAIL VTSIFFLOWSPYHIV
		1	-	1	1	I IEI DTI ARI KAVDNTCKLNGSLPVALIMUELL
- [1		1	1	1	GT A HCCL NPML YTFAGVKFRSDLSRLLTKLG
1	[.		ļ	1	- [CTGPASI COLFPSWRRSSLSESENATSLITE
		-+-	7770	670	287	FUTTO A CD WGAGARVRGGAGGMASGAAKWL
894	2244	_ A	7738	10/0	201	VI ADVRSGALRSGPSLRKDGDVSAAWSGSGR
	-	- 1				OT VPGR SVIVTR SGAILPKPVKMSFGLLKVF51
1		- 1	1			VIPFLYVGTLISKNFAALLEEHDIFVPEDDDDD
		- 1		1		ח
			7753	119	278	APYAHSQVHCLDKVCGLLPFLNPEVPDQFYR
895	2245	A	1133	117	1	I I WI SI EI HAGKEAPHCPRTRPL
	1 2046	-	7754		372	SPAWWNSQQRVVSPFLALLTLEPTFHHLLPIM
896	2246					

SSQ III DNO: in much peptide contide DNO: in much contide D						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of peptide entide sequence uence unce to the period of the period sequence uence				SEQ	Predicted		D=Acceptic Acid. F=Glutamic Acid.
nucic cutide sequence			hod				F=Phenylalanine, G=Glycine, H=Histidine,
cotide sequence 90,9496 14 18 18 18 18 18 18 18	nucl-						I=Isoleucine, K=Lysine, L=Leucine,
Sequence	cotide	-				to last amino	M=Methionine, N=Asparagine, P=Proline,
1914 Imanino acid residue of peptide sequence Peptide sequence	seq-	uence	l		•	acid residue	O=Glutamine R=Arginine, S=Serine,
	uence	'	}	914			T=Threonine, V=Valine, W=Tryptophan,
Poptide Sequence Poptide Pop	1						V=Tyrosine, X=Unknown, *=Stop codon,
### Indicated insertion Sequence			1			Soquotion	/=possible nucleotide deletion, \=possible
897 2247 A 7761 1725 445 RPERGROVEADPSEEWVQKYVSDLELSA RPERGROVEADPSEEWVQKYVSDLELSA RPERGROTHERSCUGSFRYSMERPKSTFLP, RPLSKRIFTHSSGOLSSFRYSMERPKSTFLP, RPLSKRIFTHSSGOLSSFRYSMERPKSTFLP, RPLSKRIFTSSGOLSSFRYSMERPKSTFLALGILKOK RIESTSKRISESODSEKENTKKDLLGILKOK RIESTSNAMANLTVKHGTVKY RSSALLARTKNOUGFFGTNSVCKSKDKOS RIESTSKRISESODSEKENTKKDLLGILKOK RTESTSKRIFTSSGOLSEKENTKKDLLGILKOK RTESTSKRIFTSSGOLSEKENTKKDLLGILKOK RTESTSSELWOLKARAVADSLPFKK TTKSELLSQLQGHEESERAGDAKRPKISFS SIDMKYARSATARVKRIFTSKRINFDMAAVTK APETDISPSLWOVERAKQLATVREQPLONG EELIQWTKEGKLWEPPINNEAGFDDDGSEFI EHIPLEKHLESTFROGPIRHMELLVTGLSKN VLSYKOKVEHEWRIYFINEKDLLKESNQ EELIQWTKEGKLWEPPINNEAGFDDDGSEFI EHIPLEKHLESTFROGPIRHMELLVTGLSKN VLSYKOKVEHEWRIYFINEKDLLKESNQ REKHISSLEGLLKALSQASTDPKESTSFE RIMMIDFFVOLMGKRSVQDSFTTONQENV SFGILKYPFRAE PFHGASSNTERLQVGTGESKAQKEVKMGF FSKSMAESMKOKEPMLANARLGLERQLIN QSEMRERQMAMQLAWSREFLKYRGTFGLA ASSLTANGASSNTERLQVGTGESKAQKEVKMGF FSKSMAESMKOKEPMLANARLGLERQLIN QSEMRERQMAMQLAWSREFLKYRGTFGLA ASSLTANGASSNTFIDK QSEMRERQMAMQLAWSREFLKYRGTFGLA ASSLTANGASSKRFTISK VVTPLKSYKIRSFSLHCQCEIFFEEFFTSSLQ GRINKUTTSKMAMVSEFLKQAWFIENEEQE VQTVKSSKGGPGSAVSFYTFINFSSDVAALI AKAMVKOVDEATIDLITKKNNARQOKA LQETGKFLIDETILKKALTGHLELASKT ACHEROMANDIKAFTYSEDVAALI ALAFSMASSNAALGSCSKEYNLLGQLOK TKYSKHDMINKVLDLEKGDIEGCLTATVK TSKAFFASKLHQAMKGGTTEHKALIRM RSEIDMBDIKAFTYSHQGLOVKHENEEQE VQTVKSSKGGPGSAVSFYTFINGSDVAALI GERKGTDVNVFNTILITRSYPQLRRVFOK TKYSKHDMINKVLDLEKGDIEGCLTATVK TSKAFFASKLHQAMKGGTTEHKALIRM RSEIDMBDIKAFTYSHQGLOVKHENEEQE VGTVKSSKGGPGSAVSFYTRINGSDVAALI GERKGTDVNVFNTILITRSYPQLRRVFOK TKYSKHDMINKVLDLEKGDIEGCLTATVK TSKAFFASKLHQAMKGGTTEHKALIRM RSEIDMBDIKAFTYSHQGLOVKHENE SUGRYCKWGESSINGATHERQUKGTAARRQ KOTAARROKGTAARRQKGTAARRQ KOTAARROKGTAARRQKGTAARRQ TAARROKGTAARROKGTAARRQ TAARROKGTAARROKGTAARRQ TAARROKGTAARROKGTAARRQ TAARROKG	1					į.	nucleotide insertion
A		<u> </u>			Sequence		OVSTAALAVILCTMALCNOVLSAPLAADTPT
TKRGRQVCADPSEEWQKYVSDLELSA SPRENGTHHESCUSFRVSAMFRYSTFLE SPRENGTHHESCUSFRVSAMFRYSTFLE PRISHPLSSGSPETSAAAMLLTVRHGTVXY RSSALLARTKNNORYFGTNSVICKSKDKQS RTSETSKETSESQDSEKENTKKDLLGIIKGMK VELSTVNNYTTKPFKRPLKSILEATLGRRR, TEYAFKKREPLSPELVAAASAVADSLPFKKK TTKSELLSQLQHEEESRAQRAKRPKISFS- SIDMKVARSATARVRSPLEXIPEDGYDNY GQEKTDDLKKRNIFTGKRLNIFDMMAVTK APETDISSEL MUDERAQLATIVEQLQNG EELIQWTKEGKLWEFPINBEAGFDDDGSEFH HHFLEKHLESPFKQCHATVEQLQNG EELIQWTKEGKLWEFPINBEAGFDDDGSEFH HHFLEKHLESPFKQCHATVEQLQNG EELIQWTKEGKLWEFPINBEAGFDDDGSEFH HHFLEKHLESPFKQGFRHFMELVTGGLSKN YLSVKQKVEHEWRNYTHEKDLLKESNQ VLSWKQKVEHEWRNYTHEKDLLKESNQ VLSWKQKVEHEWRNYTHEKDLLKESNQ SQRAVCKPQEEVVPGGGSKRAPDLVQL QSRGREQBLALSQSTDFKESTSFE RDMHDFFVGLMGKRSVQPDSFTDVNQENV SGULKYPFRAE S99						į	ACCESYTSROIPONFIADYFETSSQCSKPSVIFL
897 2247 A 7761 1725 445 RPRRIGITHIFSCYLOSIR NYSAMIFRY VISITLE, PLISSIPPL SSAMILATIONAL CHARTON OF THE PRISE AND ALL THE PRI			}	ļ	1		TKRGROVCADPSEEWVOKYVSDLELSA
RPISRIPI-SSGSFETSAAAMLLTVRHGTVSKKDKQSK RSSALLARTKNINGRYEGINSVCSKKDKQSK RSSALLARTKNINGRYEGINSVCSKKDKQSK RESTAKETSESQDSEKENTKKDLLGIIKGKR VELSTVAVRITFPKPRPILSLELBATLGRURR TEYAPKKRIPI-SPEL VAAASAVADSL-PTOKENT GOOKTIDDLKKRKNIFTGKRI-NIPDMAYVISFSK SISMKVARSATARVRSRPELRIOFDEGYDNY GOEKTIDDLKKRKNIFTGKRI-NIPDMAYVISFSK SISMKVARSATARVRSRPELRIOFDEGYDNY GOEKTIDLKKRKNIFTGKRI-NIPDMAYVISFSK APETISPSIL WDVEFARQLATVNEOPLONG RELIQWYKGKL-WEPPINNEAGFDDLGSEN RELIQWYKGKL-WEPPINNEAGFDDLGSEN RELIQWYKGKL-WEPPINNEAGFDDLGSEN RELIQWYKGKL-WEPPINNEAGFDDLGSEN RELIQWYKGKL-WEPPINNEAGFDDLGSEN RELIQWYKGKL-WEPPINNEAGFDDLK-SINGRANG-PHINNEAGFDDLGSEN RELIQWYKGKL-WEPPINNEAGFDDLK-SINGRANG-PHINNEAGFDDLK-SINGRANG-PHINNEAGFDDLK-SINGRANG-PHINNEAGFDDLK-SINGRANG-PHINNEAGFDDLK-SINGRANG-PHINNEAGFDDLK-SINGRANG-PHINNEAGFD-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFDLK-SINGRANG-PHINNEAGFD-	<u> </u>		ļ.,—	0001	1725	445	PPPRRGTHHESCYLGSFRYSAMFPRYSTFLPL
RSSALLARTKNNIQRYFGTNSVICSKROKY	897	2247	A	//01	1723	177	RDI SRHPI SSGSPETSAAAIMLLTVRHGTVRY
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GERRKGTDVNVFNTILTTRSYPQLRRVFQK TKYSKHDMNKVLDLELKGDIEKCLTAIVKC TSKPAFFAEKLHQAMKGVGTRHKALIRIMV RSEIDMNDIKAFYQKMYGISLCQAILDETKC YEKILVALCGGN VEFHPQRARAGARAPSMGVLLTQRTLLSLV ALLFPSMASMAAIGSCSKEYRVLLGQLQKC DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAF NILGLRNNIYCMAQLLDNSDTAEPTKAGRC SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR 721 TAARRQKGTAARRQKGTAARRQKGTA RRQKGTAARRQKGTAARRQKGTA QKGTAARRQKGTAARRQKGTAARRQ TAARRQKGTAARRQKGTAARRQCCA AGGVRGAGSRLRAMAPKVFRQYWDIPDG CHRKAYSTTSIASVAGLTAAAYRVTLNPPG LEGVAKVGGYTFTAAAVGAVFGLTTCISAL	1		1		1		VEID DINR VYREELKRDLAKDITSDTSGDFKN
GERRKGTDVNVFNTILTTRSYPQLRRVFQK TKYSKHDMNKVLDLELKGDIEKCLTAIVKC TSKPAFFAEKLHQAMKGVGTRHKALIRIMV RSEIDMNDIKAFYQKMYGISLCQAILDETKC YEKILVALCGGN VEFHPQRARAGARAPSMGVLLTQRTLLSLV ALLFPSMASMAAIGSCSKEYRVLLGQLQKC DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAF NILGLRNNIYCMAQLLDNSDTAEPTKAGRC SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR 721 TAARRQKGTAARRQKGTAARRQKGTA RRQKGTAARRQKGTAARRQKGTA QKGTAARRQKGTAARRQKGTAARRQ TAARRQKGTAARRQKGTAARRQCCA AGGVRGAGSRLRAMAPKVFRQYWDIPDG CHRKAYSTTSIASVAGLTAAAYRVTLNPPG LEGVAKVGGYTFTAAAVGAVFGLTTCISAL	1		1		1		ALT STAKEDRSEDFGVNEDLADSDARALYEA
TKYSKHDMNKVLDLELKGDIEKCLTAIVKC TSKPAFFAEKLHQAMKGVGTRHKALIRIMV RSEIDMNDIKAFYQKMYGISLCQAILDETKC YEKILVALCGGN VEFHPQRARAGARAPSMGVLLTQRTLLSLV ALLFPSMASMAAIGSCSKEYRVLLGQLQKC DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAF NILGLRNNIYCMAQLLDNSDTAEPTKAGRC SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR 721 TAARRQKGTAARRLQKGTAARRRQKGTA RRQKGTAARRQKGTAARRRQKGTAARRQ QKGTAARRRQKGTAARRRQKGTAARRRQ TAARRRQKGTAARRRQKGTAARRRQ CHRKAYSTTSIASVAGLTAAAYRVTLNPPGG CHRCATARTRUCHTAGLT CHRCATARTRUCHTAGLT CHRCATARTRUCHTAGLT CHRCATARTAGLT CHRCATART			1	1	1	1	GERRYGTDVNVFNTILTTRSYPQLRRVFQKY
PO1 2251 A 7796 2 807 VEFHPQRARAGARAPSMGVLLTQRTLLSLV ALLFPSMASMAAIGSCSKEYRVLLGQLQKQ DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAF NILGLRNNIYCMAQLLDNSDTAEPTKAGRQ SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSK WGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR TAARRRQKGTAARRLQKGTAARRRQKGTA QKGTAARRRQKGTAARRRQKGTAARRQK TAARRRQKGTAARRRQKGTAARRRQKGTAARRQ CKGTAARRRQKGTAARRRQKGTAARRQV TAARRRQKGTAARRRQKGTAARRQV TAARRRQKGTAARRQKGTAARRQV CHRKAYSTTSIASVAGLTAAAYRVTLNPPOG CHRKAYSTTSIASVAGLTAAAYRVTLNPPOG				1	1	1	TRYSKHDMNKVLDLELKGDIEKCLTAIVKCA
PO1 2251 A 7796 2 807 VEFHPQRARAGARAPSMGVLLTQRTLLSLV ALLFPSMASMAAIGSCSKEYRVLLGQLQKQ DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAF NILGLRNNIYCMAQLLDNSDTAEPTKAGRQ SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSK WGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR TAARRRQKGTAARRLQKGTAARRRQKGTA QKGTAARRRQKGTAARRRQKGTAARRQK TAARRRQKGTAARRRQKGTAARRRQKGTAARRQ CKGTAARRRQKGTAARRRQKGTAARRQV TAARRRQKGTAARRRQKGTAARRQV TAARRRQKGTAARRQKGTAARRQV CHRKAYSTTSIASVAGLTAAAYRVTLNPPOG CHRKAYSTTSIASVAGLTAAAYRVTLNPPOG			1		1	į	TSKPAFFAEKLHQAMKGVGTRHKALIRIMVS
901 2251 A 7796 2 807 VEFHPQRARAGARAPSMGVLLTQRTLLSLV ALLFPSMASMAAIGSCSKEYRVLLGQLQKQ DLMQDTSRLLDPYIRIQGLDVPKLREHCREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAR NILGLRNNIYCMAQLLDNSDTAEPTKAGRO SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR 721 TAARRQKGTAARRLQKGTAARRQKGTAAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARAYRVTLNPPGC CHRKAYSTTSIASVAGLTAAAYRVTLNPPGC LEGVAKVGGYTFTAAAVGAVFGLTTCISAL	1	1	- 1	1	1		RSEIDMNDIKAFYQKMYGISLCQAILDETKGD
ALLFPSMASMAAIGSCSKEYRVLLGQLQRQ DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAR NILGLRNNIYCMAQLLDNSDTAEPTKAGRO SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR 721 TAARRRQKGTAARRLQKGTAARRRQKGTAARRQKGTAARRQKGTAARRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARAPKVFRQYWDIPDGGCHRKAYSTTSIASVAGLTAAAYRVTLNPPGGLITCISAL		1	1		1		YEKILVALCGGN
ALLFPSMASMAAIGSCSKEYRVELOULOKO DLMQDTSRLLDPYIRIQGLDVPKLREHCREI GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAR NILGLRNNIYCMAQLLDNSDTAEPTKAGRO SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR 721 TAARRRQKGTAARRLQKGTAARRRQKGTAARRQKGTAARRQKGTAARRQKGTAARRRQKGTAARRRQKGTAARAYRQTLNPPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYSTTSIASVAGLTAAAYRVTLNPGCHRKAYTTNPGCHRTATATATATATATATATATATATATATATATATATATA	-001	2251		7796	2	807	VEFHPQRARAGARAPSMGVLLIQKILLSLVL
GAFPSEETLRGLGRRCFLQTLNATLGCVLH ADLEQRLPKAQDLERSGLNIEDLEKLQMAF NILGLRNNIYCMAQLLDNSDTAEPTKAGRC SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR TAARRQKGTAARRLQKGTAARRRQKGTA RRQKGTAARRPQKGTAARRRQKGTAARRQ QKGTAARRPQKGTAARRRQKGTAARRRQ TAARRQKGTAARRRQKGLAIASRGCPCA AGGVRGAGSRLRAMAPKVFRQYWDIPDG' CHRKAYSTTSIASVAGLTAAAYRVTLNPPG LEGVAKVGGYTFTAAAVGAVFGLTTCISAL	901	2231	1^	1 '''	_		ALLFPSMASMAAIGSCSKEYKYLLGQLQKQI
ADLEQRLPKAQDLERSGLNIEDLEKLQMAR NILGLRNNIYCMAQLLDNSDTAEPTKAGRO SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGV TRPSRKGKRLMTRGQLPR 902 2252 A 7802 2 721 TAARRRQKGTAARRLQKGTAARRQKGTAARRQKGTAARRQKGTAARRRQKGTAARRQKGTAGATATATATATATATATATATATATATATATATATA	-	- 1		1	1 ·	1	DLMQDTSRLLDPYIKIQULDVPALKERCKERF
902 2252 A 7802 2 721 TAARRQKG]	1	1	GAFPSEETLROLGKRCFLQILNAILUCVLARL
SQPPTPTPASDAFQRKLEGCRFLHGYHRFM SVGRVFSKWGESPNRSRRHSPHQALRKGVI TRPSRKGKRLMTRGQLPR TAARRRQKGTAARRLQKGTAARRQKGTA RRRQKGTAARRPQKGTAARRRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQKGTAARRRQTAAAGGVRGAGSRLRAMAPKVFRQYWDIPDGGCHRKAYSTTSIASVAGLTAAAYRVTLNPPGGLTGSAL	Ì				1		ADLEQRIPKAQULERSGLNIEULEALQIMARP
902 2252 A 7802 2 721 TAARRRQKGTAARRLQKGTAARRQCPCAAGGVRGAGSRLRAMAPKVFRQYWDIPDGGCHRKAYSTTSIASVAGLTAAAYRVTLNPPGGAGSACKAAVGGVFFTAAAAVGAVFGLTTCISAL			1	1	1		NILGLRINIYCMAQLLDINDDIAEPIKAGROA
902 2252 A 7802 2 721 TAARRRQKGTAARRLQKGTAARRQKGTAARGKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQK	j		- [1	1	SQPPTPTPASDAFQKKLEGCKFLHG I FIGVED
902 2252 A 7802 2 721 TAARRRQKGTAARRLQKGTAARRQQKGTAARRQQKGTAARQQKGTAARQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQXGQTAARQQQXGQTAARQQQXGQTAARQQQXGQTAARQQQQXGQTAARQQQQQXGQTAARQQQXGQQQXGQQQQXGQQQQXGQQQQQQQQQQQQQQQ		1	1				SVGRVFSKWGESPNRSKRHSPHQALKKGVKK
902 ZZSZ A 780Z Z RRRQKGTAARRPQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGTAARRQKGLAIASRGCPCA AGGVRGAGSRLRAMAPKVFRQYWDIPDG CHRKAYSTTSIASVAGLTAAAYRVTLNPPGLEGVAKVGQYTFTAAAVGAVFGLTTCISAL			1_	1	1		TRPSRKGKRLMTRUQLPK
RRRQKGTAARRPQKGTAARRRQKGTAARRQCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	000	2252	- _	7802	2	721	TAARROKGTAARKLOKGTAARKKOKGTAA
TAARRRQKGTAARRRQKGLAIASRGCPCA AGGVRGAGSRLRAMAPKVFRQYWDIPDG CHRKAYSTTSIASVAGLTAAAYRVTLNPPC	902	2232	\ \ \ \	1 1002	-		RRRQKGTAARRPQKGTAARKKQKGTAARKK
AGGVRGAGSRLRAMAPKVFRQYWDIPDG CHRKAYSTTSIASVAGLTAAAYRVTLNPPG LEGVAKVGOYTFTAAAVGAVFGLTTCISAI	1						QKGTAARRQKGTAARRPQKGTAAKRRQKG
CHRKAYSTTSIASVAGLTAAAYRVTLNPPG LEGVAKVGOYTFTAAAVGAVFGLTTCISAI	l		i				TAARROKGTAARROKGLAIASKGCPCASK
			1	1	1	ļ	AGGVRGAGSRLRAMAPKVFKQYWDIPDGTD
LEGVAKVGQYTFTAAAVGAVFGLITCISA			- 1		-		CHRKAYSTTSIASVAGLTAAAYKVILNPPGT
	İ		1				LEGVAKVGQYTFTAAAVGAVFGLI ICISAHV
REKPDDPLNYFLGGCAGGLTLGARIHNIO	1				}	Ì	REKPDDPLNYFLGGCAGGLTLGARTHNYGIG
AAACVYFGIAASLVKMGRLEGWEVFANT	1		l		1		AAACVYFGIAASLVKMGRLEGWEVFAKPKV

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide	1	/=possible nucleotide deletion, \=possible
	j	1	1	sequence		nucleotide insertion
002	2253	A	7807	1	584	PWLPWSDGRAARSSRKCPRSRFPVQVGKMA
903	22.55	^	1007	-		VSTVFSTSSLMLALSRHSLLSPLLSVTSFRRFY
	Ĭ		ļ			RGDSPTDSQKDMIEIPLPPWQERTDESIETKR
	İ	[[ARLLYESRKRGMLENCILLSLFAKEHLQHMT
	1	ļ.	1	l		EKQLNLYDRLINEPSNDWDIYYWATEAKPAP
	1	1			ì	EIFENEVMALLRDFAKNKNKEQRLRAPDLEY
		l			ţ.	LFEKPR
904	2254	A	7813	40	821	GAGRALGHLETGAGDVAAALPARKFPRSLLG
904	22.54	\ ^	7025			AGARLTGWTMNVFRILGDLSHLLAMILLLGK
		1		1	İ	IWRSKCCKGISGKSQILFALVFTTRYLDLFTNF
	1	1	i	1	1	ISIYNTVMKVVFLLCAYVTVYMIYGKFRKTF
1	1	1	i	1		DSENDTFRLEFLLVPVIGLSFLENYSFTLLEIL
•	ì	1	1	}	i	WTFSIYLESVAILPQLFMISKTGEAETTTTHYL
l	-	1	1			FFLGLYRALYLANWIRRYQTENFYDQIAVVS
1	1	}	1	I		GVVQTIFYCDFFYLYVTKGRSWDDSNADTGL
•		ì				RSYSSI
905	2255	A	7817	1399	881	LSNKDVLSPQLKDENSKLRRKLNEVQSFSEA
703		1				QTEMVRTLERKLEAKMIKEESDYHDLESVVQ
		1		1	ì	QVEQNLELMTKRAVKAENHVVKLKQEISLL
].	ł	1	1	1	ĺ	QAQVSNFQRENEALRCGQGASLTVVKQNAD
1		1	1	i		VALQNLRVVMNSAQASIEQLVSGAETLNLVA
İ	l		1		<u> </u>	EILKSIDRISEVKDEEEDS DSPRNRFEILGRPTRTPTRPGPRPAMEDLDAL
906	2256	A	7822	3	1462	LSDLETTTSHMPRSGAPKERPAEPLTPPPSYG
1,,,,		1	1	·		HQPQTGSGESSGASGDKDHLYSTVCKPRSPK
	1.	l	Ì	1		PAAPAAPPFSSSSGVLGTGLCELDRLLQELNA
1	1			Į.	1	TQFNITDEIMSQFPSSKVASGEQKEDQSEDKK
1		İ		1	1	RPSLPSSPSPGLPKASATSATLELDRLMASLSD
		1		1		FRVQNHLPASGPTQPPVVSSTNEGSPSPPEPTG
						KGSLDTMLGLLQSDLSRRGVPTQAKGLCGSC
) .		1			NKPIAGQVVTALGRAWHPEHFVCGGCSTAL
Į.		1	1			GGSSFFEKDGAPFCPECYFERFSPRCGFCNQPI
	1		.}	}	į.	RHKMVTALGTHWHPEHFCCVSCGEPFGDEG
1	l l		1		į.	FHEREGRPYCRRDFLQLFAPRCQGCQGPILDN
1	}])	l	YISALSALWHPDCFVCRECFAPFSGGSFFEHE
1		İ		1	}	GRPLCENHFHARRGSLCATCGLPVTGRCVSA
1	1	1			1	LGRRFHPDHFTCTFCLRPLTKGSFQERAGKPY
1		1		1		COPCELKLEG
		 	7000	1792	1671	FIYVNQSFAPSPDQEVGTLYECFGSDGKLVLH
907	2257	A	7828	1/32	1077	YCKSOAWG
	10000	+	7042	110	1172	KI SCPCSHGTRVTAVRGPRLKAGVQWHDLG
908	2258	A	7842	110	1	ST OPPPSGLKOSSHLSLSSSWDFRHAPTHPET
1	1	1		}	1	VTCPKMTEMROAEAOLAELDLLASMFPGENE
1	1.			1	1	LIVNDOLAVAELKDCIEKKTMEGRSSKVYFTI
1		1	1	1	1	NIMNI DVSDEKMAMFSLACILPFKYPAVLPEL
	.					TVRSVLLSRSOOTOLNTDLTAFLQKHCHGDV
	1	1				CII NATEWVREHASGYVSRDTSSSPTTGSTVQ
1		1	1		1	SVDLIFTRI.WIYSHHIYNKCKRKNILEWAKEL
1	1	1		1	1	SLSGFSMPGKPGVVCVEGPQSACEEFWARLR
1		1		1		KI NWKRII IRHREDIPFDGTNDETERQRKFSIF
1		- 1	1	1		EEKVFSVNGARGNHMDFGQLYQFLNTKGCG
1	1	- 1	1	1		DVFOMFI.WV
1	0050		7870	3067	2923	EGICVYTFIYVHMYTRTCMHTYPYMYMNSV
909	2259	Α	/8/0	3007		LISSETLIPSKYLFESK
			7004	212	4874	GALTWSHPLLAVCPOGVWLGSTPSGSPALLP
910	2260	Α	7884	1 212	10/1	PSHRVNARPGCVVTNACASGPCPPHANCRDL
		1		1	1	WOTESCTCOPGYYGPGCVDACLLNPCQNQG
1						COLI DGAPHGYTCDCVGGYFGHHCEHKMU
					1	QQCPRGWWGSPTCGPCNCDVHKGFDPNCNK
1	_1					

			•			(A-Aloning C-Curtoing
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Į i			amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		nucleotide insertion
				sequence	ļ <u>-</u>	TNGOCHCKEFHYRPRGSDSCLPCDCYPVGST
	1	l				SRSCAPHSGOCPCRPGALGRQCNSCDSPFAEV
	ì	1		l		TASGCRVLYDACPKSLRSGVWWPQTKFGVL
	}			İ	j	ATVPCPRGALGLRGAGAAVRLCDEAQGWLE
	1	1	Í	ĺ	1	PDLFNCTSPAFRELSLLLDGLELNKTALDTME
	1		ł	l	-	AKKLAORLREVTGHTDHYFSQDVRVTARLL
		1	1			AHLLAFESHOOGFGLTATQDAHFNENLLWA
		1		1		GSALLAPETGDLWAALGQRAPGGSPGSAGLV
		ł		Ì	1	RHLEEYAATLARNMELTYLNPMGLVTPNIML
	1	1				SIDRMEHPSSPRGARRYPRYHSNLFRGQDAW
		İ			1	DPHTHVLLPSQSPRPSPSEVLPTSSSIENSTTSS
	1					VVPPPAPPEPEPGISIIILLVYRTLGGLLPAQFQ
		1]	l	1	AERRGARLPONPVMNSPVVSVAVFHGRNFLR
	1		1	1		GILESPISLEFRLLQTANRSKAICVQWDPPGLA EQHGVWTARDCELVHRNGSHARCRCSRTGT
	ì	1	\	ľ		FGVLMDASPRERLEGDLELLAVFTHVVVAVS
		1		1	1	VAALVLTAAILLSLRSLKSNVRGIHANVAAA
		1		1	1	LGVAELLFLLGIHRTHNQLVCTAVVILLHYFF
				i .		LSTFAWLFVQGLHLYRMQVEPRNVDRGAMR
	ļ	1	1	1		FYHALGWGVPAVLLGLAVGLDPEGYGNPDF
		1)		CWISVHEPLIWSFAGPVVLVIVMNGTMFLLA
	1	1	1	1		ARTSCSTGOREAKKTSALTLRSSFLLLLLVSA
	İ		1			SWIEGLIAVNHSILAFHYLHAGLCGLQGLAV
l				1		111 FCVI NADARAA WMPACLGRKAAPEEAR
		1		1		PAPGLGPGAYNNTALFEESGLIRITLGASTVSS
]	1	1		ł	1	VSSARSGRTQDQDSQRGRSYLRDNVLVRHGS
	1	1		1		AADHTDHSLQAHAGPTDLDVAMFHRDAGA
	'	1		1	ì	DSDSDSDLSLEEERSLSIPSSESEDNGRTRGRF
1	1	1	1		1	QRPLCRAAQSERLLTHPKDVDGNDLLSYWPA
Į.		1]	1	LGECEAAPCALQTWGSERRLGLDTSKDAAN
1	1	1		1		NNQPDPALTSGDETSLGRAQRQRKGILKNRL QYPLVPQTRGAPELSWCRAATLGHRAVPAAS
١.						YGRIYAGGGTGSLSQPASRYSSREQLDLLLRR
			İ	i		QLSRERLEEAPAPVLRPLSRPGSQECMDAAPG
i		[1	l		RLEPKDRGSTLPRRQPPRDYPGAMAGRFGSR
l	1	- [ł		DALDLGAPREWLSTLPPPRRTRDLDPQPPPLP
1		Ì	1	1	1	DALDED TO THE TOTAL THE CONTROL TO
ļ ·	ı		1	1	1	1 SPOROLSRDPLLPSRPLDSLSRSSNSREQLDQ
1		1	i	ļ		LSPQRQLSRDPLLPSRPLDSLSRSSNSREQLDQ VPSRHPSREALGPLPQLLRAREDSVSGPSHGP
1						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEOLDILSSILASFNSSALSSVOSSSTPLGPHT
1						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR
						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTOALLSATOAMDLRRDYHMERPLLNQEH
						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHOWRTWLOCSRARAYAL
						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL
						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMOLPOGLAYALLAGLPPVFGLYSSFYPVFIY
						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FI FGTSRHISVESLCVPGPVDT
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911	2261	A	7890	21	806	VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FLFGTSRHISVESLCVPGPVDT EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCPPKARSSSARWALTCCLVLLPFLAGLTTYL
911	2261	A	7890	21	806	VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEP DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FLFGTSRHISVESLCVPGPVDT EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCRPKARSSSARWALTCCLVLLPFLAGLTTYL LVSOLRAOGEACVOFOALKGQEFAPSHQQV
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911	2261	A	7890	21	806	VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FLFGTSRHISVESLCVPGPVDT EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCRPKARSSSARWALTCCLVLLPFLAGLTTYL LVSQLRAQGEACVQFQALKGQEFAPSHQVY YAPLRADGDKPRAHLTVVRQTPTQHFKNQFF ALHWEHELGLAFTKNRMNYTNKFLLIPESGD VEIVSQVTFRGMTSECSEIROAGRPNKPDSITV
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911	2261	A	7890	21		VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FLFGTSRHISVESLCVPGPVDT EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCRPKARSSSARWALTCCLVLLPFLAGLTTYL LVSQLRAQGEACVQFQALKGQEFAPSHQQV YAPLRADGDKPRAHLTVVRQTPTQHFKNQFF ALHWEHELGLAFTKNRMNYTNKFLIPESGG YFIYSQVTFRGMTSECSEIRQAGRPNKPDSITV VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ PIYLGAMFSLQEGDKLMVNVSDISLVDYTKE DKTFFGAFLL
		A	7890	1263	806	VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FLFGTSRHISVESLCVPGPVDT EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCRPKARSSSARWALTCCLVLLPFLAGLTTYL LVSQLRAQGEACVQFQALKGQEFAPSHQQV YAPLRADGDKPRAHLTVVRQTPTQHFKNQFF ALHWEHELGLAFTKNRMNYTNKFLIPESGD YFIYSQVTFRGMTSECSEIRQAGRPNKPDSITV VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ PIYLGAMFSLQEGDKLMVNVSDISLVDYTKE DKTFFGAFLL ACGIRHEGALPGLTATPEAMLRFLPDLAFSFL
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						VPSRHPSREALGPLPQLLRAREDSVSGPSHGP STEQLDILSSILASFNSSALSSVQSSSTPLGPHT TATPSATASVLGPSTPRSATSHSISELSPDSEPR DTQALLSATQAMDLRRRDYHMERPLLNQEH LEELGRWGSAPRTHQWRTWLQCSRARAYAL LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY FLFGTSRHISVESLCVPGPVDT EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCRPKARSSSARWALTCCLVLLPFLAGLTTYL LVSQLRAQGEACVQFQALKGQEFAPSHQQV YAPLRADGDKPRAHLTVVRQTPTQHFKNQFF ALHWEHELGLAFTKNRMNYTNKFLLIPESGD YFIYSQVTFRGMTSECSEIRQAGRPNKPDSITV VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ PIYLGAMFSLQEGDKLMVNVSDISLVDYTKE DKTFFGAFLL ACGIRHEGALPGLTATPEAMLRFLPDLAFSFL LILALGQAVQFQEYVFLQFLGLDKAPSPQKFG

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Accordic Acid. F=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I-Isoleucine K=Lysine L=Leucine.
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence			ng to first	acid residue	O-Glitamine R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ļ '	residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	1			peptide	Joques	/=possible nucleotide deletion, \=possible
	į	ĺ	İ	sequence		nucleotide insertion
				Sequence		PWPQGAVHFNLLDVAKDWNDNPRKNFGLFL
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residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion vilrftdfgddyvkiydglee LlrvltafdshapltvvsssgqlrvhfgNaArgfnatyQvdgfclpweipcggn TeQQrcdgywhcpngrdetnctmcQ CSRNGvCyprsDrcnyQnhcpngsde CQPgnfhcknnrcvfeswvcdsQddd	CADKV WGCY KEEFP KNCFF
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GLRWVRFTLGRSSSLSQNQSPLRQLDI	ות ו זם
REDDDDVEMLIPISDGSSDFDVNDCSP	TUDU
ASDQGQGLRQPYNATNPGVRPSNRDQ	JECERC
GIVHTAQIPDTCLEVTLKNETSDDEAL	CAULAC
919 2269 A 7951 1674 1839 VVRVTCCPPARSTTERTNAYDEEDCV	EMVAS
1919 12209 A 1754 1 GGWNDVACHTTMYFMCEFDKKNM	
920 2270 A 7953 47 572 GGRASWPEQAKEPRREGHTDKQQTE	DVLAA
920 2270 A 7333 THE GENERAL PRICAR MSPAFRAMOVE	PRAKU
VLLEPFVHQVGGHSCVLRFNETTLCK	PLVPRE
HOFVETI.PAEMRKFTPOYKGKSQLLE	GLPHW
RGDVRDRGHGRPWQPSLEPSLPPTLC	FPSLSS
FSSSWPSAOHLTPSVFNPW	
PSGRTVVTGIGYSKALOSSNRNTKSL	LQNEF
921 2271 A 7957 612 812 RSGRT V V GG T SKALQDS RATTOLE MMVYSFRALSFKESTWATFQHGGEA	TKSRSL
l l l · l l sgro	
1660 ENITEK WK EIWMCRGNKKSCCWTFII	DRHLT
922 2272 A 7967 1443 1660 ENTIER WREIWINGROUNDSCOW III	IRGFSN
WELVKPN	
CCAPRAATAMARARPPPPPSPPPGLL	LLPPLL
923 2273 A 7981 1 3023 GSAPRAATAMARARPPPPSPFOLLS	ELAWT
SHPESGWEEVSGYDEAMNPIRTYQV	NVRES
SQNNWLRTGFIWRRDVQRVYVELKF	TVRDC
NSIPNIPGSCKETFNLFYYEADSDVAS	ASSPEW
MENPYVKVDTIAPDESFSRLDAGRVI	JTKVRS
MENPYVKUDITATUESTSKUDAUKS	ARVKK
FGPLSKAGFYLAFQDQGACMSLISVR	
CASTTAGFALFPETLTGAEPTSLVIAP	CTCATG
AVEVSVPLKLYCNGDGEWMVPVGA	CICKIO
HEPAAKESQCRPCPPGSYKAKQGEG	CLICIF
NSRTTSPAASICTCHNNFYRADSDSA	DSACII
VPSPPRGVISNVNETSLILEWSEPRDL	GAKDD
LLYNVICKKCHGAGGASACSRCDDN	VEFVPR
OI.GI.SEPRVHTSHLLAHTRYTFEVQA	VNGVS
GK SPI PPR YA A VNITTNOA APSEVPT	LRLHSS
	TEKSEG
	QVRART
VAGYGOYSRPAEFETTSERGSGAQQ	LQEQLP
	QRHGS
Defytekt.OOYIAPGMKVYIDPFTYI	DPNEA
VREFAKEIDVSCVKIEEVIGAGEFGE	VCRGRL
KOPGRREVFVAIKTLKVGYTERQRR	DFLSEA
SIMGQFDHPNIIRLEGVVTKSRPVMII	TEFME
SIMGQFDHPNIRLEGVV TKSKT VIVII NCALDSFLRLNDGQFTVIQLVGMLR	GIAAGM
NCALDSFLRLINDGQF I VIQLVOMLIK KYLSEMNYVHRDLAARNILVNSNLV	CKACUE
KYLSEMNYVHKDLAARNILVNSNLV	LV ADE VI
GLSRFLEDDPSDPTYTSSLGGKIPIRV	CEDDA
AYRKFTSASDVWSYGIVMWEVMSY	OBKF I

			220	vi distad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
			i 1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide	į	nucleotide insertion
	}		1.	sequence		WDMSNQDVINAVEQDYRLPPPMDCPTALHQ
			1		ļ	LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA
		1	1]	ļ	SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD
	i .	l	l	1	ļ	SLKVIASAQSGNISQPLLDRI VIDITITITIVOS
			İ	l .		WLDAIKMGRYKESFVSAGFASFDLVAQMTA
	}	1		l		EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT
			1	1		LPVQV
201	2274	A	7985	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNF
924	22/4	^	1705	-		QLMRELDQRTEDKKAEIDILAAEYISTVKTLS
	1	1	ŀ			PDQRVERLQKIQNAYSKCKEYSDDKVQLAM
	1	į.	ľ	}		OTVEMVDKHIRRLDADLARFEADLKDKMEG
	1	1	İ	1		SDFESSGGRGLKKGRGQKEKRGSRGRGRRTS
		1	1			EELLEKKKKHKGG
				 	589	LPCSFCAQCMSSFERVWLQQSHFHNPRWNSR
925	2275	A	7994	447	289	CDIDCYCOHWPHCVHC
				J		CPCK VCCITI AIMLOCHSFYRKDVOVEHPKS
926	2276	A	7996	925	582	LNPKYSQIENFLSADMALKRKCLLSISDLDFW
,			1		\	IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQI
	I		1	1	ļ	RDTQPILPLGGRYYITIRQ
	1	1	1			RIQRPLNSRSPNHSLFVKAELTAKQATMKLSV
927	2277	A	7998	2	353	RIORPLNSKSPNHSLF VKAELTAKQATIMES
927	2211	1 **	1	1		CLLLVTLALCCYQANAEFCPALVSELLDFFFI
	1	ł			1	SEPLFKLSLAKFDAPPEAVAAKLGVKRCTDQ
ļ	l		1	1		MSLQKRSLIAEVLVKILKKCSV
	2000	A	8004	130	588	LAPLRCQPGTRTQPRSHPAANDPSAAMSAAG
928	2278	Α.	8004	1 200		ARGLRATYHRLLDKVELMLPEKLRPLYNHPA
		1	1	1	ì	GPRTVFFWAPIMKWGLVCAGLADMARPAEK
1		1	1		ì	I STAOSAVI MATGFIWSRYSLVIIPKNWSLFA
1	1	1		1		VNFFVGAAGASOLFRIWRYNQELKAKAHK
					1016	TELADDRIVEIA AREMSLLRSLRVFLVARIUS YF
929	2279	A	8007	2	1010	AGSLI ROSPOPRHTFYAGPRLSASASSKELLM
1	ı	1	1			L RI DDKTGYSEVNCKKALETCGGDLKQALIWL
ļ.	1	1		İ		LIKEAOKEGWSKAAKLOGRKTKEGLIGLLQE
		1	1	1		GNTTVLVEVNCETDFVSRNLKFQLLVQQVAL
	1	1.	Ì	1	'	GTMMHCQTLKDQPSAYSKGFLNSSELSGLPA
1		ì	- 1		1	GPDREGSLKDQLALAIGKLGENMILKRAAWV
	ì	1	1	1		KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG
1	Ì	1		Į		ALVICETSEQKTNLEDVGRRLGQHVVGMAPL
ì	ł	1		1		SVGSLDDEPGGEAETKMLSQPYLLDPSITLGQ
1	- (1	- 1	ł		SVGSLDDEFGGEAETRINESQT 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESQUE 2 DESCRIPTION OF THE SVGSLDDEFGGEAETRINESCUE TE
020	2280	- A	8008	3	1679	NSRVWGPWTEPSAGSLRPMARKQNRNSKEL
930	2200	1	0.00			GLVPLTDDTSHAGPPGPGRALLECDHLRSGV
1		1	1	1	1	PGGRRKDWSCSLLVASLAGAFGSSFLYGYN
1		ı			1 .	LSVVNAPTPYIKAFYNESWERRHGRPIDPDTL
1	-	1	1	1	1	TI I WSVTVSIFAIGGLVGTLIVKMIGKVLGKK
	1	1	i			TITT I ANNOPAISAALLMACSLOAGAFEMLIV
			1			GPEIMGIDGGVALSVLPMYLSEISPKEIRGSLG
1		ı	i	{		OVERTRICIGVETGOLLGLPELLGKESTWPYLF
		1		1	1	CVTVVPAVVOLLSLPFLPDSPRYLLLEKHNEA
	1	1				RAVKAFQTFLGKADVSQEVEEVLAESRVQRS
1		1	1	1		IRLVSVLELLRAPYVRWQVVTVIVTMACYQL
1	-	- 1	1	1		CGLNAIWFYTNSIFGKAGIPPAKIPYVTLSTGG
1		1	1		1	IETLAAVFSGLVIEHLGRRPLLIGGFGLMGLFF
	ľ	- 1			l	IETLAAVISGLVIEHLUKKILLIGUIGETATIA CECCO
	1	1	1	1		GTLTITLTLQDHAPWVPYLSIVGILAIIASFCSG
1	-	- 1			İ	PGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSN
ı			1	1	· I	FAVGLEPPIOKSLDTYCFLVFATICITGALYL,
	l .	- 1	1		İ	YFVLPETKNRTYAEISQAFSKRNKAYPPEEKI
1	1			- 1		DEANTDGKINGRP
	ļ		i			
					200	AAGAVVSAMPKAKGKTRROKFGYSVNRKKL
931	2281	A	8009	861	300	AAGAVVSAMPKAKGKTRRQKFGYSVNRKRL
931	2281	A	8009	861	300	AAGAVVSAMPKAKGKTRRQKFGYSVNRKRL NRNARRKAAPRIECSHIRHAWDHAKSVRQNL AEMGLAVDPNRAVPLRKRKVKAMEVDIEER

		24.	ara	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	поа	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq- uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
nence		\		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
'	1			peptide		/-possible nucleotide deletion, \-possible
			Į.	sequence		nucleotide insertion
						PKELVRKPYVLNDLEAEASLPEKKGNTLSRD
		1	Ì	Į.	İ	LIDYVRYMVENHGEDYKAMARDEKNYYQD
	ļ	ĺ		ļ	ļ	TPKQIRSKINVYKRFYPAEWQDFLDSLQKRK
		ĺ	1	ļ		MEVE
932	2282	A	8011	412	1	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG
,,,,		1				DIRGSHFSSPQRQRSQRVPGKETARVLRAGK
	1		Ī		Ì	QGRGQIPIPCPWPPPPPPPPPPPGSPGPGCRQFHQ SLEAKARHPASVREMRGKVKMRRALRRAPA
			!	1		SLEAKAKHPAS V KENIKUK V KWIKKALIKATA
	1					STRASSRQPNPK PPVPPASRSDMAQNLKDLAGRLPAGPRGMGT
933	2283	Α	8012	147	1077	ALKLLLGAGAVAYGVRESVFTVEGGHRAIFF
-						NRIGGVQQDTILAEGLHFRIPWFQYPIIYDIRA
		1		Į.	1	RPRKISSPTGSKDLQMVNISLRVLSRPNAQEL
•	1				1	PSMYQRLGLDYEERVLPSIVNEVLKSVVAKF
	ł	Ì	}		}	NASQLITQRAQVSLLIRRELTERAKDFSLILDD
	1	1				VAITELSFSREYTAAVEAKQVAQQEAQRAQF
		1	1			LVEKAKQEQRQKIVQAEGEAEAAKMLGEAL
		1		1	ì	SKNPGYIKLRKIRAAQNISKTIATSQNRIYLTA
		}	Ì	1	1	DNLVLNLQDESFTRGSDSLIKGKK
		.l		 	982	SQFSLSQVLVDSAEEGSLAAAAELAAQKREQ
934 -	2284	A	8023	255 .	982	RLRKFRELHLMRNEARKLNHQEVVEEDKRL
			ì			KLPANWEAKKARLEWELKEEEKKKECAARG
	İ	1	ļ.	ļ		EDYEKVKLLEISAEDAERWERKKKRKNFDLG
	1	1	1			FSDYAAAOLROYHRLTKOIKPDMETYERLRE
	ì	1	1	1	<u> </u>	KHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLE
	1	1	ł	İ	İ	KQIEKRDKYSRRRPYNDDADIDYINERNAKF
	1	1 .	1	ļ		NKKAERFYGKYTAEIKONLERGTAV
	10005	-	8027	59	310	LVSSTVNLLTEKAPWNSLAWTVTSYVFLKFL
935	2285	A	0027	1 33	} "	OGGGTGSTGMRDSALTLLGIGPSHRHSLSIRL
		1		1		SOHSSPAPMYSOTFHILVLG
026	2286	A	8032	1	639	SGRECNMAKTYDYLFKLLLIGDSGVGKTCVL
936	2280	ΙΛ.	8032	1.	***	FRESEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ
		İ		- (IWDTAGOERFRTITTAYYRGAMGIMLVYDIT
	ì		1.			NEKSFDNIRNWIRNIEEHASADVEKMILGNKC
	Ì	-		1		DVNDKRQVSKERGEKLALDYGIKFMETSAK
	}	1		1	}	ANINVENAFFTLARDIKAKMDKKLEGNSPQG
-	 .	ļ	1			SNQGVKITPDQQKRSSFFRCVLL
937	2287	A	8039	393	311	EETIHSENSYILEKYIPISANLTLTIA
938	2288	HÃ	8052	675	-1334	LHPAATSTAWLHVPPGLSMALSWVLTVLSLL
1,20		1 -		1		PLLEAQIPLCANLVPVPITNATLDRITGKWFYI
}	1	1	1 .	1	1	ASAFRNEEYNKSVQEIQATFFYFTPNKTEDTIF
1		1	1			LREYQTRQDQCIYNTTYLNVQRENGTISRYV
1				1		GGQEHFAHLLILRDTKTYMLAFDVNDEKNW
!				1	1	GLSVYADKPETTKEQLGEFYEALDCLRIPKSD
1						VVYTDWKKDKCEPLEKQHEKERKQEEGES SSVAEFPERVQLSQPQNWNFSGAGGAWSLDF
939	2289	A	8055	12	1039	22 APLICATION OF THE CECIT WORLD COMPOSED
1				- {		AEQLKWSAELARLGESIMDGKQGGMDGSKP AGPRDFPGIRLLSNPLMGDAVSDWSPMHEAA
1	1	1	l		1	AUTKUTTUIKLLSINTLINIUUAVSUNTSI MITLAN
1		1			1	IHGHQLSLRNLISQGWAVNIITADHVSPLHEA CLGGHLSCVKILLKHGAQVNGVTADWHTPL
	1	-		1	1	FNACVSGSWDCVNLLLQHGASVQPESDLASP
}	.1	- [1	1	}	IHEAARRGHVECVNSLIAYGGNIDHKISHLGT
ľ	1	1	[1	1	PLYLACENQQRACVKKLLESGADVNQGKGQ
1						DSPLHAVARTASEELACLLMDFGADTQAKN
			1			AEGKRPVELVPPESPLAQLFLEREGPPSLMQL
		}	J.	1	1	CRLRIRKCFGIQQHHKITKLVLPEDLKQFLLH
	1	- 1				
į			1	l l		
					1000	i.
940	2290	A	8058	2	1203	

					S 18.4 3 4.4	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
401100	}			amino acid	of peptide	T=Threonine, v=vaine, w=1typtopilat,
			}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
•				sequence		nucleotide insertion
	ļ		 			VVDTVMCPNMPNKSVLLYTLSFIYIFIFVIGMI
	1	ì			j	ANSVVVWVNIQAKTTGYDTHCYILNLAIADL
	1	ĺ		ĺ	ł	WVVLTIPVWVVSLVQHNQWPMGELTCKVTH
•	i	ŀ		ì		LIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS
		i		1		RKKMVRRVVCILVWLLAFCVSLPDTYYLKT
	1	1	1		1	VTSASNNETYCRSFYPEHSIKEWLIGMELVSV
	1	ĺ	\	1	į	VI.GFAVPFSIIAVFYFLLARAISASSDQEKHSS
	ł.	l	ì	1		RKITESYVVVYELVCWLPYHVAVLLDIFSILHYI
1	Ì		•		1	PETCRIEHALFTALHVTOCLSLVHCCVNPVL
	· ·	j		İ		YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA
		ł				SRVSETEYSALEQSTK
	l			<u></u> _	420	DMAGLMTIVTSLLFLGVCAHHIIPTGSVVLPS
941	2291	Α	8059	73	432	PCCMFFVSKRIPENRVVSYQLSSRSTCLKAGV
	1	}			ľ	IFTTKKGQQFCGDPKQEWVQRYMKNLDAKQ
	1	Į.	İ	Į.	1	KKASPRARAVAVKGPVQRYPGNQTTC
		1				GGIGEIKQRPSCLGRCLDPSLSVLMNISLGLGS
942	2292	Α	8067	278	1262	VFSAVISQKPSRDICQRGTSLTIQCQVDSQVT
						MMFWYRQQPGQSLTLIATANQGSEATYESGF
ļ		1	ł	1	.[VIDKFPISRPNLTFSTLTVSNMSPEDSSIYLCSA
İ	1	1	}	1	1	GRQGTYEQYFGPGTRLTVTEDLKNVFPPEVA
1	1	1	1	İ	1	VFEPSEAEISHTQKATLVCLATGFYPDHVELS
1	l l	1		1	Į.	WWVNGKEVHSGVSTDPQPLKEQPALNDSRY
1.						CLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
İ	1	1		}	· ·	NDEWTQDRAKPVTQIVSAEAWGRADCGFTS
j		Į.		1		ESYQQGVLSATILYEILLGKATLYAVLVSALV
ì		1		l		ESYQQQVLSATILTEILLORATLTAVLYSADY
		1		1	1	LMAMVKRKDSRG MVKVVPATRGNLPRSQLTGTHQHCQPREPKI
943	2293	A	8070	1	879	TASERLRRRPRATARLRAHAAPPEPPLAVFAP
/ "	====	1		[ļ	TASERLRRRPRATARLRAHAAFFEFFEAVIA
1	1	1	İ	1		PSDRKELLALPVACDPVIASVMSWVQAASLI PSDRKELLALPVACDPVIASVMSWVQAASLI
	1	1	-	1		QGPGDKGDVFDEEADESLLAQREWQSNMQR
l	- 1	į			ĺ	RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA
1		1			İ	EVILNYGRLRGTLSALLSWCHLHNNNSTLINK
	1 .	1	1	1		INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL
1						DSIEDMDLCHVVPAEKKIDEAKDERLCENNA
ì		1				EFNKNCSKSHSGIDCSYVECCRTQEHAHSGK
	1	1			Į.	PKPHMDFGTDSQF
944	2294	A	8073	1	797	ESARWSRQLRRTLIRLSFPISCGRSHAFGGCK
744	2234	10	1 30,3	1		MAATSGTDEPVSGELVSVAHALSLPAESYGN
1		1				DPDIEMAWAMRAMQHAEVYYKLISSVDPQF
1		1			1	LKLTKVDDOIYSEFRKNFETLRIDVLDPEELK
1			1		1	SESAKEKWRPFCLKFNGIVEDFNYGTLLRLD
1			ļ		1	CSOCYTEENTIFAPRIOFFAIEIARNREGYNKA
1		Į.	i		1	VYISVODKEGEKGVNNGGEKRADSGEEENT
		1	1		1	KNGGEKGADSGEEKEEGINREDKTDKGGEK
1	1			1	1	GKEADKEINKSGEKAM
						GAATLLRSASSAARKAAEAEQVWLHLHRYL
945	2295	Α	8074	2	505	SADRRVLGLREWGRPASERECSLCQRLKREL
1	1	1		1		NMGDVEKGKKIFIMKCSQCHTVEKGGKHKT
1	ļ	- 1	1	1		GPNLHGLFGRKTGQAPGYSYTAANKNKGIIW
1		1	1.	1		GEDTLMEYLENPKKYIPGTKMIFVGIKKKEER
1	1	1	- 1	l	1	ADLIAYLKKATNE
				1		EGRRGKFGGKLCNFLFYFHSNSAESRMDVLF
946	2296	A	8081	42	590	EGREGEL GENERAL CENTRAL STATES OF THE STATES
1		1				VAIFAVPLILGQEYEDEERLGEDEYYQVVYY
1	1	1	i	1	1	YTVTPSYDDFSADFTIDYSIFESEDRLNRLDK
1			1	1	l	DITEAIETTISLETARADHPKPVTVKPVTTEPQ
1		1		1		SPRSEAMPCPVLRSPIPLPPVRVPLFRWGCISC
1		- 1		1		KKVGRRLLMTLWMGVWQEEIGR
043	2207	+-	8084	322	549	GGGSSPRELAGAAGLTVTSQAVAARRQQPSF
947	2297	^	3007	1		SRARAPAHSLRAALSLASSARSWGAVSRDRG
947	2297	TA	8084	322	349	SRARAPAHSLRAALSLASSARSWGAVSRL

			4			
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
})	1		peptide	{	nucleotide insertion
1		l		sequence		PCPPAIMYQSSNKC
				L	<u> </u>	MEPGEVKDRILENISLSVKKLQSYFAACEDEI
948	2298	В	8093	3905	846	PAIRNHDKVLQRLCEHLDHALLYGLQDLSSG
	ì			_	1	YWVLVVHFTRREAIKQIEVLQHVATNLGRSR
	1					AWLYLALNENSLESYLRLFQENLGLLHKYYV
	l	}		1	1	KNALVCSHDHLTLFLTLVSGLEFIRFELDLDA
		1				PYLDLAPYMPDYYKPQYLLDFEDRLPSSVHG
1	1	}				SDSLSLNSFNSVTSTNLEWDDSAIAPSSEDYD
	ł	1	1			FGDVFPAVPSVPSTDWEDGDLTDTVSGPRST
		1	1			ASDLTSSKASTRSPTQRQNPFNEEPAETVSSS
İ	1	1			1	DTTPVHTTSQEKEEAQALDPPDACTELEVIRV
	1			1		TKKKKIGKKKKSRSDEEASPLHPACSQKKCA
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1		1	1		1	GPSSTTESSERSEPGLLIPEMKDTSMERLGQPL
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SVDLSHIPLKDPLLFKSASDTNLQKGISFMD T LSDKHLGKISEDESSGLVYKSGSGEIGSETSD KYDSEYTDSSSVI NYREDSNILSFDSDGNQNI	l	i	1		1		CDET SCREKOISEDINKIRSVI VNHMODINKOM							
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LSSTLTSKGNETIESIFKAEDLLPEAASLSENL	1		1		1	1	KANGERALDESSAL MANEURINI SEDSDONONI							
LSSILISKONE IESIFAAISUM DIVISEE	1		- 1		1	1	LOCAL TOP CHETTERIER ARDI L PEAASLSENL							
	i		-		1		LSSTLISKONE HESIFKAEDEGI EAGAGEGEI (2							

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	The Accountic Acid. E=Glutamic Acid.
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	\			amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1		Ì	residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
		I		sequence		DISKEETPPVRTLKSQSSLSGKPKERCPPNLAP
					Ì	LCVSYKNMKRSSSQMSLDTISLDSMILEEQLL
						ESDGSDSHMFLEKGNKKNSTTNYRGTAESVN
]	j	ł		AGANLQNYGETSPDAISTNSEGAQENHDDLM
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	1	1		Į.		DQLGNISLRHYLCNRPVGSDQKAVIHSKSSPE
	1	1	1	1		DOLGNISLRHYLCHRY VOSDQRAVITISROSI D
		i	1	İ		ISLRFESGPGAVIHSLLAEKNGFLQCHIENFST
}	}	i .				EFLTSSLMNIQHFLEDETVATVMPMKIQVSNT
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961	2311) ^	01/2	1		ACYKNKVVGWRSGVEKDLDEVLQTHSVFVN
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Į.		1		1		ETKRPYTVILIERAMKDIHYSVKTNKSTKQQA
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ì	1	}	}		.4	KEKI KPI IKVIESEDYGQQLEIVCLIDPGCFREI
	-	1		1	1	DELIKKETKGKGSLEVLNLKDVEEGDEKFE
		 	8175	286	587	NISNKAEVSSHPSVISHSMDSFGQPRPEDNQS
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	2313	À	0.0.	1.5		GMDLVWSAWYGKCVKGKGSLPLSAHGIVV
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	2313		0.01			GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDFLRLLYGMALVRFVNLISERKTKFAK
	2515	ķ	0.01			GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPI K CLAOEVNIPDWIVDLRHELTHKKMPHI
		,				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRGCYEVI.DWLOKTYWCRQLENSLRET
		Ģ				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WEI EFFREGIEEEDOEEDKNIVVDDITEQKPE
		Ģ				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PODDGKSTFSDYKADGDSKGSEEVDSHCKK
	2313	Ġ.				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERAREILVSYEEEOFTVLEKFRYL
	2313	4				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEGFTVLEKFRYL PK AIK AWNNPSPRVECVLAELKGVTCENREA
*	2313					GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VI DAFI DDGFLVPTFEOLAALQIEYEENVDL
*	2313	Ġ.	GIGI			GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVI VPKPFSOFWOPLLRGLHSQNFTQALLE
*	2313	Ġ.				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMI.SELPALGISGIRPTYILRWTVELIVANTKT
	2313	C.				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGOWEARRGWRLFNCSASLDWP
	2313	<i>C</i> ·				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP
	2313	C				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP
*	2313	C.				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRTVFELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EFOEKLLRICSIYTOSGENSLVQEGSEASPIGK
·	2313	C.				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTI DSI YWSVKPASSSFGSEAKAQQQEEQ
	2313	C.				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ
	2313					GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEKEEKEVLPDQVEEEEENDDQE
	2313					GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPITEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVOFFSTGQESPTA
						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEOFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPIFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTTP PLGRMPGOTEDPAELMLENYDTMYLLDQPV
	2313	c				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEOFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPIFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEORLEPSTCKTDTLGLSCGVGSGNCSNSSSS
	2313	c				GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDRMEVGPFSTGGESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS
OCA					1393	GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASFQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEENDDQE EEEEDEDDEDDEEDRMEVGPFSTGGESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF
. 964	2314	A A	8184			GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALINRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASFQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEDEDDDEDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQQQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLBSILLPPRLOLPAGFFSRCRWDPVSSPR
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEDEDDEDDEEDRMEVOPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEENDDQE EEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRGGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPITFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFSEAKAQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGFFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPITEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFNVLTNSQASAENFFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDLAG
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEOFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPIFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDEMMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDLAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPITEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDDDDEEDRMEVOFFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EFRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDOKKPVRFYHDWNDKEIEVLNKHLFLTS
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEDEDDEDDEEDRMEVOPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGYGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDFVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGFHLTRA FEDDDITHVEGSVDPIRDIEIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS
964						GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQVTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPITEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDDDDEEDRMEVOFFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EFRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI

		3.64	Lego	Predicted	Predicted end	Amino acid sequence (A=Alanine O=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ł	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	,	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ .			Sequence	/=possible nucleotide deletion, \=possible
	ł	l		peptide		nucleotide insertion
		<u> </u>	<u> </u>	sequence	ļ <u> </u>	ANMTQSALPKIKAGFAALQLEYFFTAGPDEV
	Į	1		l	1	RAWTIRKGTKAPQAAGKIHTDFEKGFIMAEV
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	Í	ļ	1		}	EDGDIIFFKFNTPQQPKKK
					1004	RSFSLSFSLLSPSEMMALGAAGATRVFVAMV
965	2315	Α	8195	1437	594	AAALGGHPLLGVSATLNSVLNSNAIKNLPPPL
		1			ì	GGAAGHPGSAVSAAPGILYPGGNKYQTIDNY
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	1	1				LACRKRRKRCMRHAMCCPGNYCKNGICVSS
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			j		<u> </u>	KFKLIKIMLLTLIILLPVVSKFSFVSLSAPQHW
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						DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM DVEHKMSIRILK

					To disk d and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	Ì	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide)	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-	!	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l			acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence)	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1		1	amino acid	of peptide	1=Inreonine, v=vaine, w=itypiophan,
1	1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
l		1	1	peptide	· •	/=possible nucleotide deletion, \=possible
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İ	1	J	<u>1</u>	sequence		ISSCPHTAYEGSMSTLSNFTQTLEDVFRRIFIT
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FORSOMALKOMOLSKNEGEREAQLIHURMIAS HTAAAARTQAPPTPKVOMTWTPKIKLAEAK HTAAAARTQAPPTPKVOMTWTPKIKLAEAK HTAAAARTQAPPTPKVOMTWTPKIKLAEAK KLNGVVLAKSODAQLVLLIMPGGGREVTUT STRRVTMEFLEVLTEGLARVLLVRGGGREVTUT STRRVTMEFNEVTSDRSKNEKRENAPSSTW RKIMSSPLSKER RQKYNVRSAPTRKDDEVQ VVRGHYKGQQIGKVVQVYRKKVTYTERVQ REKAMSSPLSKER RQKYNVRSAPTRKDDEVQ VVRGHYKGQQIGKVVQVYRKKVTYTERVQ REKAMSRQVGKEGETVRELIEKMOB 973 2323 A 8237 873 4610 GCPHGAGGGGREVTGGLTGGRTWSPSAAPRSC GPHGAGGGGRTVTGGLTGGRTWSPSAAPRSC PRPGPTPAGAMDKLPPSMKKRLYSLPQQV AKAWINDEEDABEEGAGGGDPSRSSIRLR PLPSPSSAAAGGTESRSSALGAADSEGPARG AGKSTNODCRIFRGSLASLGSAGGSGGTG SGSSHGHLIDSAEERALGAGDASPEDRIPP GLAAEPERPGASAQPAASPPPQQPPQPASA CQPFMQRGGAAAGQULPEAFULD QAGFMQRGGAAMQQULPEAFULD QAGFMQRGGAAMQQULPEAFULD QAGFMQRGGAAMQQULPEAFULD QAGFMQRGGAAMQULPEAFULD QAGFMCRGGAAAGQULPEAFULD QAGFMCRGGAAAGQULPEAFULD QAGFMCRGGAAAGQULPEAFULD QAGFMCRGGAAAGQULPEAFULD QAGFMCRGGAAAGQULPEAFULD QAGFMCRGGAAAGQULPEAFULD QAGFMCRGVAFWINIPYSDRFYWDLTML LLMYGNLIHVGUVEDINIPYSDRFYWDLTML LLMYGNLIHVGUVEDINIPYSDRFYWDLTML LLMYGNLIHVGUVEDINIPYSDRFYWDLTML LLMYGNLIHVGUVEDINIPYSDRFYWDLTML PRINTIPAL SILLIFLLISLELIKHRIQUE EIFHNTYDLASAVVRIVALIGMMLLCHVOG CLQFLVPMLQDFPDCVSINNAVNINSWGK QYSYALFFAAMSIMLCIGYGRQAPVGMSDV WLTMLSMINGATCYAMFGHATALIGSLISS RRQYGEKYRQVGYMSFHKLPPDTRQRIBD QUVQHREMAHACHEVQAAASATPTPTVW TYLQAPLQAAAATTSVAAIALTHHPRLPAAAG ASPASSPSOVDTSSSSFHIQQLAGFSAAAGGI PPLPSSSSSPPGAGGGGGAGSPSATFSAGVAATTIA GFGHFHKALGGSLSSSDSFLLTFLQPGARSPQ AAQPSAPPGAGGGGGSPSATFSAGVAATTIA GFGHFHKALGGSLSSSDSFLLTFLQPGARSPQ AAQPSAPPGAGGGGGGSPSATFSAGVAATTIA GFGHFHKALGGSLSSSDSFLLTFLQPGARSPQ AAQPSAPPGAGGGGLGLPHEHTPSSSSPPPQVPQR RGTPLTTGRLTQDLKLLIASASQALPQDGQGL LRRASPHSGGSGGGSGGS GGLGPPGRYGGIFGGGLGLPFARTSSSSPPPQVPQR RGTPLTTGRLTQDLKLLIASASQALPQDGQT LRRASPHSGGSGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGG	Į.	!	1				KVWRKCRMRIFTVAOVDDNSIQMKKDLQMF
HTAAAARTQAPPTPDKVQMTWRRSLIANS YRSRDTSLGSFEDLFSMKPQSWRRMITTAV KLNGVYLNKSQDAQLVLLNMPGPPKNRQGGEVITTYS PRETERVTEGLENKVLLVRGGGREVITTYS TSRTVTMKFNFPFYTSDRSKNRKKHPNAPSTY RRKIMSSPLSKELQKYNVRSKNPFKDDEVQ VRGMFYKGQQIGKVVQVYRKKYVYTERVC RRKANGTYTHYGIHPSKVVITRLKLDKDRKKI LERKAKSRQVVGKKGKYREELIEKMQB 973 2323 A 8237 873 4610 GCPHAGGGRVPTGGLTGGRTWSPSAAPRSC PROPTPAPGAMDKLPSMKKKLYSLPQQVG AKAWINDEEDAEEGAGGRQDPSRSRSIK PLPSPSSAAAGGTESRSSALGAADSGCPARG AGKSTNODCRFRGSLSJ.GSRGGGGGTG SGSSIGHLIDSAEERRLLAEGDSEARG AGKSTNODCRFRGSLSJ.GSRGGGGGTG GAGGMRQFGAMLQPGVMKFSLRMFGSQA VEREGERVKSAGFWIHPYSDRFFYWDLTMA LLMVGNLIHVGGTFFKDENTTPWIVTNVVSD TFFLIDLVLNFKTGIVVEDNTEILLDPQRKM YLKSWFMVDPTSSISPVYDFILVETRIDSEVYX TARALRIVRTFKLSLLRLLSLSKLRKTHGWG QYSYALFKAMSHMCLGVGRQAVYOMSDV WLTMLSMIVGATCYAMFGHATALICSLDSS RRYQBEKYRCOVYMSFHKLPPDTRQRHD YYGHRYQGKYGCVYMSFHKLPPDTRQRHD YYGHRYQGKYGCVYMSFHKLPPDTRQRHD YYGHRYGCKYGNYSFHKLPPDTRQRHD YYGHRYGCKYGNYSFHKLPPDTRQRHD YYGHRYGCKYGNYSFHKLPPDTRQRHD YYGHRYGCKYGNYSFHKLPPDTRQRHD YYGHRYGCKYGNYSFHKLPPDTRQRHD YYGHRYGCKYGCYMSFHKLPPDTRQRHD YYGHRYGCKYGCYMSFHKLPPDTRQRHD YYGHRYGCKYGCYMSFHKLPPDTRQRHD YYGHRYGCKYGCYMSFHKLPPDTRQRHD YYGHRYGCKYGCYMSFHKLPPDTRQRHD YYGHRYGCKYGCYMSFHKLPPDTRQRHD YYGHRYGCKYGCTARAFTYALDRL DRIGKKNSILLIKKVQHDLNSGVFNYQENSILD DRIGKKNSILLIKKVQHDLNSGVFNYQENSILD QIVQHDREMAHGAGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ł		1			Į.	LYHLRISAEVEVVEMVENDISAFTYERTLMM
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VEREGERVKSAGFWILHPYSDTRETYWIDTINL LLMVGNLIIIPVGITIFKDENTTEWIVFNVSD TFFLDLVLNRTIGIVVEDNTEIILDPQRIKMK YLKSWFMYDFISIFVDYIFLIVETRIDSEYYK TARALRIVRFTKILSLLRLLRLSRLBRVHQWE EIFHMTYDLASAVVRIVNLIGMMLLCHWDG CLQFLVPMLQDFPDDCWVSINNMYNNSWGK QYSYALFKAMSHMLCIGYGRQAPVGMSDV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRHD YYEHRYQGKMFDEESLGELSEPLREEINFNC RKLVASMPLANADPNFVTSMLTKLREEVFQ PGDYIIREGTIGKKMYFIQHGVVSVLTKGNKE TKLADGSYFGEICLLTRGRTTASVRADTYCE LYSLSVDNFNEVLEEYPMMRRAFETVALDRL DRIGKKNSILLHKVQHDLNSGVFNYQENEIIQ QIVQHDREMAHCAHRVQAAASATPTPTEVTW TPLIQAPLQAAAATTSVALALTHHPRLFPAHFR PPPGSGLGNLGAGQTPRHLKRLQSLIPSALGS ASPASSPSQVDTFSSSSFHIQQLAGFSAFAGLS PILLPSSSSSPPPGACGSPSAFTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGPFHFLPPPSSRSPSS SFGQLGQPPGBLSIGLATGFLSTPETPPRQPEP PSLVAGASGGASPVGFTRGGLSPFGHSFOPP RTTPSAPPRASGSHGSLLLPPASSPPPQVPGR RGTPPLTPGRLTQDLKLISASQFALPQDGAU LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPFGRPYGAIRGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	}.		1		1	1	OAGEMOROFGAMLOPGVNKFSLRMFGSQK.A
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PPPGSGLGNLGAGQTPRHLKRLQSLIPSALOS ASPASSPSQVDTTPSSSSFHIQQLAGFSAPAGLS PLLPSSSSSPPGACGSPSAPTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGELSLGLATGPLSTPETTPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL			1	1			TRI IOARI OA A ATTSVAIAI.THHPRLPAAIFR
ASPASSPSQVDTPSSSSFHIQQLAGFSAPAGLS PLLPSSSSSPPPGACGSPSAPTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	1	1	- 1	}			DDDCCCI GNI GAGOTPRHLKKLUSLIPSALUS
PLLPSSSSSPPPGACGSPSAPTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL		1	ĺ			1	ASPASSPSOVDTPSSSSFHIOOLAGFSAPAGLS
GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSSSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	1	-	-1				PLI PSSSSSPPPGACGSPSAPTPSAGVAATTIA
AAQPSPAPPGARGGLGLPEHFLPPPPSSKSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGSGGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	1		1			1	GEGHEHK ALGGSLSSSDSPLLTPLQPGARSPQ
SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL			1		1	[AAODSDADPGARGGLGLPEHFLPPPPSSKSPSS
PSLVAGASGGASPVGFTPRGGLSPPGHSPGFP RTFPSAPPRASGSHGSLLLPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGSGGSGSSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL			1			l	SPGOLGOPPGELSLGLATGPLSTPETPPRQPEP
RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL]		-	1	1		PSI VAGASGGASPVGFTPRGGLSPPGHSPGPP
LRRASPHSSGESMAAFPLFPRAGGGSGSGSSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL		1	1	1		}	RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR
GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	1	1	- 1	1			RGTPPLTPGRLTQDLKLISASQYALYQDGAQ1
USLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL 974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL		1	- 1	- {			LRRASPHSSGESMAAFPLFFRAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
974 2324 A 8247 279 468 EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	1		1	1	- 1		LOT ECAPATES GOPPI TAGPOREPGARPEPVR
974 2324 A 8247 279 468 EYKQWERRFLSCONRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL			ĺ			1	
974 2324 A 6247 LVPVKDASRICSLTYLLGSHWNNLVVRSPVL		_ L				160	FYKOWERRFLSCONRNDLGYGKPRKGGGLL
	974	2324	A	8247	279	400	LVPVKDASRICSLTYLLGSHWNNLVVRSPVL
							G

			Coro	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	De Agnartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
401,00]	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophian,
ì	1	}	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	{		peptide		/-possible nucleotide deletion, \-possible
	ļ	l		sequence		nucleotide insertion
		<u> </u>	10040	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYM
975	2325	Α	8249	02	13/1	MTKVLGMAPVLGPRPPQEQVGPLMVKVEEK
1	1	í	1	ļ	1	EEKGKYLPSLEMFRQRFRQFGYHDTPGPREA
1	1	1	!	ł	ł	LSQLRVLCCEWLRPEIHTKEQILELLVLEQFLT
1	l.	l	1	ŀ	1	ILPQELQAWVQEHCPESAEEAVTLLEDLEREL
1	1	1	1	i i		ILPQELQAW VQENCI ESALLIAV I EBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB
	ł	1	1	Į.		DEPGHQVSTPPNEQKPVWEKISSSGTAKESPS
1	1	i	1	1	1	SMQPQPLETSHKYESWGPLYIQESGEEQEFAQ
	1	1	1		1	DPRKVRDCRLSTQHEESADEQKGSEAEGLKG
1	1	1				DIISVIIANKPEASLERQCVNLENEKGTKPPLQ
1	1	1	1		(FAGSKKGRESVPTKPTPGERRYICAECGKAFS
1	ì	1	1	ł	0.0	NSSNLTKHRRTHTGEKPYVCTKCGKAFSHSS
1	1	1	1		1	NLTLHYRTHLVDRPYDCKCGKAFGQSSDLLK
1	1	1		ł	ì	HORMHTEEAPYOCKDCGKAFSGKGSLIRHYR
1.	1	1	1	1	1	IHTGEKPYQCNECGKSFSQHAGLSSHQRLHT
1	1		1	1	1	GEKPYKCKECGKAFNHSSNFNKHHRIHTGEK
	1]		i		PYWCHHCGKTFCSKSNLSKHQRVHTGEGEA
i	1	1		1 .		1
		1	1			P TENDROTCOLLE
076	2326	A	8257	298	7086	GNMACWPQLRLLLWKNLTFRRRQTCQLLLE
976	2320	1,	025.			VAWPLFIFLILISVRLSYPPYEQHECHFPNKAM
	!	٠ .	1		1	PSAGTLPWVQGIICNANNPCFRYPTPGEAPGV
1	İ	1	i	ľ		VGNFNKSIVARLFSDARRLLLYSQKDTSMKD
1	ì	1	l l			MRKVLRTLQQIKKSSSNLKLQDFLVDNETFS
1	1	1	}		į.	GET VHNI ST.PKSTVDKMLRADVILHKVFLQG
	1	1		1		VOI HI TSI CNGSKSEEMIOLGDQEVSELCGLP
		1	1	1	Į.	REKLAAAERVLRSNMDILKPILRTLNSTSPFPS
İ	ì				\	KELAEATKTLLHSLGTLAQELFSMRSWSDMR
į.	- {	1		1	1	QEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEG
ľ	- 1	[1			GGLKIKSLNWYEDNNYKALFGGNGTEEDAE
1	i	1	1			TFYDNSTTPYCNDLMKNLESSPLSRIIWKALK
ŀ	\	1	1	1		PLLVGKILYTPDTPATRQVMAEVNKTFQELA
1	Į.	l l	1	Ĭ	1	PLLVGKILI IPDIPATKŲ IMAEVISOEMOI VR
1	İ	- [-		1	VFHDLEGMWEELSPKIWTFMENSQEMDLVR
			i			MLLDSRDNDHFWEQQLDGLDWTAQDIVAFL
			1	•		AKHPEDVQSSNGSVYTWREAFNETNQAIRTIS
1	1		1	}		RFMECVNLNKLEPIATEVWLINKSMELLDER
1		1	1	1		KFWAGIVFTGITPGSIELPHHVKYKIRMGIDN
1	I	1	1		1	VERTNKIKDGYWDPGPRADPFEDMRYVWGG
1				1	1	FAVLODVVEOAIIRVLTGTEKKTGVYMQQMP
		1		1	1	VPCVVDDIFLRVMSRSMPLFMILAWIYSVAV
- I		1		1		IIKGIVYEKEARLKETMRIMGLDNSILWESWEI
1		- 1	1	1		COLIDIT VSAGLI VVILKLGNLLPYSDPSVVFV
1	-		1	1	1	FI CVEAVATII OCFLISTLESRANLAAACGGII
	1	- 1		ļ	j	VETT VI PVVI CVAWODYVGFTLKIFASLLSP
i	1	- 1	1		}	VAFGFGCEYFALFEEQGIGVQWDNLFESPVE
-	ı	- [1	1	EDGFNLTTSVSMMLFDTFLYGVMTWYIEAVF
-	1	- 1	· ·		1	FDQLWF119A9WMMTLD11F1GAMMIL TOPATA
.	1		1	· 1	1	PGQYGIPRPWYFPCTKSYWFGEESDEKSHPGS
ł	1	1		1	1	NOKRISEICMEEEPTHLKLGVSIQNLVKVYRD
		ı			ł	GMKVAVDGLALNFYEGQITSFLGHNGAGKT
			1	1	1	TTACH TGI EPPTSGTAYILGKDIRSEMSTIRQ
			-	1	1	NT GVCPOHNVLFDMLTVEEHIWFYAKLKGLS
		- 1	- 1			EVUVK A FMEOMALDVGLPSSKLKSKTSQLS
1	1	- 1	1	l	1	GCMORKI SVALAFVGGSKVVILDEPTAGVDP
1	1	- 1		· I		VCDPCIWEI LI KYROGRTIILSTHHMDEADVL
1		1				GDRIAIISHGKLCCVGSSLFLKNQLGTGYYLT
ł		- 1	I	1	ĺ	LVKKDVESSLSSCRNSSSTVSYLKKEDSVSQS
1				1		LAKKTA F29 F29 CVIA2231 A 2 LTVI TD ATA A
	1			1		SSDAGLGSDHESDTLTIDVSAISNLIRKHVSEA
i	į		1	1	1	RLVEDIGHELTYVLPYEAAKBGAFVBLFHEID
			1	1		DDI SDI GISSYGISETTLEEIFLKVAEESGVDA
1						ETERATI PARRIERAFGRICOSCLEPFTEDDA
1					1	ADDATOSOTOPESRETDLLSGMDGKGSYQVKG
			1			WKLTQQQFVALLWKRLLIARRSRKGFFAQIV
	1	1	1	ı)	

				N. distant	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in USSN	location	corresponding	I=Isoleucine K=Lvsine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	\ \	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	}	1 1	314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1			peptide	•	/-possible nucleotide deletion, \-possible
ł	<u> </u>			sequence		nucleotide insertion
				301		LPAVFVCIALVFSLIVPPFGKYPSLELQPWMY
Ì			[(NEQYTFVSNDAPEDTGTLELLNALTKDPGFG
ł		1	1		l	TRCMEGNPIPDTPCQAGEEEWTTAPVPQTIM
1		1				DLFQNGNWTMQNPSPACQCSSDKIKKMLPV
					1	CPPGAGGLPPPQRKQNTADILQDLTGRNISDY
	1		{	į.	{	LVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVS
	1	1	1		1	NTQALPPSQEVNDATKQMKKHLKLAKDSSA DRFLNSLGRFMTGLDTRNNVKVWFNNKGW
1		1	1			HAISSFLNVINNAILRANLQKGENPSHYGITAF
			1	Į		NHPLNLTKQQLSEVAPMTTSVDVLVSICVIFA
1				ł	ł	MSFVPASFVVFLIQERVSKAKHLQFISGVKPVI
1		1		1		YWLSNFVWDMCNYVVPATLVIIIFICFQQKSY
1	-	1	1		ļ	VSSTNLPVLALLLLLYGWSITPLMYPASFVFK
		1		1		IDSTAVVVI.TSVNLFIGINGSVATFVLELFION
		l	}	1	ł	KI NNINDILKSVFLIFPHFCLGRGLIDMVKNQ
1	ì	İ	1	1		AMADALEREGENREVSPLSWDLVGKNLFAM
1		İ	1		1	A VEGVVEELITVLIOYREFIRPRPVNAKLSPLN
i i		1	1			DEDEDVERERORILDGGGONDILLEIKELTKIY
	1	١.	1	1		RRKRKPAVDRICVGIPPGECFGLLGVNGAGK
1		 		1		SSTFKMLTGDTTVTRGDAFLNRNSILSNIHEV
1	1	1		1		HONMGYCPOFDAITELLTGREHVEFFALLRG
	1			1		VPEKEVGKVGEWAIRKLGLVKYGEKYAGNY VPEKEVGKVGEWAIRKLGLVKYGEKYAGNY
1		ĺ	-	1		SGGNKRKLSTAMALIGGPPVVFLDEPTTGMD
1	1			Ì		PKARRFLWNCALSVVKEGRSVVLTSHSMEEC
				1		EALCTRMAIMVNGRFRCLGSVQHLKNRFGD GYTIVVRIAGSNPDLKPVQDFFGLAFPGSVPK
ļ	ľ	1	1	1		EKHRNMLQYQLPSSLSSLARIFSILSQSKKRLH
	İ	1				IEDYSVSQTTLDQVFVNFAKDQSDDDHLKDL
1	Ì			1		SLHKNQTVVDVAVLTSFLQDEKVKESYV
1		İ			1500	IPGSTISFSLCFIFPPCVPTMVRKPVVSTISKGG
977	2327	A	8260	3	1567	YLQGNVNGRLPSLGNKEPPGQEKVQLKRKV
		- {	ì		1	TI I RGVSIIIGTIIGAGIFISPKGVLQNTGSVGM
1		}	1			STITIWTYCGYLSLFGALSYAELGTTIKKSGGH
<u>'</u>		1	1	1		VTVII EVEGPLPAFVRVWVELLIIRPAATAVIS
	1		1	1		LAFGRYILEPFFIOCEIPELAIKLITAVGITVVM
	1	- 1		1		VI NSMSVSWSARIOIFLTFCKLTAILIIIVPGV
	,	}		1	}	MOLIKGOTONFKDAFSGRDSSITRLPLAFYYG
i		1	į			MYAYAGWFYLNFVTEEVENPEKTIPLAICISM
1		1		1	1	AIVTIGYVLTNVAYFTTINAEELLLSNAVAVT
1	-	1		1	1	FSERLLGNFSLAVPIFVALSCFGSMNGGVFAV
1	1	1	-		1	SRLFYVASREGHLPEILSMIHVRKHTPLPAVIV
1			ì	i		LHPLTMIMLFSGDLDSLLNFLSFARWLFIGLA
		1	1	1	1	VAGLIYLRYKCPDMHRPFKVPLFIPALFSFTC LFMVALSLYSDPFSTGIGFVITLTGVPAYYLFII
		1	1	1		WDKKPRWFRIMSEKITRTLQIILEVVPEEDKL
] .		1		1		RGGSLRCVLGKLLGQLLCFQSERCVRFPEGLL
978	2328	A	8261	2	2165	RGGSLRCVLGKLLGQLLCFQSERCVKITEGES RHRGCGLLSSRLSAGKPPLRTSFFGSWGVLPP
1		1				LADAASMSGVRAVRISIESACEKQVHEVGLD
				1		GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE
	1	1	1		1	EEAAGTEGDAQEWPGAGSSADQDDEEGVVK
		1	1 .	(Ì	FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI
	1	1	- 1	1		VRDKKFMTI.DPVSODALPPKQNPQTLQLISK
1		1	- [1	1	PRST AGA AOTLIKGAERLTKSVTENQENKLQ
1		1		[PDENSELLRI.ROHWKLRKVGDKILGDLSYKS
- 1		l	ì	- 1	1	AGGI FPHHGTFEVIKNTDLDLDKKIPEDYCPL
		١.	1		1	DVOIDSDI EGSAYIKVSIOKOAPDIGDLGI VN
i	- 1	.	1			I EKRPI PKSKPGSPHWOTKLEAAQNVLLCKEI
l					}	EACT SPEAVOIKSOVPHIVVKNOIISQPFPSLQ
1	}		}	1		I SISI CHSSNDKKSOKFATEKOCPEDHLY VLE
	1			1		HNLHLLIREFHKQTLSSIMMPHPASAPFGHKR
	i i	ł	1	ı	1	

SEQ ID SEQ ID With SEQ I Properties Properties DeAspartic Acid, E=Glutamic Acid,				OTIC I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
much colde social continuous per	SEQ ID			- 1			D=A spartic Acid. E=Glutamic Acid,
Second S	NO: of		uoa	1			F=Phenylalanine, G=Glycine, H=Histidine,
See- Uence 1946					•		I=Isoleucine, K=Lysine, L=Leucine,
Beg		-				to last amino	M=Methionine, N=Asparagine, P=Proline,
mino soid residue of peptide residue of peptide sequence esidue of residue of	•	uence			•		Q=Glutamine, R=Arginine, S=Serine,
Presiduc of peptide pe	uence			214			T=Threonine, V=Valine, W=Tryptophan,
Popsible nucleotide ediction, \(\foatign{center} \)		1					Y=Tyrosine, X=Unknown, *=Stop codon,
							/=possible nucleotide deletion, \=possible
MRI.SGPQAFDKNEINSLQSSEDLEKIIKQAK HIFLRSRAAATIDSLASREDPQQAFWSNINDD		}		}			nucleotide insertion
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VTDDFAAHLTLEHRAPRDLDESSGVRHVRR MFHPGRGI.GGPRARRSNMHFTSSSTGGLSSS QSSYSPSNREAMDPIAELLSQLSGVRRSAGGQ LNSSGPSASQL.QQLQMQLQLERQHAQAARQ QLETARNATRRTNTSSVTTITIQSTATTNIAN TESSQQTLQNSQFLLTRLNDPKMSETERQSM ESERADRSLFVQELLLSTLVREESSSSDEDDR GEMADFGAMGCVDIMPLDVALENLNLKESN KGNEPPPPPL 982 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEPRAGGRPRRRRDLGS RLQAQRAQRVAWAEADENEEAVILAQEE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAEREERKRLESQREAEWKKEEERLR LEEEQKEEEERKAREEQAQREHEEYLKLKEA FVVEEEGVGETMTEEQSQSTLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA 983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPLRSPSI.DNPTPFPNLGFSENPLKRLLVPG			1	ì	}	}	FDLYYGGEAFSVEQPQSFICFICGAMGIIEI
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982 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFITRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEPRAGGRPRRRDLGS RIQAQRRAQRVAWAEADENEEAVILAQEE EGVEKPAETHLSGKIGAKKLRLEEKQARKA QREAEEAEREERKRLESQREAEWKKEEERLR LEEEQKEEERKAREEQAQREHEEYLKLKEA FVVEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFTYTTPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA 983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DILPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYTEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPPGPPSLAVAPEP CPOPLRSPSI.DNPTPFPNLGPSENPLKRLLVPG	1	1	1			1	VTDDFAAHLTLEHRAPRDEDESSGVRTVRC
P82 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFILTSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEEAVILAGE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAREERKRLESQREAEWKEEERLR LEEEQKEEERKAREQAQREHEEYLKLKEA FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA P83 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPPSLAVAPEP CPOPL RSPSL DNPTPFFPNLGFSENPLKRLLVPG	1		1	1		ł	MEHPURGLOGERARCHIMIT 1991 GOLGO
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TESSQQTLQNSQFLLTRLNDPKMSETERQSM ESERADRSLFVQELLLSTLVREESSSSDEDDR GEMADFGAMGCVDIMPLDVALENLNLKESN KGNEPPPPPL 982 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEAVILAQEE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAEREERKALESQREAEWKKEEERLR LEEEQKEEEERKAREEQAQREHEEYLKLKEA FVVEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFTYTTPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA 983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPPSLAVAPEP CPOPL RSPSL DNPTTFFPNLGFSENPLKRLLVPG				l	1	j	OF ETARNATRETNISSYTTITOSTATINIAN
P82 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEAVILAQEE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAERERKRLESQREAEWKKEEERLR LEEEQKEEERKAREEQAQREHEEYLKLKEA FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFTYTTPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA P83 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPL RSPSL DNPTTFFPNLGFSENPLKRLLVPG	1	1	1	1	1	1	TESSOOTI ONSOFILTRLNDPKMSETEROSM
982 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEAVILAQEE EGVEKPAETHLSGKIGAKKLRLEEKQARKA QREAEEAEREERKRLESQREAEWKKEEERLR LEEEQKEEEERKAREEQAQREHEEYLKLKEA FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFTYTTPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA 983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPLRSPSLDNPTTFFPNLGFSENPLKRLLVPG			1	}		1	FSFRADRSLFVOELLLSTLVREESSSSDEDDR
SCHEPPPPPL			.1	1		1	GEMADFGAMGCVDIMPLDVALENLNLKESN
982 2332 A 8315 1 1004 GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEEAVILAQEE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAERERKRLESQREAEWKKEEERLR LEEBQKEEERKAREEQAQREHEEYLKLKEA FVVEEBGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA PRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAFEF CPOPLRSPSLDNPTTFFPNLGFSENPLKRLLVPG	1		1	1			KGNEPPPPPL
AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEEAVILAQEE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAERERKRLESQREAEWKKEEERLR LEEBQKEEEBCKAREEQAQREHEEYLKLKEA FVVEEBGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPPSLAVAFEF CPOPLRSPSLDNPTTFFPNLGFSENPLKRLLVPG		1	+	9215	 	1004	GSTHASADAWAOWFCTEALVMGAPVWYLV
AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEEAVILAQEE EGVEKPAETHILSGKIGAKKLRKLEEKQARKA QREAEEAEREERKRLESQREAEWKKEEERLR LEEEQKEEEERKAREEQAQREHEEYILKLKEA FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYTTPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA PRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPPSLAVAPEP CPOPL SPSI DNPTFFPNLGFSENPLKRLLVPG	982	2332	A	6212	1.	1,004	AAALLVGFILFLTRSRGRAASAGQEPLHNEEL
PRIQAQRRAQRVAWAEADENEEEAVILAQEE EGVEKPAETHILSGKIGAKKLRKLEEKQARKA QREAEEAEREERKRLESQREAEWKKEEERLR LEEEQKEEEERKAREEQAQREHEEYILKLKEA FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA PRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPL SPSI DNPTPFPNLGFSENPLKRLLVPG	1]			1	AGAGRVAOPGPLEPEEPRAGGRPRRRRDLGS
BEGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEEAEREERKRLESQREAEWKKEEERLR LEEBQKEEEERKAREEQAQREHEEYLKLKEA FVVEBEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPPPGPPSLAVAPEP CPOPL SPSL DNPTPFPNLGPSENPLKRLLVPG	1	1	1				RI OAORR AORVAWAEADENEEEAVILAQEE
QREAEEAERERKRLESQREAEWKKEEERLR LEEEQKEEERKAREEQAQREHEEYLKLKEA FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLTQDTINRIQDLLAEGTIT GVIDDRGKFIYTTPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA PRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPL RSPSL DNPTTFFPNLGPSENPLKRLLVPG			1				FGVEKPAETHILSGKIGAKKLRKLEEKQAKKA
P83 2333 A 8320 244 1420 RRRWRARGGLYTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPL RSPSL DNPTPFPPLGPSENPLKRLLVPG	1	-			[(OREAEEAEREERKRLESOREAEWKKEEERLK
FVVEEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASINSLIAWGRESPAQAPA 983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPL SPSL DNPTTFFPNLGPSENPLKRLLVPG			1				LEFEOKEEEERKAREEQAQREHEEYLKLKEA
VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA 983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPPSLAVAPEP CPOPLRSPSLDNPTTFFPNLGFSENPLKRLLVPG		1	1	1.	1		FVVEREGVGETMTEEOSOSFLTEFINYIKQSK
983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPSLAVAPEP CPOPL SPSL DNPTPFPNLGFSENPLKRLLVPG			-	1	1		VVILEDI.ASOVGLRTODTINRIQDLLAEGTIT
983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDFGPPSLAVAPEP CPOPL SPSL DNPTPFPNLGFSENPLKRLLVPG)			1	l		GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA
983 2333 A 8320 244 1420 RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPLRSPSLDNPTPFPNLGPSENPLKRLLVPG	1	- [i		1	}	FLAGASNSLIAWGRESPAQAPA
DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPLRSPSLDNPTPFPNLGPSENPLKRLLVPG				9220	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKP
PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPLRSPSLDNPTPFPNLGPSENPLKRLLVPG	983	2333	A	0320	1277	1 7	DI.PTWKRNFRSALNRKEGLRLAEDRSKDPHD
TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPOPLRSPSLDNPTPFPNLGPSENPLKRLLVPG	1		1		1	1	PHKIVEFVNSGVGDFSOPDTSPDTNGGGSTSD
CPOPI_RSPSI_DNPTPFPNLGPSENPLKRLLVPG			1			1	TOEDILDELLGNMVLAPLPDPGPPSLAVAPEP
EEWEFEVTAFYRGRQVFQQTISCPEGLRLVGS	1			1	1	{	CPOPLESPSI DNPTPFPNLGPSENPLKRLLVPG
				Ι΄.			EEWEFEVTAFYRGRQVFQQTISCPEGLRLVGS

650 m	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1 401.00	ì			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ŀ	l		peptide		/=possible nucleotide deletion, \-possible
		1	١.	sequence		nucleotide insertion
						EVGDRTLPGWPVTLPDPGMSLTDRGVMSYV
		1			1	RHVLSCLGGGLALWRAGQWLWAQRLGHCH
		Ì				TYWAVSEELLPNSGHGPDGEVPKDKEGGVF
}		ļ			l	DLGPFIVGSLGPPDLITFTEGSGRSPRYALWFC
1		1	ļ	ļ		VGESWPQDQPWTKRLVMVKVVPTCLRALVE
		1 1		1		MARVGGASSLENTVDLHISNSHPLSLTSDQY
						KAYLQDLVEGMDFQGPGES
984	2334	TA	8321	1	1243	ANMAPVEHVVADAGAFLRHAALQDIGKNIY
170.		1	1		· .	TIREVVTEIRDKATRRRLAVLPYELRFKEPLPE
.	}				i	YVRLVTEFSKKTGDYPSLSATDIQVLALTYQL
		1	1		1	EAEFVGVSHLKQEPQKVKVSSSIQHPETPLHIS
i	ļ				ļ	GFHLPYKPKPPQETEKGHSACEPENLEFSSFM
1	1			1		FWRNPLPNIDHELQELLIDRGEDVPSEEEEEE
}		1		ŀ	1	NGFEDRKDDSDDDGGGWITPSNIKQIQQELE
i		l				QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV
		[LAVNGMLIREARSYILRCHGCFKTTSDMSRV
1	1	1				FCSHCGNKTLKKVSVTVSDDGTLHMHFSRNP
ŀ	Ì	1				KVLNPRGLRYSLPTPKGGKYAINPHLTEDQRF
1 .		1				POLRLSQKARQKTNVFAPDYIAGVSPFVENDI
i				1		SSRSATLQVRDSTLGAGRRRLNPNASRKKFV
		l		<u> </u>		KKR RRNNIRQFIMKVCISGQARWLTPVVPVLWET
985	2335	Α	8322	352	529	EAGRSLELKSLRPAWATWGNPISTKINK
ł				<u> </u>		KMNPTDIADTTLDESIYSNYYLYESIPKPCTKE
986	2336	Α	8325	89	1172	GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL
1		1		1	ļ	FKYKRLRSMTDVYLLNLAISDLLFVFSLPFWG
		1	i	1		YYAADQWVFGLGLCKMISWMYLVGFYSGIF
1		1				FVMLMSIDRYLAIVHAVFSLRARTLTYGVITS
	}	ļ				LATWSVAVFASLPGFLFSTCYTERNHTYCKT
	i	1	Ì			KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCY
1	ļ	1	1	1		SMIRTLQHCKNEKKNKAVKMIFAVVVLFLG
İ	1	1			1	FWTPYNIVLFLETLVELEVLQDCTFERYLDYA
		1		1		IQATETLAFVHCCLNPIIYFFLGEKFRKYILQL
	1	1	1	1		FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS
	1	1			1	TMDHDLHDAL
	1	1	0226	1,	470	SLSAMRFLAATFLLLALSTAAQAEPVQFKDC
987	2337	Α	8326	3	1 470	GSVDGVIKEVNVSPCPTQPCQLSKGQSYSVN
-	1	1				VTFTSNIQSKSSKAVVHGILMGVPVPFPIPEPD
Ί	1	1		1		GCKSGINCPIQKDKTYSYLNKLPVKSEYPSIK
1	1				1	LVVEWQLQDDKNQSLFCWEIPVQIVSHL
	1		10005	1205	323	VIKMALAARLLPQFLHSRSLPCGAVRLRTPA
988	2338	Α	8335	1205	323	VAEVRLPSATLCYFCRCRLGLGAALFPRSAR
			1		1	ALAASALPAQGSRWPVLSSPGLPAAFASFPAC
1	1		1		1	PQRSYSTEEKPQQHQKTKMIVLGFSNPINWV
		1	1	1		RTRIKAFLIWAYFDKEFSITEFSEGAKQAFAH
1		1	1.	1	-[VSKLLSQCKFDLLEELVAKEVLHALKEKVTS
		1	1	Į	1	LPDNHKNALAANIDEIVFTSTGDISIYYDEKG
	1			1	1	RKFVNILMCFWYLTSANIPSETLRGASVFQVK
1					1	LGNQNVETKQLLSASYEFQREFTQGVKPDWT
						IARIEHSKLLE
000		1	0240	67	185	MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL
989	2339	A	8349	67	103	KSLHPMS
			10000	1210	1115	ASPFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ
990	2340	A	8361	210	"13,13	ITLOGSRRRQGRTAFPASGKKRETDYSDGDPL
				1	1	DVHKRLPSSTGEDRAVMLGFAMMGFSVLMF
		1		1	1 .	FLLGTTILKPFMLSIQREESTCTAIHTDIMDDW
}		1	1	1	1	LDCAFTCGVHCHGQGKYPCLQVFVNLSHPG
	1	1			1	OKALLHYNEEAVQINPKCFYTPKCHQDRNDL
	1	1		1	1	LNSALDIKEFFDHKNGTPFSCFYSPASQSEDVI
1	1			<u> </u>	ــــــــــــــــــــــــــــــــــــــ	

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	}	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	}	l		amino acid	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i				residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
	<u> </u>		<u> </u>	sequence	 	TIKKYDOMAIFHCLFWPSLTLLGGALIVGMV
						RLTQHLSLLCEKYSTVVRDEVGGKVPYIEQH
Ì		ì		1		OFKI CIMRRSKGRAEKS
·		<u> </u>	-	ļ	921	T COVVEESAL SVSMACLSPSOLOKFQQDGFLVL
991	2341	A	8369	9	721	LEGEL SAFECVAMOORIGEIVAEMDVPLHCKT
	1	l	1			FESTOFFFOLRAOGSTDYFLSSGDKIRFFFEK
		1			}	GVEDEK GNET VPPEKSINKIGHALHAHDPVIK I
	1	İ		1	Ì	citustivoti ARSLGLOMPVVVOSMYIFKQP
1		1	1		1	LUEGGEVSPHODASFLYTEPLGRVLGVWIAVE I
1		1.	}			DATE FNGCLWFIPGSHTSGVSRRMVRAPVG5
1	}	}	İ	İ		APGTSFLGSEPARDNSLFVPTPVQRGALVLIH
i		1	-	1	1	GEVVHKSKQNLSDRSRQAYTFHLMEASGTT
1						WSPENWLQPTAELPFPQLYT
1000	2342	· A	8370	906	4	MALSGNCSRYYPREQGSAVPNSFPEVVELNV
992	4344	1^	1 35,0	1		GGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN
1	1	1	1	ł		DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVV
	1	1		}	1	LPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI KQSPDEFCHSDFEDASQGSDTRICPPSSLLPAD
1		1	Į.			RKWGFITVGYRGSCTLGREGQADAKFRRVPR
-		1	ł	1	1	ILVCGRISLAKEVFGETLNESRDPDRAPERYTS
,)		.v			RFYLKFKHLMGAPASNFILGFWGLGQNQDK
1	Ì	ì	!	1	1	HPVNIYLQQRSVIRPDLTSKKAGDLKGKGDA
ì	1	1	1	Į.		OEVGRRRRWI.GDPEHL
			1		2204	TARMORHICNDTMDFGDSGKRIGGGVLCLLHQ
993	2343	A	8379	1	2794	CNITCEIK I NINGFEDIVIVIDES VEEDEKIIEQIE
ì					1	DMOTTA STYLFEATEKRFFFKNVSILIPENWK
ì		j	1		İ	ENDOVERPRHENHKHADVIVAPPTLPGRUEP
1		1		ł	Į.	VTKOFTECGEKGEYIHFTPDLLLGKKQNEYG
	İ	l l		1		DDGKI FVHEWAHLRWGVFDEYNEDQPFIKA
	ł	1	l	1		KSKKIFATRCSAGISGRNRVYKCQGGSCLSKA
}		i	ŀ			CRIDSTTKLYGKDCQFFPDKVQTEKASIMFM
1	1	İ		1		QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRST
		1	İ	l l	}	WEVISNSEDFKNTIPMVTPPPPPVFSLLKIRQRI
- {				ĺ		VCLVLDKSGSMGGKDRLNRMNQAAKHFLLQ
		- 1				TVENGSWVGMVHFDSTATIVNKLIQIKSSDER NTLMAGLPTYPLGGTSICSGIKYAFQVIGELH
		- 1	1	1		SQLDGSEVLLLTDGEDNTASSCIDEVKQSGAI
	1	1	1	1		VHFIALGRAADEAVIEMSKITGGSHFYVSDEA
	[1		QNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
1		1		1		LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPP
		1		1	1	CICL WIDDSGTIMENFTVDATSKMAYLSIPGIA
			1	1 .		LYCTWAYNI OAKANPETLTITYTSKAANSSV
			l	1		DDITTVN AKMNKDVNSFPSPMIV Y AEILQU Y VP
		1	1	1	1	VI CANVTAFIESONGHTEVLELLDNGAGADS
1		ì	- [1	FUNDGVYSRYFTAYTENGRYSLKVKAHUUA
		1	-		1	NITARI KI RPPI NRAAYIPGWYVNGELEANPP
]	1	- } ·	- 1	1	1	PREIDED TOTTLED FSRTASGGAFVVSQVPSL
}		- 1	1	ł	1	DI POOVPPSOITOLDATVHEDKILLIWIAPOD
1		1		- 1	1	NEDVCKYOR VITRISASTI DLRDSFDDALQVN
l l	1	1	1	1	1	TTDI SPKEANSKESFAFKPENISEENATHIFIAI
1		j	l	1	1	VOIDE ONI TOK VONIAOVIL FIPOANPUDIDPI
	- 1	1		1		PTPTPTPDKSHNSGVNISTLVLSVIGSVVIV
		1	1	i		NEIL STTI
				1221	644	DISCOPTOR DHOELNLHTERDSRSORAVLKIP
994	2344	A	8385	231	044	PONDCIEVWIEI PSRSHSASHGSROROVSCQG
		1	1	1		TODELL KMRNTFAELKNSLEALSSRMDQALL
	- 1		1			RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSL
					1	
ł	l	- 1				PSSWDYRACLS
995	2345		8390	194	3421	PSSWDYRACLS AWRKSSVVPPRGTRRGEKSDQDKSGQKNKR

						(A. I.) O-Curtains
SEQ ID	SEQ ID	Met	SEO I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	_	in	nucleotide	location	F=Phenylatanine, G=Glycine, n=ristitute, I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ		[residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ	1		peptide		nucleotide insertion
,	l	1		sequence	ļ	DFLSMKQSPALAPEERCRRAGSPKPVLRADD
					,	NNMGNGCSQKLATANLLRFLLLVLIPCICALV
!]	1				LLLEILLSYVGTLQKVYFKSNGSEPLVTDGEI
		1		1		OGSDVII.TNTIYNOSTVVSTAHPDQHVPAW1
i		1	ì			TDASLPGDOSHRNTSACMNITHSQCQMLPYH
}				}	}	ATI TPLI SVVRNMEMEKFLKFFTYLHRLSCY
		1		l	1	OHIMLEGCTLAFPECIIDGDDSHGLLPCRSFCE
	\ .	1		1		AAKEGCESVLGMVNYSWPDFLRCSQFRNQT
		l .	1	ł	1	FRANVSRICESPOOENGKOLLCGRGENFLCAS
ł		1	1	ì	1	GICTPGKLOCNGYNDCDDWSDEAHCNCSENL
		1	Ì	1	\	FHCHTGKCLNYSLVCDGYDDCGDLSDEQNC
	1	1	1	l		DCNPTTEHRCGDGRCIAMEWVCDGDHDCVD
1		1	1			KSDEVNCSCHSQGLVECRNGQCIPSTFQCDG
1		1		1		DEDCKDGSDEENCSVIQTSCQEGDQRCLYNP CLDSCGGSSLCDPNNSLNNCSQCEPITLELCM
1		1		1	1	CLDSCGGSSLCDPNNSLNNCSQCEFTTELECH NLPYNSTSYPNYFGHRTQKEASISWESSLFPA
	1		j	j	}	LVQTNCYKYLMFFSCTILVPKCDVNTGEHIPP
1	1			1		CRALCEHSKERCESVLGIVGLQWPEDTDCSQ
		1			Ì	FPEENSDNQTCLMPDEYVEECSPSHFKCRSGQ
		ł	1	}	·,	
	1	1		1		WECPSNKOCLKHTVICDGFPDCPDYMDEKN
	}	l l		1		CSECODDELECANHACVSRDLWCDGEADCS
1	}	1	1	İ		DSSDEWDCVTLSINVNSSSFLMVHRAATEHH
	1	1	1			VCADGWOEILSOLACKOMGLGEPSVTKLIQE
i			ļ	1		OFKEPRWITLHSNWESLNGTTLHELLVNGQS
1	1	1	1			CESRSKISLLCTKQDCGRRPAARMNKRILGGR
1	1	1		ļ		TSRPGRWPWQCSLQSEPSGHICGCVLIAKKW
1	-	1		-		VLTVAHCFEGRENAAVWKVVLGINNLDHPS
		1	1	1		VFMQTRFVKTIILHPRYSRAVVDYDISIVELSE
		- }	1	1		DISETGYVRPVCLPNPEQWLEPDTYCYITGW GHMGNKMPFKLQEGEVRIISLEHCQSYFDMK
1	j	- 1	j	1		TITTRMICAGYESGTVDSCMGDSGGPLVCEK
1	į .	-	ľ	1		PGGRWTLFGLTSWGSVCFSKVLGPGVYSNVS
	1	-	j	1		YFVEWIKRQIYIQTFLLN
1]	١.			1005	KVILSSEMSKTNKSKSGSRSSRSRSASRSRSRS
996	2346	A	8392	199	3085	FSKSRSRSRSLSRSRKRRLSSRSRSRSYSPAHN
						DEDNIHDRVVONRDFRGHNRGYRRPYYFRGR
1			1	- [1	NDCEVPWGOYNRGGYGNYRSNWQNYKQAY
'	1	.	1	1	1	CDDD CD CD CD CD CD CD CD CD CD CD CD CD
1	1	1		1	-	DD CD R CCCCR CCCNHSR VESSKRKSAKEKKOO
	1	- 1		1		KDSBBSOA AGDNOGDEVKEOTFSGGTSQDTK
	1	l		1	1	ACECCK PWPDATYGTGSASRASAVSELSPKER
	1		1	1	Į.	CDAI KSPLOSVVVRRRSPRPSPVPKPSPPLSST
			- [1		L COMOCATI POGAGYOSGTHOGOFDHGSGSLSP
	1	- 1				SKKSPYGKSPPSTGSTYGSSQKEESAASGGAA
l	ł	- 1	İ	İ	1	YTKRYLEEQKTENGKDKEQKQTNTDKEKIKE
		ļ	- 1			KGSFSDTGLGDGKMKSDSFAPKTDSEKPFRG
- 1		1				SQSPKRYKLRDDFEKKMADFHKEEMDDQDK SQSPKRYKLRDDFEKKMADFHKEEMDDQDK
- 1	1	1			1	DKAKGRKESEFDDEPKFMSKVIGANKNQEEF DKAKGRKESEFDDEPKFMSKVIGANKNQEEF
	1	1			Ì	KSGKWEGLVYAPPGKEKQRKTEELEESFPE KSGKWEGLVYAPPGKEKQRKTEELEESFPE
1	- 1	1	- 1	1	1	RSKKEDRGKRSEGGHRGFVPEKNFRVTAYK AVQEKSSSPPPRKTSESRDKLGAKGDFPTGKS
	1	1	1	1	- 1	SFSITREAQVNVRMDSFDEDLARPSGLAQEI
	1	ł			l	SFSITREAQVNVKMDSFDEDLARFSGESKSE KLCRDLVHSNKKEQEFRSIFQHIQSAQSQRSP
		1	1		1	SELFAQHIVTIVHHVKEHHFGSSGMTLHERFI
1	1	1	1			KYLKRGTEQEAAKNKKSPEIHRRIDISPSTFRI
- 1	ļ	ĺ	1.	1		THE AUTHORIAN SPREPGYKAEGKYKDDP VDLI
	- [1		l		I DIEDDKKLIKERDI KRGKSRESVDSKDSSHSI
1	1			1		DDGAEVTEVTUVGSKKOKKHRRARDKSKSSS
	1	Į		- 1		SSSQSSHSYKAEEYTEETEEREESTTGFDKSR
	1	L				000000000

						Amino acid sequence (A=Alanine C=Cysteine,
	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
	peptide		in USSN	location	corresponding	I=Isoleucine K=Lysine L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			7,4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
}		}	j	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
			1	peptide		/=possible nucleonide deterion, v=possible nucleotide insertion
				sequence		GTKDFVGPSERGGGRARGTFQFRARGRGWG
					1	RGNYSGNNNNNSNNDFQKRNREEEWDPEYT
		i	1	1	1	PKSKKYYLHDDREGEGSDKWVSRGRGRGAF
		1]			PRGRGRFMFRKSSTSPKWAHDKFSGEEGEIE
		1				DDESGTENREEKDNIOPTTE
	00.45	 	8398	202	552	CPAL GGRODLOGTRLLWAHDSGVGGQKAKS
997	2347	A	0370	202		VOENT EST EATGREEEGGOGPPVTTKGVLLA
		1	1	1		LLMAGLALQPGTALLCYSCKAQVSNEDCLQ
		1			·	VENCTQLGEQCWTARIREWGDDSRQA
998	2348	A	8400	697	301	NPPSACTPGSCDSCSGRGRDLAFDSVWSTNN MSDPRRPNKVLRYKPPPSECNPALDDPTPDY
,,,,						MSDPRPNRVLRTRTTSECTI ALBERT MILLGMIFSMCGLMLKLKWCAWVAVYCSFI
	ļ .	İ			1	SFANSRSSEDTKQMMSSFMLSISAVVMSYLQ
	l	1		1		NTDOPMTPPW
		_	0401	93	1126	A SA SHITSGHI RCPPGSEGVGTMARCFSLVLL
999	2349	A	8401	. 33	1120	I TSIWTTRI I VOGSLRAEELSIOVSCRIMGITL
	1	1	1	1	1	VSKKANQQLNFTEAKEACRLLGLSLAGKDQ
			1	1.	İ	VETALKASFETCSYGWVGDGFVVISRISPNPK
	j	1	}		1	CGKNGVGVLIWKVPVSRQFAAYCYNSSDTW TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYS
1		.]		\ <u>'</u>		VASPYSTIPAPTTTPPAPASTSIPRRKKLICVTE
	i .					VASPISTIFATTITIALASISTICKNEAAGFGG
ļ		1	1	ļ		VPTALLVLALLFFGAAAGLGFCYVKRYVKAP
		1	-	Į.		PETNKNOOKEMIETKVVKEEKANDSNPNEES
l	1		ļ			KKTDKNPEESKSPSKTTMRCLEAEV
1000	2350	A	8406	12	777	KERCQFVVKPMLSTVGSFLQDLQNEDKGIKT
1000	2330	1^	0,00	1		AAIFTADGNMISASTLMDILLMNDFKLVINKI
	1	1	1	Ì		AYDVQCPKREKPSNEHTAEMEHMKSLVHRL FTILHLEESQKKREHHLLEKIDHLKEQLQPLE
1 .	1	1				QVKAGIEAHSEAKTSGLLWAGLALLSIQGGA
i		ŀ		Ì		I AWI TWWVYSWDIMEPVTYFITFANSMVFF
1		1		1		AVFIVTRODYTYSAVKSROFLQFFHKKSKQQ
		- {			Ì	HFDVQQYNKLKEDLAKAKESLKQARHSLCL
į.	1	j	-			OMOVERLNEKN
1001	2351	+A	8410	1400	264	VGFWERPLRSSRWFRRSLRRWEMLARAARG
1001	2331	1	1 0470			TGALLLRGSLLASGRAPRRASSGLPRNTVVLI
	1	l			-	VPQQEAWVVERMGRFHRILEPGLNILIPVLDI IRYVQSLKEIVINVPEQSAVTLDNVTLQIDGV
1	ł	1	1	1	1	LYLRIMDPYKASYGVEDPEYAVTQLAQTTM
1	1	1			1	DOEL GKI SI DKVFRERESLNASIVDAINQAAL
1						CWGIRCI RVEIKDIHVPPRVKESMQMQVEAL
]	1		-		1	DDVDATVI ESEGTRESAINVAEGKKQAQILA
ì	1.					FARKAROINOAAGEASAVLAKAKAKAEAIKI
1	1			İ		I LAAALTOHNGDAAASLTVAEQYVSAFSKLA
	1		1	1		POSNTII I PSNPGDVTSMVAOAMGVYGALI
	1		1		1	KAPVPGTPDSLSSGSSRDVQGTDASLDEELDI
1		-				VKMS NRENLLESRMMDPCSVGVQLRTTNECHKTY
1002	2352	A	8421	134	941	YTRHTGFKTLQELSSNDMLLLQLRTGMTLSC
}					1	NNTICFHHVKIYIDRFEDLQKSCCDPFNIHKK
1	1	-			1	AKKNI.HVIDLDDATFLSAKFGRQLVPGWKL
1	1				1	PKCTOINGSVDVDTEDROKRKPESDGRTAK
1	j		1		Į	ALRSLOFTNPGROTEFAPETGKREKRRLTKN
1		1		- 0		ATAGSDROVIPAKSKVYDSOGLLIFSGMDLC
		- 1	- 1			DCLDEDCLGCFYACPACGSTKCGAECRCDR
1	1				1	WI_YEOTETEGGETHNKHAG
1		1			1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRILR
1003	2252	Δ	8427	- 13	1410	TEN GEOGRAPH : COOK I NO INVINCTOR
1003	2353	A	. 8427	3	1410	CRRLPEPSPFLTQPNLAQSQPPAPVPVTDPSV MHPAVFLSLPDLRCSLLLLVTWVFTPVTTET

EQ ID				- 1. ·	D . J: 4- J J	Amino acid sequence (A=Alanine C=Cysteine,
	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	location	r=Pnenylaiannie, G-Glycine, 11-1115teme,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	иепсе		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uciicc	i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			7.4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1 1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
į		,	·	residue of	Sequence	/=possible nucleotide deletion, \=possible
			1 1	peptide		nucleotide insertion
				sequence	<u> </u>	SLDTENIDEILNNADVALVNFYADWCRFSQM
+					1	SEDIENIDEITUNADAATANI LADACALPOIT
- 1	ì	i			1	LHPIFEEASDVIKEEFFNENQVVFARVDCDQH
	Ì	1	Į.			SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ
	1	1	1	· ·		RSVKALADYIRQQKSDPIQEIRDLAEITTLDRS
ļ	1	Į.	ì	1		KRNIIGYFEOKDSDNYRVFERVANILHDDCAF
	Ì	l	1	ļ	Į.	LSAFGDVSKPERYSGDNIIYKPPGHSAPDMVY
İ	l	l			1	LGAMTNFDVTYNWIQDKCVPLVREITFENGE
	1	1				ELTEEGLPFLILFHMKEDTESLEIFQNEVARQL
	Į.	1	1		1	EL LEGGEFFEILFRINGED TEDEBLI QUE TRADCP
	1	(į	i		ISEKGTINFLHADCDKFRHPLLHIQKTPADCP
	ļ		1	Í		VIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDL
	1		1		1	HSGKLHREFHHGPDPTDTAPGEQAQDVASSP
	1		1	(PESSFQKLAPSEYRYTLLRDRDEL
			10400	010	387	GI SRKI RAGELPGFCRVSPCGSWVVETLVKM
1004	2354.	Α	8432	910	1 30'	ACAAARSPADODRFICIYPAYLNNKKTIAEGR
		ł		l	1	RIPISKAVENPTATEIQDVCSAVGLNVFLEKN
	1	ł		1		KMYSREWNRDVQYRGRVRVQLKQEDGSLC
	1	1	1	1		LVQFPSRKSVMLYAAEMIPKLKTRTQKTGGA
	Į	1	İ	1	1	LACING COCCOUNT LAYER WELL STATE OF THE STAT
	1	1				DQSLQQGEGSKKGKGKKKK
1005	2355	A	8453	90	530	QSHETKMQSGTHWRVLGLCLLSVGVWGQD
1005	2333	10	0433	1 2	1	GNEEMGGITQTPYKVSISGTTVILTCPQYPGSE
	i .		1 .	1	ł	II. WOHNDKNIGGDEDDKNIGSDEDHLSLKEF
	1	1	1	[SELEOSGYYVCYPRGSKPEDANFYLYLRARG
	1	1	1	1		NPGLONRYHRLFREDHSKGHSQ
					307	AVQRIRHEMNIFRLTGDLSHLAAIVILLLKIW
1006	2356	Α	8458	3	307	KTRSCAGISGKSQLLFALVFTTRYLDLFTSFIS
	1				i	LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC
	1	1	-50-	l	1	
	ł	1	1		l	QLCIFN GAGAGGDWAAMDKLKKVLSGQDTEDRSGL
1007	2357	A	8459	43	553	GAGAGGDWAAMDKLKKVLSGQDIEDKSGE
1007	1 2337	1			1	SEVVEASSLSWSTRIKGFIACFAIGILCSLLGT
	Į.	1	. 1	ł		VLLWVPRKGLHLFAVFYTFGNIASIGSTIFLM
	1	1		ł		GPVKQLKRMFEPTRLIATIMVLLCFALTLCSA
			-1	Į.	ł	FWWHNKGLALIFCILQSLALTWYSLSFIPFAR
	1	1				DAVKKCFAVCLA
				400	150	AQDIRSVHSLGQKSTFVKHFRTLSHLHGLPDP
1008	2358	Α	8462	487	130	PPHWPPQERSPPSHPCMPSHRPQIPQLSNSGPS
		1	1	1	1	DPRWGCVGPSMPTSTCLPGAVEASTTKASLP
	i i	1	1	ì		KCPVDSSLPTPEACFL
						KCPVDSSLFIFEACID
1009	2359	A	8465	134	954	ETRVKTSLELLRTQLEPTGTVGNTIMTSQPVP
1007	2333	1	0.00			NETIIVLPSNVINFSQAEKPEPTNQGQDSLKKH
	1	1	l	1		LHAEIKVIGTIQILCGMMVLSLGIILASASFSPN
	1	1	1	1		FTOVTSTLLNSAYPFIGPFFFIISGSLSIATEKKL
	1		- 1	1		TKI LVHSSLVGSILSALSALVGFIILSVKQATL
	- }	1	1	ł		NPASLQCELDKNNIPTRSYVSYFYHDSLYTTD
	1	-	1	1	1	CYTAKASLAGTLSLMLICTLLEFCLAVLTAVL
		1	1	1	1	RWKQAYSDFPGSVLFLPHSYIGNSGMSSKMT
Í				1		KWKQAYSDPPUS YLFLPHS I IGHSGWISSKWII
		1		1		HDCGYEELLTS
1010	2360	A	8468	2	473	KYRYRRPYPVMRKICQVGPAGLAFILNISPVA
1010	2300	'A	0400	1-		HRVALCHLAGCQEQAAWYHTLQILFFLVSAY
1	1	1	1	1		FESCHVPEKYFPGSCDIVGHGHOIFHAFLSICT
ł	ŀ	ì	1	1		I SOLEAILLDYOGROEIFLORHGPLSVHMACL
l		1			1	SEFFI AACSAATAALLRHKVKARLTKKDS
!	1	1.				TELSQLEKAHPPADMGRRKSKRKPPPKKKMT
1011	2361	A	8478	5	409	GTLETOFTCPFCNHEKSCDVKMDRARNTGVI
		1				GILETURICIFICATERACE VANDARACTOR
1		1	1			SCTVCLEEFQTPITCILGNLGFFQRVGRGLESG
l		j			1	PCSSGPLCALVQGQSRPEEQVPPSDFCGVRRC
	1	1	1 .	1	ĺ	PAGEOCO
1		1	1 _		17.00	RTSTQKWQSVFNDSQEHLERFYCNPENDRM
			0401	1 2010	1 1657	KISIOKWQSVI WOOQLIMBBIG 1011
1012	2362	A	8481	2810	1652	PMKYGGORFWADLNAMNVYETTEFDQLKK
1012	2362	A	8481	2810	1652	RMKYGGQEFWADLNAMNVYETTEFDQLRR LSTPPSSNVNSIYHTVWKFFCRDHFGWREYPH

SSQ ID No. of much-odd graphide sequence of peptide sequence of peptide sequence of sequen				- C-22	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO. 21 In	SEQ ID	SEQ ID	Met	SEQ			D=A spartic Acid, E=Glutamic Acid,
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uence 9/496 uence		1 * *				corresponding	I=Isoleucine, K=Lysine, L=Leucine,
mence 914 ng to first amino acid residue of peptide pepti		, -					M=Methionine, N=Asparagine, P=Proline,
amino acid residue of peptide residue of peptide sequence peptide sequence peptide sequence peptide sequence per solution of the sequence per solution of the sequence per solution of the sequence per solution of the sequence per solution of the sequence sequence sequence per solution of the sequence per s	•	ucaice				acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of peptide pep	uence		ļ	7.4		of peptide	T=Threonine, V=Valine, W=Tryptophan,
Peptide sequence		1				sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1		peptide		
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PPVINPLGTSFPDDTA/OPSGVGVELSTIPKS NASVNVSHAPGDWFVAAHLPPSSQKIELKG LAPTCAYYPQPELLVTRVVEISIMEPDVPLPQ TLLSHPSYLKVVPVDYTRELLLELRDCVSNGS LGCPVRLTVGPVTLPSNFGKVLTCTGAPWPC RLLLPSPPWDRWLQVTAESLVGPLGTVAFSA VAALTACRPRSVTIQPLLQSSQNQSFNASSGL LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIPYPETDNWYLSLQLMCPENAEDCEQ AVHVETTLYLVPCLNDCGPYGQCLLLRRHS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRRFFLVEASVY AYTMFSTFYHACDQPGGAVLCILSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHLI AGSAALLIPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KGGEKKGRSANEVVTREYTINHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVLSKRKNEDEDSP NKLYTLVTVYVYVTTFKNLQTVNVDEN LSAKWADNFMAEGCGSKEHSFQHFFLQAV GMFLGFFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVGLADLLSKHDSOHKLSSVIT GDLLIIMAQIIVAIQMVLEEKFVYKINVPPLR AVGTEGLFGFVILSLLLVPMYYIRAGSPSGNP	1015	2365	A	8504	13		AVITEWILOVSRESGAACTDAEITVHERSGA
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TILSHPSYLKVFVPYTRELLERLOVSUNG LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPC RILLPSPPWDRWLQVTAESLVGPLGTVAFSA VAALTACRPRSVTIQPLQSSQNQSFNASSGL LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRRIS YLYASCSCKAGWRGWSCTDNSTAQTVAQQG AATLLLTLSNLMFLAPIAVSVRFFLVEASVY AYTMFFSTFYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASSMYAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEWACSQKFPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSANEVVTREYTINHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRJSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN LSAKWADNFMAEGCGGSKEHSFOHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIMAQIIVAIQMVLEEKFVYKHNVHPLR AVGTEGLFGFVULSLLVPMYYPAGSFSGNP	1	ļ	l	1	j		NASYNVSHPAPGDWFVAAHLPPSSQKIELKG
LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPC RLLPSPPWDRWLQVTAESLVGPLGTVAFSA VAALTACRPRSVTIQPLLQSSQNQSFNASSGL LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLAWSR RANLIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRRIS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRRFFLVEASVY AYTMFFSTFYHACDQPGBAVLCLLSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKPPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKRGRSAINEVVTREYTINIHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTYYPVTTFKNLQTVNVDEN NKLYTLVTYYPVTTFKNLQTVNVDEN NKLYTLVTYYPVTTFKNLQTVNVDEN LSAK WADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIIMAQIIVAIQMVLEEKFYYKHNVHPLR AVGTEGLFGFVILSLLLVPMYYPAGSFSGNP	İ	Ì	-{ .	1	ì		LAPTCAYVFQPELLVTRVVEISIMEPDVPLPQ
RLLLPSPPWDRWLQVTARESLVGPLGTVAFSA VAALTACRPRSVTIQPLLQSSQNQSFNASSGL LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSWRLRL NTGMDSGGSLTISLAANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRRHS YLYASCSCKAGWRGWSCIDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRRFFLVEASVY AYTMFFSTPYHACDQPGEAVLCLSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDBRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSANDEVVTREYTNIHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTYYPVTTFKNLQTVNVDEN LERTPASADMAWTKYQLFLAGLMLVTGSNY LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIFTGLFSVAFLGRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIIMAQIIVAIQMVLEEKFYYKHNVHPLR AVGTEGLFGPVILSLLLVPMYYPAGSPSGNP			1			ŀ	TLLSHPSYLKVFVPDYTRELLLELRDCVSNGS
VAALTACRPRSYTIQPLLQSSQNQSFNASSGL LSPSPDHQDLGRSGRVDRSPFCLTNYPYTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIPYPETDNWYLSLQLMCPENAEDCEQ AVYHVPETTLYLVPCLNDCGPYGQCLLLRRHS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLLTISNLMFLAPIAVSVRRFFLVEASVY AYTMFFSTPYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIATYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KWYPSGFVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSANEVVTREYTINHKRHGVG FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGRINVPYVRIRVRLSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN LERTPASADMAWTKYQLFLAGLMLVTGSINT LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVISQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIMAQIIVAIQMVLEEKFYYKHNVHPLR AVGTEGLFGFVLSLLLVPMYYPIPAGSPSGNP PGTL ETDALDAFCQVGQOPLLAVALLGNISSIA	1	-	1	!		l	LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPC
LSPSPDHQDLGRSGRVDRSFFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASFFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETITLYPCLNDCGPYQCCLLLRHIS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRRFFLVEASVY AYTMFFSTPYHACDQPGEAVLCLLSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLOPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KWYPSOPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSAINEVVTREYTINIHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRDEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN LERTFASADMAWTKYQLFLAGLMLVTGSINT LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAFYLLRCRAAGQSDSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GGLLIIMAQIIVAIQMVLEEKFYYKHNVHPLR AVGTEGLFGFVILSLLLVPMYYJPAGSFSGNP PGTL ETDALDAFCQVGQOPLLAVALLGNISSIA		1	1			ļ	RLLLPSPPWDRWLQVTAESLVGPLGTVAFSA
MDVVSVHFQPLDRVSVRVCSDTPSVMRLKL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRHGS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLITLSNLMFLAPIAVSVRFFLVEASVY AYTMFFSTFYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTLCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDRELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSAINEVVTREYTINIHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIVRLSRKRNEDEDSP NKLYTLVTYVPVTTYKNLQTVNVDEN LERTPASADMAWTKYQLFLAGLMLVTGSINT LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIETGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIMAQIIVAIQMVLEEKFYYKHNVHPLR AVGTEGLEFFVILSLLLVPMYYIPAGSPSGNP PGTI EDAI DAFCOVGOOPLIAVALLGNISSIA			Ì	ļ.	Į.		VAALTACRPRSVTIQPLLQSSQNQSFNASSGL
NTGMDSGGSLTISLRANKTEMRNETVVVACN NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIIPYPETDNWYLSLOLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRHIS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLTLSNLMFLAPIAVSVRRFFLVEASVY AYYMFSTFYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWYTLLCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT 1016 2366 A 8511 1 453 KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSAINEVVTREYTINHKRHIGVO FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTVYPVTTFKNLQTVNVDEN LSAKWADNFMAEGCGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SFFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVTI GDLLIMAQIIVAIQMVLEEKFVYKHNVHIPS AVGTEGLFGFVILSLLLVPMYYIPAGSFSGNP PGTI EDALDAFCOVGOOPLIAVALLGNISSIA	1		1			1	LSPSPDHQDLGRSGRVDRSFFCLINII VIRLD
NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRHIS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRFFLVEASVY AYTMFSTFYHACDQPGEAVLCLSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSAINEVTREYTINIHKRHIGVO FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN 1017 2367 A 8513 54 1196 LERTPASADMAWTKYQLFLAGIMLVTGSINT LSAKWADNFMAEGCGGSKEHSFQHFFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVTI GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR AVGTEGLIFFVILSLLLVPMYYIPAGSPSGNP PGTI FDALDAFCOVGOOPLIAVALLGRISSIA	ł		1	1	ĺ	1	MDVVSVHFQPLDKVSVKVCSD115VMCMCV
RANLIIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETTLYLVPCLNDCGPYGQCLLLRRHS YLYASCSCKAGWRGWSCTDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRFFLVEASVY AYTMFFSTFYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTLCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAF KGGEKKGRSAINEVVTREYTINIHKRIHGVO FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVLSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVTI GDLLIIMAQIIVAIQMVLEEKFYYKHNVHPLR AVGTEGLFGPVILSLLLVPMYYPAGSPSGNP PGTI EDAL DAFCOVGOOPLIAVALLGNISSIA	1	1	1		'	1	NIGMDSGGSLISERAINTENACTIVE STATES NCTTAFFOGYPI SLSAWSR
AVVHVETTLYLVPCLNDCGPYGQCLLLRANGY YLYASCSCKAGWRGWSCIDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRFFLVEASVY AYTMFFSTPYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKPPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSAINEVVTREYTINIHKRIHGVC FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN LSAKWADNFMAEGCGGSKEHSFQHFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR AVGTEGLFGFVILSLLLVPMYYIPAGSFSGNP PGGTLEDALDAFCOVGOOPLIAVALLGNISSIA	1	1 .	1	1)	1	PANT UPVERTENTIALIS OF MCPENAEDCEO
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AATLLTLSNLMFLAPIAVSVRRFFLVEASVY AYTMFFSTFYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAR KGGEKKKGRSAINEVVTREYTINHKRIHGVG FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN LERTPASADMAWTKYQLFLAGLMLVTGSINT LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR AVGTEGLFGFVILSLLLVPMYYIPAGSPSGNP PGTI EDALDAFCOVGOOPLIAVALLGNISSIA		1	1	1			VIVASCSCKAGWRGWSCTDNSTAOTVAQQR
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CRVPYCSVVCFRKHKEQCNI ALPTKTVKPVENKDDDDSIA VSLQNLKNLGESATLRSLLI DQGEDKAKLMRAYMQEPLE EPSQNEES VGMELPAVNLKVILLGHWL YAWANFTILALGVWAVAQF LLATIFLDIVHISIFYPRVSLTI SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP. GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	PETRPVEKKIRS DFLNSDEEEDR NPHLRQLMVNL PVEFADCCLGIV LTTWGCIVFSGS RDSIDAISMFLGG DTGRFGVGMAIL
ALPTKTVKPVENKDDDDSIA VSLQNLKNLGESATLRSLLL DQGEDKAKLMRAYMQEPLE EPSQNEES VGMELPAVNLKVILLGHWL YAWANFTILALGVWAVAQF LLATIFLDIVHISIFYPRVSLTT SLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	DFLNSDEEEDR NPHLRQLMVNL EVEFADCCLGIV LTTWGCIVFSGS RDSIDAISMFLGG DTGRFGVGMAIL
VSLQNLKNLGESATLRSLLL DQGEDKAKLMRAYMQEPLE EPSQNEES VGMELPAVNLKVILLGHWL YAWANFTILALGVWAVAQE LLATIFLDIVHISIFYPRVSLTI SLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADPL GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	NPHLRQLMVNL FVEFADCCLGIV LTTWGCIVFSGS RDSIDAISMFLGG DTGRFGVGMAIL
DQGEDKAKLMRAYMQEPLE EPSQNEES VGMELPAVNLKVILLGHWL YAWANFTILALGVWAVAQE LLATIFLDIVHISIFYPRVSLTI SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	FVEFADCCLGIV LTTWGCIVFSGS RDSIDAISMFLGG DTGRFGVGMAIL
1026 2376 A 8547 1078 594 VGMELPAVNLKVILLGHWL YAWANFTILALGVWAVAQE LLATIFLDIVHISIFYPRVSLTI SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP. GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	LTTWGCIVFSGS RDSIDAISMFLGG DTGRFGVGMAIL
1026 2376 A 8547 1078 594 VGMELPAVNLKVILLGHWL YAWANFTILALGVWAVAQF LLATIFLDIVHISIFYPRVSLTI SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	NDSIDAISMFLGG DTGRFGVGMAIL
1026 2376 A 3577 A 3577 A 3557 1 340 YAWANFTILALGVWAVAQE LLATIFLDIVHISIFYPRVSLTI SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP: GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	NDSIDAISMFLGG DTGRFGVGMAIL
LLATIFLDIVHISIFYPRVSLTT SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP: GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	DTGRFGVGMAIL
SLLLKPLSCCFVYHMYRERG SSQDRSAYQTIDSAEAPADP. GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT. FSRYSGSEGSTOTLTKGELK	OCH I MUTCEI C
SSQDRSAYQTIDSAEAPADP GY 1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	**************************************
	FAVPEGRSODAR
1027 2377 A 8557 1 340 DFLGPASPQEEGGSESSTMT FSRYSGSEGSTOTLTKGELK	LY AL FORMÓDI ME
102/ 23// A 655/ FSRYSGSEGSTOTLTKGELK	CT ET A MCMITTY
I I I I I I I I I I I I I I I I I I I	THE PROPERTY OF THE PROPERTY O
	A TIMEVETI OLITA
SGKDKDAVDALEXDEAN	DAQVDF3E1111
VAAITSACHKYFEKAGLK	- O A D D C C D D I I I
1028 2378 A 8569 20 963 KMAATLGPLGSWQQWRRC	LSAKDUSKKLLL
LLLLGSGOGPOOVGAGQTF	EYLKREHSLSKP
YQGEAPRPCFLRDWELQVH	FKIHGQGKKNL
HGDGLAIWYTKDRMQPGPV	FGNMDKFVGLG
VFVDTYPNEEKQQERVFPYI	SAMVNNGSLSY
DHERDGRPTELGGCTAIVR	ILHYDTFLVIRY
VKRHLTIMMDIDGKHEWRI	CIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISI	LKLFELTVERTPE
	EMTAPLPPLSGL
ALFLIVFFSLVFSVFAIVIGIII	_YNKWQEQSRK
RFY	
578 AAAASHRSRARSRPRRVSSO	PAPRRAQSSAG
1029 2379 A 0372 RVASGLDSAPLCTMARALC	RLPRRGLWLLLA
HHLFMTTACQEANYGALLF	ELCLTOFOVDM
EAVGETLWCDWGRTIRSYR	ELADCTWHMAE
KLGCFWPNAEVDRFFLAVH	GRYFRSCPISGR
AVRDPPGSILYPFIVVPITVT	I.I.VTAI.VVWOS
AVKUTTOSIL ITTIV VIII VI	
KRTEGIV JOSO 3280 A 8574 1352 372 DSSTVKGGSESRHLCLIPDLI	KCKARTREASSC
1030 2380 A 8574 1352 372 DSSTVKGGSESKHLCLIPDL	VD CCDI GMUGIRU
1 STTCGRRINLCISANSWID	COL CINCODDI EL
THLTITQALRQPLHRAPLLP	CEL VECCELCEUR
NKAMGRPLLLPLLLLQPPA	ALTALARA I CONTROL
SYLYGVTQPKHLSASMGGS	VEIPPORTITION
AIVPNVRISWRRGHFHGQSI	AZIKAKZIHKDA
VNRLFLNWTEGQESGFLRIS	NLRKEDQSVYF
CRVELDTRRSGRQQLQSIKO	JTKLTTTQAVT1T
TTWRPSSTTTIAGLRVTESK	GHSESWHLSLDT
AIRVALAVAVLKTVILGLLC	LLLLWWRRRKG
SRAPSSDF	
2600 006 240 RRTAGIYPCFPKPGRTRHAL	CSVVLLLLTGQL
1031 2381 A 8580 905 340 RRTAGIYPCFFRFORTRIAL AFDDFQESCAMMWQKYAC	SRRSMPLGARIL
FHGVFYAGGFAIVYYLIQKI	HSRALYYKLAV
EQLQSHPEAQEALGPPLNIH	YLKLIDRENEVDI
VDAKLKIPVSGSKSEGLLYV	/HSSRGGPFORW
VDAKLKIPYSUSKSEULLY	CCENCIDENKKE
HLDEVFLELKDGQQFVFKI	DADMCCGAKAD
1032 2382 A 8593 2558 961 RRRPRLLPGAEPCEPRVGFR	ANVIATOR IRU
1032 2382 A 8593 2558 901 WAAGALGVAGLLCAVLGA	A MIT A IM A TOTAL

			C000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	E-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide	ļ	in USSN	location	corresponding	I=Icoleucine K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Glutamine R=Arginine, S=Serine,
uence	1	1	714	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
1	1		,	residue of	sequence	V=Tyrosine X=IInknown, *=Stop codon,
]	1	l		peptide		/=possible nucleotide deletion, \=possible
	1	1	l	sequence	į.	nucleotide insertion
		 		Sequence	· · · · · ·	QVLKNVRIDPSSLSFNMWKEIPIPFYLSVYFFD
1	}	1	1	\ `		VMNPSEILKGEKPQVRERGPYVYREFRHKSNI
ł	1	1	i	ĺ		TFNNNDTVSFLEYRTFQFQPSKSHGSESDYIV
		1			ļ	MPNILVLGAAVMMENKPMTLKLIMTLAFTTL
1	1	ì		ì	ł	GERAFMNRTVGEIMWGYKDPLVNLINKYFP
		l	ļ	1	1	GMFPFKDKFGLFAELNNSDSGLFTGFTGVQNI
}	1	i	1	}	İ	SRIHLVDKWNGLSKVDFWHSDQCNMINGTS
	1	1	\	1	1	GQMWPPFMTPESSLEFYSPEACRSMKLMYKE
1)	}	ì	1	SGVFEGIPTYRFVAPKTLFANGSIYPPNEGFCP
1		1	1	1		CLESGIQNVSTCRFSAPLFLSHPHFLNADPVL
1	ł			1		AEAVTGLHPNQEAHSLFLDIHPVTGIPMNCSV
1	1	1	1	İ		KLQLSLYMKSVAGIGQTGKIEPVVLPLLWFA
1						ESGAMEGETLHTFYTQLVLMPKVMHYAQYV
1 .	ļ	1		i	i	LLALGCVLLLVPVICQIRSQEKCYLFWSSSKK
		1	}		, <u> </u>	GSKDKEAIQAYSESLMTSAPKGSVLQEAKL
1033	2383	IA	8595	595	767	AHLPDTLLLPPHSPTVPTPKSFQCSQKACFSRS
1055	2505	1				FCLLLSLVSSSLVSLSLCPPLTQA VTTSCIIPFAFGLGVRASERLAEIDMPYLLKYQ
1034	2384	A	8597	640	164	PMMQTIGQKYCMDPAVIAGVLSRKSPGDKIL
1034		1	1	j	1	VNMGDRTSMVQDPGSQAPTSWISESQVFQTT
1	1	i	1		1	EVLTTRITELQRRFPTWTPDQYLRGGLCAYSG
1		1	Ì	ì	· I	GAGYVRSSQDLSCDFCNDVLARAKYLKRHG
1		Ì	1	1		,
1		1.	<u> </u>			F AMASTLEYSPSPLRRLVGPAAGFSRAARADL
1035	2385	A	8603	936	204	CWDPMAFFTGLWGPFTCVSRVLSHHCFSTTG
	l l	1			.	SLSAIQKMTRVRVVDNSALGNSPYHRAPRCI
	Ì	1				HUVKKNGVGKVGDOILLAIKGOKKKALIVG
1	Ì	1	1	1	-X-	HCMPGPRMTPRFDSNNVVLIEDNGNPVGTRI
-		1	1	1	1 .	KTPIPTSLRKREGEYSKVLAIAQNFV
		4	000	 	562	PTP A HSFDI CCSPCRRRLLGREEAGEEPTSPV
1036	2386	A	8606	1.	1 302	TOYLOPESPEECKMFACAKLACTPSLIRAGSR
		ı		1	}	VAVRPISASVI SRPEASRTGEGSTVFNGAQNG
1	1	i	- (1	1	VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG
i	į		1	1		VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY
İ	Ì	J	į .			AILGFALSEAMGLFCLMVAFLILFAM
1000	2387	A	8615	1.2	2364	SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT
1037	2307	1^	3013	_		GMVAHINNSRLKAKGVGQHDNAQNFGNQSF
-		-{	1			EELRAACLRKGELFEDPLFPAEPSSLGFKDLG
		1	İ	1		PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI
i	- [- 1	1	-		CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG
1	-	ı				QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL
1	ŀ	1		1	ĺ	PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP
1				1	}	GSYEALSGGSIMEGLEDFIGGYAQSFQLQAT
ļ	- 1	1	1	1	1	PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI
- (- [1	1	-	1	RVRNPWGRIEWNGAWSDSAREWEEVASDIQ
1		1	-		1	MOLLHKTEDGEFWMSYQDFLNNFTLLEICNL
j			-	1	1	TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC
1			İ	İ	1 .	RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV
		l				VVCTCLVALMQKNWRHARQQGAQLQTIGFV
	[1	- 1			LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI
	- [1		'		FINSREVSSQLRLPPGEYIIPSTFEPHRDADFL
į			ì	1		LRVFTEKHSESWELDEVNYAEQLQEEKVSED
1	1	- 1	1	1		DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR
-	-			- 1	1	MAIKFKSFKTKGFGLDACRCMINLMDKDGSG
		- 1	Ì	- [}	KLGLLEFKILWKKLKKWMDIFRECDQDHSGT
1		- 1	- }	1		LNSYEMRLVIEKAGIKLNNKVMQVLVARYA
		- 1	- 1		Ì	DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT
			- 1			GHICLSLEQVLGEGWEGICRIAPACPSTPPPPS
						10.200

				-2	Deadisted and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	l	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	\	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	[amino acid	of peptide	1=1 hreonine, v=vaine, w=1 typiopilai,
1		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	<u> </u>	i	l	peptide		/=possible nucleotide deletion, \=possible
		1	ì	sequence		nucleotide insertion
	 	 	 	 		SDVPGPASCPRLFPPWDLLPVSTVAADDHVGI
						EAL
1000	10200	A	8621	3	1494	RSRMARAPLGVLLLLGLLGRGVGKNEELRLY
1038	2388	^	0021	1	1	HHLFNNYDPGSRPVREPEDTVTISLKVTLTNL
	ł	1		ļ		ISLNEKEETLTTSVWIGIDWQDYRLNYSKDDF
		1	1	İ	Ì	GGIETLRVPSELVWLPEIVLENNIDGQFGVAY
]		l	1	ì	j	DANVLVYEGGSVTWLPPAIYRSVCAVEVTYF
}	1	1	1	1	ļ	PFDWQNCSLIFRSQTYNAEEVEFTFAVDNDG
1	i	1	1	1		KTINKIDIDTEAYTENGEWAIDFCPGVIRRHH
· ·		1		1	1	GGATDGPGETDVIYSLIIRRKPLFYVINIIVPCV
		1			1	LISGLVLLAYFLPAQAGGQKCTVSINVLLAQT
	1		1	1	1	VFLFLIAQKIPETSLSVPLLGRFLIFVMVVATLI
1		1	1	1		VMNCVIVLNVSQRTPTTHAMSPRLRHVLLEL
		1.]	1	LPRLLGSPPPPEAPRAASPPRRASSVGLLLRAE
	1	ſ		1		ELILKKPRSELVFEGQRHRQGTWTAAFCQSL
1	ļ	1	ļ			GAAAPEVRCCVDAVNFVAESTRDQEATGEE
1 .	}	ì	1	1	ļ	VSDWVRMGNALDNICFWAALVLFSVGSSLIF
1	1	1	1			LGAYFNRVPDLPYAPCIQP
		1		<u> </u>		PGRERPGGGGARRRPQHLPALLPSERPDCATL
1039	2389	A	8636	1	900	QAMENELPVPHTSSSACATSSTSGASSSSGCN
	j	}		1	ŀ	NSSSGSGRPTGPQISVYSGIPDRQTVQVIQQ
1	1	ł		1	1	ALHRQPSTAAQYLQQMYAAQQQHLMLQTA
	1	-	1	l .	1	ALHKUPSTAAQTLQQMTAAQQQTLIMIDQTP
1	1	1				ALQQHLSSAQLQSLAAVQQASLVSNRQGST
ļ	1	j			1	SGSNVSAQAPAQSSSINLAASPAAAQLLNRA
1	1	1	}			QSVNSAAASGIAQQAVLLGNTSSPALTASQA
	1	1	ļ			QMYLRAQMLIFTPTATVATVQPELGTGSPAR
		1	}	1		PPTPAQVQNLTLRTQQTPAAAASGPTPTQPVL
İ	Į.	1				PSLALKPTPGGSQPLPTPA
1040	2390	TA-	8645	98	1388	ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSF
1040	20,00	1		ł		HEHRHQSGRCLSTGMAPNLKGRPRKKKPCPQ
		1	1	ł	· '	RRDSFSGVKDSNNNSDGKAVAKVKCEARSA
		1		ì		LTKPKNNHNCKKVSNEEKPKVAIGEECRADE
		1	1		l	QAFLVALYKYMKERKTPIERIPYLGFKQINLW
ł	Ì		1	İ		TMFQAAQKLGGYETITARRQWKHIYDELGG
Ì	l l	i		1	Ì	NPGSTSAATCTRRHYERLILPYERFIKGEEDKP
1	- 1	1	j			LPPIKPRKQENSSQENENKTKVSGTKRIKHEIP
	1		l			KSKKEKENAPKPQDAAEVSSEQEKEQBILISQ
1	1		1	1		KSIPEPLPAADMKKKIEGYQEFSAKPLASRVD
	1			1		PEKDNETDOGSNSEKVAEEAGEKGPTPPLPSA
1		1		1	}	PLAPEKDSALVPGASKQPLTSPSALVDSKQES
	1	1		1		KLCCFTESPESEPQEASFPRLPHHTGHRWQTR
		1		1	1	MRRRMTNCPPWOITLPTAP
			10000	112	1492	LLOEMCTKTIPVLWGCFLLWNLYVSSSQTIYP
1041	2391	A	8646	113	1772	GIKARITORALDYGVOAGMKMIEQMLKEKK
}		ì		1	1	LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP
		1	1		1	NTSLAFVPGVGIKALTNHGTANISTDWGFESP
				}	1	LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVK
l		1	1	1		ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE
	-	1	}	1		NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER
1	1	1	1	ĺ		SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS
	1	1]		TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM
1			1 .			VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK
		- [1	1		AKIWA I ELLIMITAL GULL I IDIL VOMI MAGI 6
1	1	1	1	1		NSTVETIVSMDFVASTSVGLVILGQRLVCSLS
		1		1		LNRFRLALPESNRSNIEVLRFENILSSILHFGVL
l		- 1	1	1		PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF
		1				LLISTDLKYETSSKQQPSFHVWEGLNLISRQW
1				1		RGKSAP
1045	3200	A	8672	538	170	ARRIARTRESKAAVSQDNVPALQPGKKKKLR
1042	2392	^	3072	1 223	1	LGGKKKKFKFFRLPKEFKKQLMYSPSNFKKM
	1					

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in	nucleotide location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	1	USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l	914	ng to first	acid residue	O=Ghitamine, R=Arginine, S=Serine,
uence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ľ	peptide		/=possible nucleotide deletion, \=possible
j	}]	_	sequence		nucleotide insertion TSLAGNTVQCLNKLKYVIYSAQYPAYGNITT
	1	 				LDMITSTDHVLEQDFWICFTFYSVKERQI
	İ				1	GLKTRAPATPTFQREVLGPAKQDMQRRCPRI
1043	2393	Α	8688	359	17	GLMTSLLKPIKRRWRDYKRWKSGGFTGESC
					ł	HHADTLGDRGGLQGDHSELLQWQKRILRTE
'	-	ì		Į		GEPSPKYISKNIFPICSYITGFL
	2394	A	8718	292	1490	GTVKTSVATPITAGHSCSSGGVLQVKSPATQS
1044	2394) ^	8/16	1		GFKFTSKMEDFNMESDSFEDFWKGEDLSNYS
		ì	1	\		YSSTLPPFLLDAAPCEPESLEINKYFVVIIYAL
		1	1	1	i .	VFLLSLLGNSLVMLVILYSRVGRSVTDVYLL
	1	1	1		İ	NLALADLLFALTLPIWAASKVNGWIFGTFLC KVVSLLKEVNFYSGILLACISVDRYLAIVHA
	1		1	}		TRTLTQKRYLVKFICLSIWGLSLLLALPVLLFR
		1				RTVVSSNVSPACYEDMGNNTANWRMLLRIL
1	1					POSEGEIVPLLIMLFCYGFTLRTLFKAHMGQK
1	1	1	1	0.		HRAMRVIFAVVLIFLLCWLPYNLVLLADTLM
		1				RTOVIOETCERRNHIDRALDATEILGILHSCLN
	'	1	1	(PLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDS
]]	1				RPSFVGSSSGHTSTTL
1045	2395 ·	A	8724	254	3184	FRANLAITVANRRGAQGGKMHTCCPPVTLEQ DLHRKMHSWMLQTLAFAVTSLVLSCAETIDY
				1		YGEICDNACPCEEKDGILTVSCENRGIISLSEIS
1		1	 .	1		PPRFPIYHLLLSGNLLNRLYPNEFVNYTGASIL
		1	İ		1	HLGSNVIODIETGAFHGLRGLRRLHLNNNKL
ł		ł	İ	1		FILEDDTFLGLENLEYLQVDYNYISVIEPNAF
1	1.	i				GKLHLLQVLILNDNLLSSLPNNLFRFVPLTHL
}	1	1				DLRGNRLKLLPYVGLLQHMDKVVELQLEEN
1						PWNCSCELISLKDWLDSISYSALVGDVVCETP FRLHGRDLDEVSKQELCPRRLISDYEMRPQTP
1	1	[LSTTGYLHTTPASVNSVATSSSAVYKPPLKPP
	1	1		İ		KGTRQPNKPRVRPTSRQPSKDLGYSNYGPSIA
	1	1 .	.		1	VOTKSPVPLECPTACSCNLQISDLGLNVNCQE
1		1		ł		RKIESTAELOPKPYNPKKMYLTENYLAVVRRT
-		1	ł	1		DILEATGLDLLHLGNNRISMIQDRAFGDLTN
		ı		- [ļ.	LRRLYLNGNRIERLSPELFYGLQSLQYLFLQY
	İ	1	1	İ		NLIREIQSGTFDPVPNLQLLFLNNNLLQAMPS
	İ	ļ		{	1	GVFSGLTLLRLNLRSNHFTSLPVSGVLDQLKS LIQIDLHDNPWDCTCDIVGMKLWVEQLKVG
1	ļ	1		1	Ì	VLVDEVICKAPKKFAETDMRSIKSELLCPDYS
Ì	ŀ		} .]		DVVVSTPTPSSIQVPARTSAVTPAVRLNSTGA
1	1 .			1		PASLGAGGGASSVPLSVLILSLLLVFIMSVFVA
1		1		1		AGLEVI VMKRRKKNOSDHTSTNNSDVSSFN
		1		1		MOYSVYGGGGGTGGHPHAHVHHRGPALPK
1		1		1	1	VKTPAGHVYEYIPHPLGHMCKNPIYRSREGN
1	İ	İ	1		- {	SVEDYKDLHELKVTYSSNHHLQQQQQPPPPP
	1					QQPQQQPPPQLQLQPGEEERRESHHLRSPAYS VSTIEPREDLLSPVQDADRFYRGILEPDKHCST
	-	1		1		TPAGNSLPEYPKFPCSPAAYTFSPNYDLRRPH
	1				ļ	OYLHPGAGDSRLREPVLYSPPSAVFVEPNRNE
1			1			VLBLKAKLNVEPDYLEVLEKQTTFSQF
			000	20	452	SPSAAGGLAWVSLALGSGSRGRDHSGSGVGT
1046	2396	Α	8736	28	752	AMAGALVRKAADYVRSKDFRDYLMSTHFW
		1	1	Ì	1	GPVANWGLPIAAINDMKKSPEIISGRMTFALC
1	1		1			CYSLTFMRFAYKVQPRNWLLFACHATNEVA
	1	1		1		OLIOGGRLIKHEMTKTASA
1047	2397	HA-	8741	673	924	ALPGTPQQTVTLNTDGKVKSFTSPHSNPNLPP
1047	2091	"	1	'''		AKFFTSLQSLNWSSHLPPSPATESVGKRGNAK
				<u> </u>		PPTTKLLHSSPLWNFFAQQL PEVTKPSLSQPTAASPIGSSPSPPVNGGNNAKR
1048	2398	A	8747	3	5054	PEA IN STORE I WOOD AND CONTRACT
<u> </u>						

						(A 1 - 0 0 A 1 - 0
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		Ì	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ľ	l	ł	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	l .	i i	peptide		nucleotide insertion
	<u> </u>			sequence		VAVPNGQPPSAARYMPREVPPRFRCQQDHK .
	'	l				VLLKRGQPPPPSCMLLGGGAGPPPCTAPGAN
	1	1	ł	ł		PNNAQVTGALLQSESGTAPDSTLGGAAASNY
	1	l	ļ	ļ	1	ANSTWGSGASSNNGTSPNPIHIWDKVTVDGS
	Ì				ļ	DMEEWPCIASKDTESSSENTTDNNSASNPGSE
	ĺ	1	1	1	}	KSTLPGSTTSNKGKGSQCQSASSGNECNLGV
	ł	1		[1	WKSDPKAKSVQSSNSTTENNNGLGNWRNVS
		l	1			GQDRIGPGSGFSNFNPNSNPSAWPALVQEGTS
)		İ	1	RKGALETDNSNSSAQVSTVGQTSREQQSKME
	1	1	ł	į	İ	NAGVNFVVSGREQAQIHNTDGPKNGNTNSL
	1		1			NLSSPNPMENKGMPFGMGLGNTSRSTDAPSQ
	1			}		STGDRKTGSVGSWGAARGPSGTDTVSGQSNS
			1]	GNNGNNGKEREDSWKGASVQKSTGSKNDS
			1	1	1	WDNNNRSTGGSWNFGPQDSNDNKWGEGNK MTSGVSQGEWKQPTGSDELKIGEWSGPNQPN
	1	1	1	1	1	SSTGAWDNQKGHPLLENQGNAQAPCWGRSS
	1	1		1	ì	SSTGAWDROTH EDITAGES TO STATE OF THE STATE OF
	1	1		1		RPTHPDCQAVLQTLLSRTDLDPRVLSNTGWG
		1	}		i	QTQIKQDTVWDIEEVPRPEGKSDKGTEGWES
		1	1	1	1	AATOTKNSGGWGDAPSQSNQMKSGWGELS
				1		ASTEWKDPKNTGGWNDYKNNNSSNWGGGR
		1)		1	PDEKTPSSWNENPSKDQGWGGGRQPNQGWS
		1	l		1	SGKNGWGEEVDQTKNSNWESSASKPVSGWG
1		1	1		,	EGGQNEIGTWGNGGNASLASKGGWEDCKRS
1		1	1			PAWNETGRQPNSWNKQHQQQQPPQQPPPPQ
i	1	{		i		PEASGSWGGPPPPPPGNVRPSNSSWSSGPQPA
1	1	1	1			TPKDEEPSGWEEPSPQSISRKMDIDDGTSAWG DPNSYNYKNVNLWDKNSQGGPAPREPNLPTP
	İ		1	1		MTSKSASDSKSMQDGWGESDGPVTGARHPS
	1	1		ì		WEEEEDGGVWNTTGSQGSASSHNSASWGQG
!	1		1	1	1	GKKQMKCSLKGGNNDSWMNPLAKQFSNMG
	-	1		1		LLSOTEDNPSSKMDLSVGSLSDKKFDVDKRA
}				1	1	MNLGDFNDIMRKDRSGFRPPNSKDMGTTDS
		1	j	Į.		GPYFEKGGSHGLFGNSTAOSRGLHTPVQPLN
					}	SSPSLRAOVPPOFISPOVSASMLKQFPNSGLSP
		1	1		ļ	GLFNVGPOLSPOQIAMLSQLPQIPQFQLACQL
ł	į	- {		1	1	LLQQQQQQLLQNQRKISQAVRQQQEQQLA
1			1	1	1	RMVSALOOOOOOOOROPGMKHSPSHPVGPK
1		1			1	PLIT DNMVPNALNVGLPDLOTKGPLPGYGSGF
			1		1	SSGGMDYGMVGGKEAGTESRFKQWTSMME
	1.	}		1	1	GLPSVATQEANMHKNGAIVAPGKTRGGSPY
1	1			1		NOFDIIPGDTLGGHTGPAGDSWLPAKSPPTNK
i		1		l	1	IGSKSSNASWPPEFQPGVPWKGIQNIDPESDP YVTPGSVLGGTATSPIVDTDHQLLRDNTTGS
1	1	-		1		NSSLNTSLPSPGAWPYSASDNSFTNVHSTSAK
1	i	1		· ·	1	FPDYKSTWSPDPIGHNPTHLSNKMWKNHISS
1		1				RNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRG
		-		1		WGTQDSRLASASTWSDGGSVRPSYWLVLHN
1	1		1	1		T TPOTOGSTI RTICMOHGPLLTFHLNLTQGTA
	1	-		İ	1	LIRYSTKOEAAKAOTALHMCVLGNTTILAEF
				l		ATDDEVSRFLAGAOPPTPAATPSAPAAGWQS
				1		1 ETGONOSDPVGPALNLFGGSTGLGQWSSSA
1.	ŀ	[1		GGSSGADLAGASLWGPPNYSSSLWGVPIVED
'					1	PHRMOSPAPILLPGDLLGGGSDSI
1040	2399	- _A	8748	200	1387	VPWKRODEOLSLOVETLYLDSPAVIHLLSPIT
1049	2399	^	0/40	1 200	1	I PPSSLPPFLOIVDSSSSACTLDSFFPFLAPWDS
		1	1	1	1	PODCGFKDHOPLTLOALTVELARWTLMLLLS
	- 1	l.				
					1	TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT
						TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT ELTKLLLCAFSLLVGWQAWPQGPPPWRQAA PFALSALLYGANNNLVIYLQRYMDPSTYQVL

	0000		OF C	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ł	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł		1	1	peptide		/=possible nucleotide deletion, \=possible
1	[1		sequence	(nucleotide insertion
				Sequence		SNLKIGSTAVLYCLCLRHRLSVRQGLALLLL
	٠ .	1		•		MAAGACYAAGGLQVPGNTLPSPPPAAAASP
ŀ	}			i	1	MPLHITPLGLLLLILYCLISGLSSVYTELLMKR
		İ				MPLHIPLGLLLLIC ICLISGLSS VI TELLIVIAN
i		l				QRLPLALQNLFLYTFGVLLNLGLHAGGGSGP
j		1			1	GLLEGFSGWAALVVLSQALNGLLMSAVMKH
		}	Ì	}	}	GSSITRLFVVSCSLVVNAVLSAVLLRLQLTAA
1		1				FFLATLLIGLAMRLYYGSR
1050	2400	A	8758	3	1660	WVSSMGFEELLEQVGGFGPFQLRNVALLALP
1030	2400	^	0750	١	1	RVLLPLHFLLPIFLAAVPAHRCALPGAPANFS
ſ		ı				HODVWLEAHLPREPDGTLSSCLRFAYPQALP
		1	1		1	NTTLGEERQSRGELEDEPATVPCSQGWEYDH
1	1				1	SEFSSTIATESQWDLVCEQKGLNRAASTFFFA
	1				1	GVLVGAVAFGYLSDRFGRRRLLLVAYVSTLV
1	1	1	1			UVLVUAVARU I LODKRUKKULLVA I VOILV
	1	1	1			LGLASAASVSYVMFAITRTLTGSALAGFTIIV
	-		ľ]		MPLELEWLDVEHRTVAGVLSSTFWTGGVML
}	1	1	Ì	}	Ì	LALVGYLIRDWRWLLLAVTLPCAPGILSLWW
1 .	1		1			VPESARWLLTQGHVKEAHRYLLHCARLNGR
}		1	1	1		PVCEDSFSQEAVSKVAAGERVVRRPSYLDLF
1	ł	ł	1	ł	l	RTPRLRHISLCCVVVWFGVNFSYYGLSLDVS
1	i .	1	1	1	1	GLGLNVYQTQLLFGAVELPSKLLVYLSVRYA -
I		1		i		GRRLTQAGTLLGTALAFGTRLLVSSDMKSWS
1		1		1		TVLAVMGKAFSEAAFTTAYLFTSELYPTVLR
1			1	1	Į	QTGMGLTALVGRLGGSLAPLAALLDGVWLS
ĺ	1	1	1	1	 	LPKLTYGGIALLAAGTALLLPETRQAQLPETI
		1	1			QDVERKSAPTSLQEEEMPMKQVQN
						EIRTPVAVSSAPSGDSEGDEEETTQDEVSSHTS
1051	2401	Α	8759	515	1625	EIKTPVAVSSAPSGDSEGDEEET TQDEVSSATS
			1			EEDGGVVKVEKELENTEQPVGGNEVVEHEV
]	1		}	1	l	TGNLNSDPLLELCQCPLCQLDCGSREQLIAHV
1			1	1	ĺ	YQHTAAVVSAKSYMCPVCGRALSSPGSLGR
i				1 .		HLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
1	1		ļ		1	EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYP
1	1 .	1	1			AGILLVCNNCAAYRKLLEAQTPSVRKWALRR
1	1	1	1	1	Ī	QNEPLEVRLQRLERERTAKKSRRDNETPEERE
1		1	1	1	i	VRRMRDREAKRLQRMQETDEQRARRLQRDR
1	1		1	1		EAMRLKRANETPEKRQARLIREREAKRLKRR
1	1	1	1	1	1	LEKMDMMLRAQFGQDPSAMAALAAEMNFF
*	1	1	i	1	l .	QLPVSGVELDSQLLGKMAFEEQNSSSLH
	<u></u>			J	<u> </u>	ALL A 20 A ETT 2 OF THE DECK CONTINUED OF A
1052	2402	A	8763	1106	70	RHGHGGRDRRGGGRVARPGGLGRYPGRGAA
			1]	ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA
	1	1		1	1	HGSKHRARAAPDPPPLFDDTSGGYSSQPGGY
1	1	1	1	i		PATGADVAFSVNHLLGDPMANVAMAYGSSI
]	}	1	1]	1	ASHGKDMVHKELHRFVSVSKLKYFFAVDTA
1			1		1	YVAKKLGLLVFPYTHQNWEVQYSRDAPLPP
	1	1	1	1		RODLNAPDLYIPTMAFITYVLLAGMALGIQK
] .	1	1			1	RFSPEVLGLCASTALVWVVMEVLALLLGLYL
1	1]		1	1	ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL
	1	Ì	1		1	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
1	1	1	1	1	1	TLADARI I ANTWA TOSUTALI CA VECCI MA
1	1	1		1	1 .	GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY
		1				WLTFHLVR
1053	2403	A	8768	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVF
	1	1		1		YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW
ľ	1	1	1	(1	PEDIWPHVDKLSSAHVYLRLHKGENIEDIPKE
1	1	l				VLMDCAHLVKANSIQGCKMNNVNVVYTPW
1	1		1		1	SNLKKTADMDVGQIGFHRQKDVKIVTVEKK
1		i	1	[VNEILNRLEKTKVERFPDLAAEKECRDREER
1	1		1	1		NEKKAQIQEMKKREKEEMKKKREMDELRSY
1	1		1			
	1			<u> </u>	<u></u>	SSLMKVENMSSNQDGNDSDEFM
1054	2404	A	8769	344	527	REATTLACRNSCWVFSRCSLGACKPTVCSMP
1	1	1	1	1		SLSRQGSQTLCLRLAEYCMESVDSQRLLLS
	1	1	J			

		17	1000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	neuce		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	}		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
1				sequence		OOESPAAGAARMNCKEGTDSSCGCRGNDEK
1055	2405	A	8770	430	1104	KMLKCVVVGDGAVGKTCLLMSYANDAFPEE
						KMLKCVVVGDGAVGATCDEMSTAIDATTED
	1	1				YVPTVFDHYAVTVTVGGKQHLLGLYDTAGQ
ì		l	Ì		l	EDYNQLRPLSYPNTDVFLICFSVVNPASYHNV
1	1	Į.	1	1		QEEWVPELKDCMPHVPYVLIGTQIDLRDDPK
1	1	١.	1	l	i	TLARLLYMKEKPLTYEHGVKLAKAIGAQCYL
	1	1	ł	l		ECSALTQKGLKAVFDEAILTIFHPKKKKKRCS
1	1	l	1			EGHSCCSII
1056	0406	A	8773	261	332	NPRIQLSGNSCCAGSCRVWLSEQ
1056	2406		8778	3	477	PAGIRHEOARGADRMGKCRGLRTARKLRSH
1057	2407	A	0//0	3	777	RRDOKWHDKOYKKAHLGTALKANPFGGAS
	-					HAKGIVI.EKVGVEAKOPNSAIRKCVRVQLIK
1	į	1		1		NGKKITAFVPNDGCLNFIEENDEVLVAGFGR
		1	Ì	Į.		KGHAVGDIPGVRFKVVKVANVSLLALYKGK
1	1	1	ì	1	İ	KERPRS
			0000	 121	881	PGLSOEPSGSMETVVIVAIGVLATIFLASFAAL
1058	2408	Α	8808	171	991	VI VCRORYCRPRDLLORYDSKPIVDLIGAME
1	1					TOSEPSELELDDVVITNPHIEAILENEDWIEDA
	1	ì	1		}	SGLMSHCIAILKICHTLTEKLVAMTMGSGAK
i		1	1	1		MKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
	1	1		į.	1	DPKLLDARTTALLLSVSHLVLVTRNACHLTG
1	i	ŀ	1	ļ		GLDWIDQSLSAAEEHLEVLREAALASEPDKG
1	}	Į.	ł	ì		GLDWIDQSESAAESTEEVIAGES EN ESTE
					l	LPGPEGFLQEQSAI MRLQGAIFVLLPHLGPILVWLFTRDHMSGWC
1059	2409	A	8809	246	757	EGPRMLSWCPFYKVLLLVQTAIYSVVGYASY
,				1	1	EGPRMLSWCPF 1KVLLLVQIALISV VOTASI
	-		1	i	1	LVWKDLGGGLGWPLALPLGLYAVQLTISWT
1					•	VLVLFFTVHNPGLALLHLLLLYGLVVSTALI
ł	1	Ì	1		1	WHPINKLAALLLLPYLAWLTVTSALTYHLWR
1	İ	i				DSLCPVHQPQPTEKSD
1060	2410	A	8810	304	381	PKLSVYPLQSHHCLSEPFQSLVCCLA
1061	2411	TA A	8820	1673	848	SCKTENLLEMWWFQQGLSFLPSALVIWTSAA
1001	2411	1	***		1	FIFSYITAVTLHHIDPALPYISDTGTVAPEKCLF
	1	Į.	1			GAMLNIAAVLCIATIYVRYKQVHALSPEENVI
1	1			1		IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA
1	l	ì		1		HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH
		4	1			GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS
1	1	1		ſ	i	GNFGTDLEOKLHWNPEDKGYVLHMITTAAE
1	1			ł		WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL
	1	1		İ		TI VOTAPCPINNERTRLLSRDI
12.22			0004	$+_{i}$	763	GGAPPASVPARESPVSGAOGSSRTRGHKRAA
1062	2412	A	8824	1,	""	GARAPOLCSSWORRSAPAMSRGLQLLLLSCA
1			1	1		VSI APATPEVKVACSEDVDLPCTAPWDPQVP
		1		1		YTVSWVKLLEGGEERMETPQEDHLRGQHYH
1	1	Ì	1.	1	1	OKGONGSFDAPNERPYSLKIRNTTSCNSGTYK
		İ	1	1		CTLODPDGORNLSGKVILRVTGCPAQRKEET
1		ł	1	1		FKKYRAEIVLLALVIFYLTLIIFTCKFARLQSI
i				1		FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT
-				1	i	
					1	ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE
		A	8826	147	627	HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT
1063	2413	Į A.				HOKTHA MALOLKKA OF MALOCEDD VICEDUV
1063	2413	A	1		1	AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH
1063	2413	^		1	ž.	
1063	2413	A			İ	KCSLMCPHRSQDSLS1AIFQRS1 GAITTOIG IDIT
1063	2413	A				CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL
1063	2413					CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR
			9075	2982	1869	CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR I KDTLKSOMTOEASDEAEDMKEAMNRMIDE
1063	2413	A	8835	2982	1869	CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKOVSELSOLYKEAQAELEDYRKRKSLEDV
			8835	2982	1869	CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV TAFYIHKAEHEKLMOLTNVSRAKAEDALSE
			8835	2982	1869	CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV TAEYIHKAEHEKLMQLTNVSRAKAEDALSE MKSQYSKVLNELTOLKQLVDAQKENSVSITE
			8835	2982	1869	CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKOVSELSOLYKEAQAELEDYRKRKSLEDV

					Dundinted and	Amino acid sequence (A=Alanine C=Cysteine,
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nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		•	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
401100				amino acid	of peptide	Telhreonine, Vevaline, wellypropriati,
	į .			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ.	[peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		 				VAKLEKQLLEEKAAMTDAMVPRSSYEKLQS
		1				SLESEVSVLASKLKESVKEKEKVHSEVVQIRS
	1	l				EVSQVKREKENIQTLLKSKEQEVNELLQKFQ
		ì				OAOEELAEMKRYSESSSKLEEDKDKKINEMS
	ľ	1	1			KEVTKLKEALNSLSOLSYSTSSSKRQSQQLEA
		{	1			LOOOVKOLONOLAECKKOHQEVISVYRMHL
	1	ļ			ł	LYAVQGQMDEDVQKVLKQILTMCKNQSQK
1		1	ļ	ŀ	i	K
			,	<u> </u>	663	AAATAASLSPRGCRLRTPSSDVGPSRAPPPSA
1065	2415	Α	8841	3	003	APLPTGRAQMSPSGRLCLLTIVGLILPTRGQTL
	i	1		1	1	KDTTSSSSADATIMDIQVPTRAPDAVYTELQP
1	1	1)	}	1 .	TSPTPTWPADETPQPQTQTQQLEGTDGPLVT
	1	1	1			DPETHKSTKAAHPTDDTTTLSERPSPSTDVQT
1	1		1		1	DPQTLKPSGFHEDDPFFYDEHTLRKRGLLVA
1 .			·		1	AVLFITGIILLTSGKCRQLSRLCRNHCR
1			l			FVGEQEGGCEAGAGRGAQTYPGEAGERWFG
1066	2416	A	8853	3806	2204	RRRRGRVVSRKKMSLKSERRGIHVDQSDLL
		1		1		CKKGCGYYGNPAWQGFCSKCWREEYHKAR
ł		1	1	1	1	QKQIQEDWELAERLQREEEEAFASSQSSQGA
1	1	1		1	1	QKQIQEDWELAEKLQKEEEAA ABSQCSQR QSLTFSKFEEKKTNEKTRKVTTVKKFFSASSR
1	Į.	,.			1	QSLTFSKFEBKKINEKIKKVIIVKKIIOAGGK
	1	1		1	1	VGSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE
ì	1	1	l	1	1	FLKTFHKTGQEIYKQTKLFLEGMHYKRDLSIE
i .		1	1	1		EQSECAQDFYHNVAERMQTRGKVPPERVEKI
1		1	ł	1		MDQIEKYIMTRLYKYVFCPETTDDEKKDLAI
1	1	ì		ł	j	QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV
	1		1	1	1	KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI
1			1	1		KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI
ļ				1	ł	QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE
ł	1	1		1	1	KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES
1	İ	1				WSPDACLGVKQMYKNLDLLSQLNERQERIM
1	1	i i	1		l .	NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI
1		1	}	ł	į —	KPPNQPLAAIDSENVENDKLPPPLQPQVYAG
10/5	2417	HA	8855	1372	1513	SNMREVGCGWLVPVIPAFWEAEVGGSLEARS
1067	2417	Λ.	0033	10,2		LRQAWATKQDPISKKK
			8856	1530	1583	PCRPGMECNSMISVHCNL
1068	2418	A		1530	1583	PCRPGMECNSMISVHCNL
1069	2419	A	8857		1675	PVPOGGYPOGPYPOEGYPOGPYPQGGYPQGP
1070	2420	A	8866	293	10/3	VPOSPFPPNPYGOPOVFPGODPDSPQHGNYQ
		1		1	1	EEGPPSYYDNODFPATNWDDKSIRQAFIRKVF
1	.	1		ł	1	LVLTLOLSVTLSTVSVFTFVAEVKGFVRENV
	1		į	1		WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL
1			1	1		VALSVLTASLSYMVGMIASFYNTEAVIMAVG
1		- 1		1		ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM
}	}	}		1		VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA
1	1	1	į.	1		VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI
i	-	ı	1	1	1	FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP
	ł	- 1	1	Į.		WHGSASCTSPLSCPQAQPREKDASLQPSCMY
	1	1		ŀ	i	TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC
1	1	1	1	1		TADISIW IKCOMSWAPLVLFFFRGIRATITO
	į	- 1	1			HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ
1	}	- 1	1	1	i	EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS
1		1	1		1	GDMRSGGLIPVLSPE
1221	2421	- 	8868	2	358	ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH
1071	2421	A	3000	1~	1	DDKMGSNTFFKRNDCRYVMISCKADMAYDN
1		l	1	- 1	1	VRHPFMI*SI/KLIMEETYLNIIKAVYDRPTASII
-			1	i	1	I NGEKLKVFPVRSGT*OGCSVWP
L			- 10000	 22 - 	658	MESVI SKYEDOITIFTDYLEEYPDTDELVWIL
1072	2422	A	8870	33	056	GYOHI I KTEKSKLLSDISARLWFTYRRKFSPI
				1	1 .	GCTGPSSDAGWGCMLRCGOMMLAQALICKH
1	i			ļ		LGRDWSWEKQKEQPKEYQRILQCFLDRKDC
1						

					D distant and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=Aspartic Acid E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide.		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence	'	}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		Ì		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			[residue of	sequence	/=possible nucleotide deletion, \=possible
	}		ļ	peptide		
			_	sequence		nucleotide insertion CYSIHQMAQMGVGEGKSIGEWVLGPNTVAQ
						CASIHÓWYÓMA ARCHAINE A TANANTAL CITANANTAL CASIHÓWYÓMA A TANANTAL CITANANTAL CASIHÓWYÓMA A TANANTANTAL CASIHÓWYÓMA A TANANTANTA CASIHÓWYÓMA A TANANTANTA CASIHÓW
		1	ļ			GV*KNLAILFDEWINSLGLVYVSM\DNPSGSIA
						RFPKKLCRVLPL\SADTAGLTGP
1073	2423	Α.	8879	146	412	DFSV*GDVDIEVTCPICLQLLTEPLSLNCGLRL
1075	2423	''	1 00.5		ļ	*QVCITA*IKESVIISGG*SSSPVCHTTFQPANL
		1	1	İ	ł	RTSRYLPT*SIKSLGPDEPQEG
	0404	A	8884	67	435	HLQGRSIRTLQLTGENEKNCEVSERIRRSGPW
1074	2424	A	0004	0,	"""	KEISEGDVICHTFOGDCWADRSPLHEAAAHG
		1		1 .		RILALKTLIAOGVNVNLWTL/DRVSSLHEACL
	l	1	1	j		*GPVACAKPYWKMYPRHGGTVTGPPLLMV
				1004	248	RSGDRNGLTHOLGGLSOGSRNQSYRSRSRSR
1075	2425	Α	8896	1294	240	SRERPSAPRGIPFASASSSVYYGSYSRPYGSDK
				1	ì	PWPSLLDKEREESLRQKRLSERERIGELGAPE
		1	ŀ			VWGLSPKNPEPDSDEHTPVEDEEPKKSTTSAS
	1	1	ł			TSEEEKKKKSSRSKERSKKRRKKKSSKRKHK
	{'	i	1	1		KYSEDSDSDSDSETDSSDEDNKRRAKKAKKK
	1	1		1		EKKKHRSKKYKKKRSKKSRKESSDSSSKES
	1	1	J	J	ł	QEEFLENPWKDRTKAEEPSDLIGPEAPKTLTS
	1			1		QDDKPLNYGHALLPGEGAAMAEYVKAGKRI
	1	1		1	ì	PRRGEIGLTR*RNCHHLNAQVM**VVSRHRR
		}		1	,	MEAVRTAKREPESTVLMRREPLHPFNPRRET
		1		1		
						KERE
1076	2426	A	8899	146	789	GRSTEAEKEPAFDERTGKGRRLPRAGEFHG*E
1070	2720	}	1		1.	*APGPGPRSFQVSRKMPEEIPPGARKHPFSGKS
(1	\ `	1	1	FYLDLPAGKNLQFLTGAIQQLGGVIEGFLSKE
1	1	1	١.	1		VSYIVSSRREVKAESSGKSHRGCPSPSPSEVR
	1	1				VETSAMVDPKGSHPRPSRKPVDSVPLSRGKE
Ì		1				LLQKAIRNQK**CTVQQLSHCRLY\GEKTTAK
1	1	L		l l		RSQREHVQQQSQEHGKWPDLKGPR
1000	2427	A	8901	352	3	AKIGAYKYIQELWRKKQSDVMHFLLRVRCW
1077	2421	1^	0,0.			QYPALHRAGTEWQLSALHRAPRSTQPDKAC
1		1		1		RLGYKAKQGYIIYRICVRRGGWKCPVPKAVT
1		1		1	ŀ	\YGKPVHHGVN*LKFAQSLQSVAEEQ
		-	8905	536	781	ACPAENREVPEMAAGOAPHAGPGAGPGQPA
1078	2428	A	8905	230	/01	PALPFAATPGSRGQALCRGGRRRQHLHGPLH
	'	1		1	ĺ	RP*OAAPALHAGCOLAPHPPT
				121	376	NI.IWKLCVTERRLVILDNYDLASE/YEANKYI
1079	2429	A	8912	121	370	CNRIIQFKPGQDKYFTLGLPTGSTPL*CYPKLI
			- }		1	EVNKNGHLSFKYVKTFSMDEY
				1 20:	1788	SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG
1080	2430	. A	8920	381	1/00	GUST ESCEPITLRMCODLPYNTTFMPNLLNHY
		1 .		1	1	DQQTAALAMEPFHPMVNLDCSRDFRPFLCAL
1			1		1	VADICMEVGRVTLPCRRLCORAYSECSKLME
1				1	}	MFGVPWPEDMECSRFPDCDEPYPRLVDLNLA
1		1	1			GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY
1		1				SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS
1	1	1		1	1	IICLSATLFIFVIFLIDVTRFRYPERPIKCYAV
.	İ	- 1		1	1	WHMMVSLIFF\GFLLEDRVACNA\SIPAQYKA
1	}	-	1	1	·	WHMMVSLIFTNOTLLEDKVACHABITAQ IXA
1	1	ı		1	I	STVTQGSHNKACTMLFMILYFFTMAGSVWW
1				}		VILTITWFLAAVPKWGSEAIEKKALLFHASA
1	1	- 1	- 1	[1	WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD
1						VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR
1	1	- 1		Į		VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLI
				1.		VVIGCYFYEOAYRGIWETTWIOERC
	 		0000	56	420	FERTKMSTGPDVKATVGDISSDGNLNVAQEE
1 1001	2431	A	8922	30	720	CSRKGIVDEFFPLLSN*CIWTOPQGYPQSSYG
1081				1	1	THE PROPERTY ALTERNATION AND CHECKYTOOMN
1081	1	-	l l		1	TLANFVF(CSVKHGLALILOLCNFS) I I QQMIV
1081			ļ			TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST
1081	2432	A	8923	355	1079	LSIAIPAMVNNTAPPSQPNASTERPST PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV

SQ ID NO. of much conduction of the conduction o		050 10	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
In much cedide Sequence Seq	SEQ ID	SEQ ID	Met				D=Aspartic Acid, E=Glutamic Acid,
USSN			noa	7			F=Phenylalanine, G=Glycine, H=Histidine,
Sequence 914 914 1							I=Isoleucine, K=Lysine, L=Leucine,
1083							M=Methionine, N=Asparagine, P=Proline,
Immin seid residue of peptide residue of peptide sequence T=Threonine, V=Valine, V=Typtophae, Y=Typtophae	seq-	uence					O=Glutamine, R=Arginine, S=Serine,
Pestide of peptide Pep	uence			914 .			T=Threonine V=Valine W=Tryptophan.
Peptide			l				V-Tyrosine Y=I Inknown *=Ston codon.
			1	1		sequence	b-possible nucleotide deletion \=nossible
1083 2433 A 8948 28 385				1	peptide]	
QGTQLASDGLKGLLFEVSLADLQNDEVAFRK FELITEDVQDENCLTHYFYGMDLTCDKICSMV EKWSTMEAHVDVKTTDGYFFILECVGFTKK HNNQLKTYA*HQGSQRQIKKMBEMT*EV QTNDLKEVYNKLIPDNIOKDTEKV/CPYPLI DYFIREYKMLEPDFERMELRGGSSS DYFIREYKMLEPDFERMELRGGSSS DYFIREYKMLEPDFERMELRGGSSS DYFIREYKMLEPDFERMELRGGGSS DYFIREYKMLEPDFERMELRGGGSS DYFIREYKMLEPDFERMELRGGGSS DYFIREYKMLEPTGET QWILITESCSISPKLCSIAVH*DNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLCSIAVH*QNPAWF QWILITESCSISPKLC		1	1		sequence		nucleotide insertion
FRITTEDVQDRNC_TRYTGMDLTCDKICSMY REWSTMEAHVDWKTTGSYFFILLCVGFTKK HNNQLKTSYA*HQQSRQIQKKMMBIM*PEV DYDRKVMKLIDPIORIDTEKVCYGFTKK HNNQLKTSYA*HQQSRQIQKKMMBIM*PEV DYDRKVMKLIDPIORIDTEKVCYGFTKK HNNQLKTSYA*HQQSRQIQKKMMBIM*PEV DVFIRKVMM_BAPQFPBMBEL_RGG0SSS LTWPQFHPSCT_AMSEETLQSKL_AAASKKLP WGAVQGSRAMSDLLLLLDLTLLLLMLLGF AGYSGQLAGVASAGSPPJKKFHVEPYGET GWL_TDSCSISPRKLCSIAVP*INPAMP* WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVWQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQKSTLNLRY WGKKVQFFWKRVQFWKRVQKSTLNLRY WGKKVQFWKRVQFWKRVQKSTLNLRY WGKKVQFWKRVQFWKRVTT WGKVGFWCKTLSFWWKTQFFWKRVT WGKKVGFWKRVT WGKVGFWCKTLSFWWKTQFWKRVT WGKVGFWKRT WGKVGFWKRVT WGKVGFWKRT WGKVGFWKT WGKVGFWKRT WGKVGFWKRT WGKVGFWKRT WGKVGFWKRT WGKVGFWKT WGKVGFWKRT WGKVGFWKRT WGKVGFWKRT WGKVGFWKRT WGKVGFWKRT WGKVGFWKRT WGKVGFWKT WGKVGFWKRT WGKVGFWKT WGKVGFWK						1	GPFSKKDQYDYKAPAWITNIGNIGNICYACI
	i	1		1	1		QGTQIASDGLKGLLFEVSLADLQNDEVATAK
HNNOLLKTSYA-HQQSRQIQKKM/MEIMTEV CINDILEEVYNLIPDNIKOIDTEVIPTLH		ļ			1	l	FKLITEDVQDKNCLINF I GWDLICDKICSIVIV
		<u> </u>	ì	1			EKWSTMIEAHVDVKI IDGYFFHLFCVGF1KK
DVPRKVKMENPGFERWELRGGGSSS		İ	1		i		HNNQILKTSYA*HQQS/RQIQKKMMEIM1*EV
1083	_	1	1		1		QTNDLKEVVNKLIPDNIGKDTEKV/CPIYPLH
1083		1		1	1		DVFIRKVKMLENPGFER\MELRGGGSSS
WGAVQGSRAMSDLLLLLDT.LLLLM.	1002	2422	 	8048	28	385	LTWPQPHIPSCPAMSEETLQSKLAAAKKKLP
1084	1083	2455	^	. 6540	20	•	WGAVQGSRAMSDLLLLLLDLTLLLLLMLLGF
1084 2434 A 8990 156 318			1	1			AGYSGOLAGVAVSAGSPPI/RYKFHVEPYGET
1084	ļ			1			GWLLT/ESCSISPKLCSIAVH*DNPAWF
1084				<u> </u>	1.50	210	HYTPINTDTIENSENNKCW*GY*E\VGLIHHW
1085	1084	2434	A	8930	136		WGGKRVOPFWKRVWOKRTLNLRV
1085		i	1				TRACOL CYPIOCWWECKRLISE/WKTI*OSPAK
MFILAPFTATIKGRQLTCPL/VEERIPYMWYS HKYYTKVKRNL*VTITHTWVNLNILMFEILW YSHKYY 1087 2437 A 8985 58 330	1085	2435	A	8956	16	413	+DESTRUCTOR A TRIC/CITY DE PROSENCIA CHO ETCAR
HKYYKKRNI,*VTITHTWVNI,NILMFEIL.W YSHKYY					1	1	*TIY ISYDIAIPIS/GU TERI VEERIDVIMWYS
1086			1	1			MFILAPFIATIKG KOLTUTURUMI MIL MERIT W
1086	1	4	1				
1086	1			1			YSHKYY
1087 2437 A 8985 58 330	1086	2436	A	8962	868	1026	H*KILQVGRAQRAHXSRL*SQLLRRLRHESHL
1088	1000	2.33	1		1		NPGARGCSEARLHRC1PAW11
1088	1097	2437	A	8985	58	330	LHVKHLGHFQLVFSEVICHCILMPVS*ELQRL
1088	1007	2437	1 **	1 0700			*ERSVCAFHVCIQTYVCLQVYACMCVYYICM
1086		1	1			l	FVYSVYGCGLCTCVCMDVYICVCVQEFL
1086	1000	2420	- 	8080	394	404	N*KWILHVNVRIQSIFF/IKRNQK/INSHELKLD
YKDLSKLNRRKTE/S*/VKKWVKDLSRYFIKE	1088	2436	ΙΛ.	67,07	1 32.		KKFLDMMSNA*STKKHDKLD/LIKFKT/LCSA
1089 2439 A 8991 60 329 MALTPESPSSFPGLATGSSVPEPPGGPNATL	1				1		KYTVKRIKIHPTDLEKMLRNHLSDKD*YS/GV
1089 2439 A 8991 60 329 MALTPESPSSFPGLATGSSVPEPPGGPNATL	i		1				YKDLSKLNRRKTE/S*/VKKWVKDLSRYFIKE
1089 2439 A 8991 60 329 MALTPESPSSFOLATGSSVPEPFGGPNATL NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV GVEDNAYTLEVNSRYMRAVGIM*HL 1090 2440 A 8996 2 351 SNITTLT*MKKYDNTFCW*GCGQIG/T/LIYC WQESKFIQAFWSKIQQYLA*ISHHLFDPAFLFL GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR LLIAALFIIVQYWKQSKDHYI 1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT LVSSRKISKVIVVGDLSVGKTCLINR*GGAG AELGRVGPSLARWAGSRSQHLVPSQVCKDS FDKNYKARIGADFEMERFEVLGIFF FDKNYKARIGADFEMERFEVLGIFF FDKNYKARIGADFEMERFEVLGIFF FDKNYKARIGADFEMERFEVLGIFF FOKNYKARIGADFEMERFEVLGIFF FOKNYKARIGADFEMERFEVLGIFF FOKNYKARIGADFEMERFEVLGIFF WALHIHQHGQGPLGHGLVARVG ALLGIQQPAGSLILSRSSVMGVRGLQGFVGS TCPHICTVVNFKELAEHHRSKYPGCTPTIVVD AMCCLRYWYTFESWICGGQWREYFSALRDF VKTFTAAGIKLIFFTDGMYEQDKRDEWYKRR LKNNNEISRIFFHYIKSHKEQPGRNMFFIPSGLA VFTRFALKTLGOETLCSLQEADYEVASYGLQ HNCLGILGEDTDYLIPDTCPYFSISELCLESLD TVMLCREKLCESLGLCVADLPLLACLLGNDII PPGMFESFRYKCLSSYTSVKENFDKKGNIILA VSDHISKVLYLVQGEKKLEELPL/VTKQSSFL*RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP RVQTPNPGKKFPCVQALNP GKFPCVQALNP GKFPCVQALNP GKFPCVQALNP GKFPCVQALNP GKFPCVQALNP GKFPCVQALNP GKFPCVQALNP GKF	1		1	ł			VISMENKHKKIFSTS
NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV GVEDNAYTLEVNSRYMRAVGIM*IHL 1090 2440 A 8996 2 351 SNITTLT*MKKYDNTFCW*GCQIGIT/LIYC WQESKFIQAFWSKIQQYLA*ISHILIFDPAFLFL GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR LLIAALFIIVQYWKQSKDHYI 1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT LVSSRFKISK VIVVGDLSVGKTCLINR*GGAG AELGRVGPSLARWAGSRSQHLVPSQVCKDS FDKNYKAPIGADFEMERFEVLGIPF 1092 2442 A 8999 548 811 SSFIKRHILIFEDDWHQTTCCHPHIPAF*RCQ FHIFYVSVQNSISPSLSVSSSHPDRPDHEVHQH RAAHIHQHGQGPLGHGLVARVG 1093 2443 A 9002 3 2745 ALLGLQQPAQSLILSRSSVMGVRGLQGFVGS TCPHICTVVNFKELAEHHRSKYPGCTPTIVVD AMCCLRYWYTPESWICGQWREYFSALRDF VKTTAAGIKLIFFDGMVEQDKRDEWVKRR LKNNREISRIFHYIKSHKEQPGRNMFFIPSGLA VFTRFALKTLGGETLCSLQEADYEVASYGLQ HNCLGHLGEDTDYLIYDTCPYPSISELCLESLD TVMLCREKLCESLGLCVADLPLLACLLGNDII PEGMFESFRYKCLSSYTSVKENFDKKGNIILA VSDHISKVLYLYQGEKKLEELPLVTKQSSFL *RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP RVOTRPNGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTO- PESRREVPMCSDPEPRQEVPMCTGSEPRQEVPMCTDSEP ROFVPMYTGSEPROEVPMCTDSEPRQEVPMCTDSEP		1		9001	- 60	329	MAITPESPSSFPGLAATGSSVPEPPGGPNATL
GVEDNAYTLEVNSRYMRAVGIM*IHIL	1089	2439	A	8991	00	325	NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV
1090 2440 A 8996 2 351 SNITITLT*MKKYDNIFCW*GCGQIG/T/LIYC WQESKFIQAFWSKIQQYLA*ISHILFDPAFLFL GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR LLIAALFIIVQYWKQSKDHYI 1091 2441 A 8997 97 456 YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT LVSSRFKISKVIVVGDLSVGKTCLINR*GGAG AELGRYGPSLARWAGSRSQHLVPSQ\VCKDS FDKNYKAPIGADFEMERFEVLGIPF SSFIKRHILIFEDDWHQTTCCHHPHHPVF*RCQ FHIFYVSVQNSISPSLSVSSSHPDRPDHEVHQH RAAHHHQHGQGPLGHGLVARVG 1093 2443 A 9002 3 2745 ALGLQQPAQSLILSRSSVMGVRGLQGFVGS TCPHICTVVNFKELAEHHRSKYPGCTPTIVVD AMCCLRYWYTPESWICGGQWREYFSALRDF VKTFTAAGIKLIFFTDGMVEQDKRDEWVKRR LKNNREISRIFHYIKSHKEQPGRNMFFIPSGLA VFTRFALKTLGQETLCSLQEADYEVASYGLQ HNCLGILGEDTDYLIVDTCTYFSISELCLESLD TVMLCREKLCESLGLCVADLPLLACLLGNDII PEGMFESFRYKCLSSYTSVKENFDKKGNILA VSDHISKVLYLYQGEKKLEEILPLVTKQSSFL *RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPRQEVPMCTDSEPRQEVPMCTDSEP PESRREVPMCSDPEPRQEVPMCTDSEP ROFVPMYTGSEPRQEVPMCTDSEP ROFVPMYTGSEPROEVPMCTDSEP ROFVPMYTGSEPROEVPMCTDSEP		1	1	1	ł		GVEDNAYTLEVNSRYMRAVGIM*IHL
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
]	Ì	residue of	sequence	/=possible nucleotide deletion, \=possible
		l		peptide	1	
		İ		sequence		nucleotide insertion PICTOPISKQEDSMCTHAEINQKLPVATDFEFK
						LEALMCTNPEIKQEDPTNVGPEVKQQVTMVS
İ	1	l	j			DTEILKVARTHHVQAESYLVYNIMSSGEIECS
	1 .		İ	ĺ		NTLEDELDQALPSQAFTYRPIRQRVYSLLLED
İ	ļ	•		1	Ì	CODVTSTCLAVKEWFVYPGNPLRHPDLVRPL
1]]		}	QMTIPGGTPSLKILWLNQEPEIQVRRLDTLLA
j		ì	•	l		CFNLSSSREELQAVESPFQALCCLLIYLFVQV
ì	- 22		ì	1		DTLCLEDLHAFIAQALCLQGKSTSQLVNLQP
	1	1	ŀ	1		DYINPRAVQLGSLLVRGLTTLVLVNSACGFP
		1		}		WKTSDFMPWNVFDGKLFHQKYLQSEKGYA
		İ		l	İ	VEVI_/CRTK*ISAHOIPOPEGSRLQGLHEGEQT
1		1	ĺ	1		HHWPSPLGLTPRREVGKTGLQLPQDGLWV
100		 	0001	97	834	AREACRAKTDFPGRRFRLWPSCCCRVIVGAE
1094	2444	Α	9021	"	33",	T*HMAEPVSPLKHFVLAKKAITAIFDQLLEFV
		1		1	l	TEGSHEVEATYKNPELDRIATEDDLVEMQGY
			1	1	İ	KDKLSIIGEVLSRRHMKVAFFGRTSSGKSSVI
1	1 .	1		1	ł	NAMLWDKVLPSGIGHITNCFLSVEGTDGDKA
	1		1		1	YLMTEGSDEKKSVKTVNQLAHALHMDKDLK
	1	1	1	1	}	AGCLVRVFWPKAKCALLRDDLVLVDGPGTD
	1					VITELDSWIDKFCTKSSTREITNSGSDT
1095	2445	A	9022	1	537	LVLNSRVEDFVPPEGAGRTLPFALRPLAACW
1.0,5	1					LLHRRARRSSALCPRPRSWGVSGGEGAGARE
		1	İ	1	1	P*ITSSSCCLSAA/SHLSIQSPNMAGARRIRPQ
1	1	1	i	İ		LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV
1		İ	1	İ	1	FAYGQT\GAGKTYTMGTGFD
						FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL
1096	2446	A	9029	1	285	GQHSETPSLKKK\LAGYSGMCL*SQVLRRLRQ
İ	1		1			EDCLSPGGNCRES*SCPYTPAWITERDPV
			1		357	ARSTGFWGEILWCGFLKRSLALSPRVKCSGAI
1097	2447	Α	9032	716	357	LAHCNFRHAGFPPLSCLSLPNRWEYRRPPARP
	1			ì	1	GKFFLVFLVETGFQC/G*DGLDLLTSRSACLG
1		1	ĺ	{		LPKCWDYRREPAASIIFQTTFFINSK
1000	10440		9038	230	652	KVVVMSCEDINISGSFYRNKLKYLAFLCKRTS
1098	2448	A	1 2036	250	1002	TNPSOGPYHLWVPSHIFWQTTCGRLPHKTKQ
	.[1		1		G*AALDHLKVFDRIPLPYDKKKQMAVSATLE
1.	1	1	1	1		VVRPKP*RKFAYLGHWAQKVDWKYQAMTA
	1		1	1		TMGEKRKVYYOKICYOKK
1099	2449	A	9043	185	372	IIFYSHOOCMRV/WOGCGDIETLIHCW*E*KII
1077	2-7-75	1 ^	1			HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP
					=	RKIKTCPONSCTSMLINAIHNDQKWKKINI
1100	2450	A	9045	763	584	ROSLALSPRIECSGTISAHCRLCPLVFTPLSCL
1100	7.50	1	1			SLTSSWDYRRPPPHPANFLYFK*RRGF
1101	2451	A	9050	275	2	LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL
1		1			1	FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS
	1				1	DSPASAS*VAGITDMCRYTQLILFHAS
1102	2452	A	9053	449	1224	KTSMFWKFDLHSSSHIDTLLEREDVTLKELM
1.102		1			1	DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF
		1		1	· [N*EEPPQDMDEKIRYKYPNISCELLTSDVSQM
1		1		1		NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF
1	1		-	1		SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG
1	1			1	1	TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ
				1		RNL*HST*NVMDISKYVNLHWGLNKSHSLL*
	1		1	1		LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS
						SLV
1103	2453	A	9058	403	3	GLHVYDFQVYREHILTLNVKKCSVSFWGLRE
		J)	1	1	WLYLOMYEIKSPRFPIKMTDITKCW*GC\GA
			l		1	AGMQI/H/CW\WCVNVGKFWEMS*YYLLKLSI ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA
						21/FIDPAIPLEGITE BIKY HAFRICKRIVER

						(A Alexino C Cyptains
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide	ì	in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	amino acid residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	}	peptide	Sequence	/=possible nucleotide deletion, \=possible
1	1	1		sequence	+	nucleotide insertion
				sequence		APFVLAVNC
1104	2454	A	9064	75	393	KWLFSSLNITGRGDIIGHLKWLDCR\NCSSFPI
1104	2454	Δ.	3004	, ,	373	KRNRQTHSTESNKLKAGHSFGYN*LIH*NS\V
		ł	İ	ļ		KTDCGCGANSKGVVVVMKVKTAQQKQTTS
		l			į	YMOIGTTKNSRAT
1105	2455	A	9065	366	778	DLLILRNLAFPELKRRNCISRFYLAYHLHKIYS
1105	2433	1	3003	500	'''	RSILLCNNCSGFYILSL*QYDVFFFNYFFFRDR
			1			AWPCCPGWSAAWLTIVILAHYRRPGLERSCC
1		1		1	į	LSLSSSWDHRRVPPCPANF*/YFSMGFTAFPRL
ľ		1		İ	[VLNS*TQGI
1106	2456	A	9083	673	816	ESGSLIH*WWENKPAQPLWWEI*QHVQKLPT
1						HFPCDPAIPLLGICPED
1107	2457	A	9086	580	18	KPSSGSFIRAIYIFLSTAHVPALFSVLVRTKLT*
	- ~ .	1			1	AFSQSSVLWAHKQQKTSLSLVIR/ERLQIKTA
1	ļ	1	1	1		VRENFLPIRLAKILKLDNVKCWQG/SGSNMSL
1	1			İ		I/HCWWEYNVIHIIWNSVTFPRKVEHVYITYA
1	1		1		1	PEISVR*IHGGLPTLVHQETHTSVFRGAPSVIP
i				<u> </u>		ETR\CRPTKESINKLLHIYTMEHYGDENK GGNDCSVTPTTEPGRKEIT*KRKF*EKTDRLP
1108	2458	Α	9093	540	1	GA/PPSRTPPTPYPCPHGDRLLPPSRPLPAGPA
i	'b	1				SAFPPAERSRGHRRASL*RARWSAAVPRRSA
1	}		J	ļ	ļ	GSASEPVQSRWLRLPVGSDSPPAVPVRVCPAP
-		1	1	Ì		DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG
1						QRPPPPSGDSLSPPGCCRY
		 	0000	1266	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL
1109	2459	Α	9099	1255	1425	GAVAHSCNPSTLVGRGGRITRGQELR
1110	0460	-	9103	242	70	EEQFFFFAVGMFP*VDFLAPASGELWDRLRLT
1110	2460	A	9103	242	"	CSRPFTRHQSFGLAFLRVCSSLDSLDDSVVGP
1	1	1	.}	ı		SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS
		1	1	1 .		LLRKQRNKRMAIP
1111	2461	A	9110	189	121	SFLSVRLECNGAIMAHCALPLPG
1112	2462	A	9113	100	910	RRRGGGSRPRRTPVPAPGPGPSFGMDVRFYP
		1		1		AAAGDPASLDFAQCLGYYGYSKFGNNNNYM
		1				NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT
	1	ı				PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT
1	İ	i	1	1	[PQFPPQSLDLPSITISRNLVEQDGVLHSSGLHM
				1	1	DQSHTQVSQYRQDPSLIMR\PSST*PDAARSG
	1	ł				VMPPAQLTTINQSQLSAQLGLNLGGASMPHT
	1	1				SPSPPASKSATPSPSSSINEEDADEANRAIGEK
	<u> </u>				1000	RAAPDSGKKPKTPKK FLRPSFALVPQAGVQWCALSWLQPPSPRFK*F
1113	2463	A	9120	3452	3051	SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH
1	1	1	1	I	1	VGQAGHEPLTSGDPPASASQSAGITGVSHQA
	1			1		WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS
	1	1	1	1	1	LLKCWDY
	L		<u> </u>	1.50	227	NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS
1114	2464	A	9122	152	377	SLHP*PPG\SSDPPAPPS*VLGITGQRYHACLII
	1			1		YLYVQTVPQRV
	I	 	10104	552	1001	QRPLLRQQLGSWPTCRSLEGDLASPW**RLPG
1115	2465	.A	9124	553	981	SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM
			1	1	1	TOTOSLSFLLGSSASLDCGFSMAPGLDLISVE
1	1	1		1	1	WRLQHKGRGRGDLHLPDHHLSVPSSADHPA
1						QQPSQFNGRNLYFLPLFR
1112	1000	 	0125	48 .	410	SASHEPAEHDGGADSLSASQPPRPAGRPAGA
1116	2466	A	9135	70 .	710	OHVHVPPWTDVLAGQDRRAPTAGDGAPWP
		1	1		1	APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ
1	1					PAAPHALPAGLPHGPPAPAPAEGGGTP*GSA
	1	1	1 .			GAGGP*GSPAGRACGAAGCRPRPPRPAASSA
	1	1			1	*NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS
<u></u>				ــــــــــــــــــــــــــــــــــــــ		

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=isoleucine, K=Lysine, L=Leucine, M=Methionie, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion CPARTSVQGGTWTC*APAGRPAGLGGWEAE RESAPPSCSAGS*DAD*GAEPWGAGSRSWGS KSGHWAKECLQPRIPPRPCPICVGPHWKSDCP TCPGAVPRAPGTLPQGSLTDSFPDLLSLVAED *CCLMASEASWTITELWVTLTVEGKSVP/CL NTEATHSTLPSFQGPVSLASITVVGIDGQASKP LKTPQLWCQLGQYSFMHYFLVIPTCSS
1118	2468	A	9154	471	2	AAGQVVVEVTSHLYLCITSDAAGLRLLPPAES ERGEGGHCPAEAPLPPRPQYCLAKHPLLRKLP EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ LVEGNIGVNLQNTELKQH*INGFLDTTPEAQE TKEKTNKLNFIKKVKRQLAEWEKIFQIA
1119	2470	A	9155	124	207	ACPRLARRRR VRSLRRRGWLRARWSRGQ NNMAARRITQETFDAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSV/LRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD VTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRR KMSFDIIDKSDVFSRFGIEIIKWAGFHTIKDDIK FSQLFQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKABPEPMREBEKMIPPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAQGLRG\ WKARRA\TTGTQTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARFVAQVGPEIEQFSIENSTDNPDL WFLHDQNSSAFKFYRKKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP PREAELESPEVMPEEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGEAACHDLAGAPALSQ ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV
1121	2471	A	9166	272	523	PMSSLQGCFYTFKCIIFKGIFLLLISNLIAF**EK V/CSHITDSLKFIGKGWVGMVTHACNPGTLG
1122	2472	C	9170	442	236	G*GGWIA*VREFETSLGNM MNRRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRON*
1123	2473	A	9171	10	423	MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC LTWINALGKFFG

				m 11	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in	nucleotide		1=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	i	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	l		}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	İ	ĺ	1	peptide	Scquonoe	/=possible nucleotide deletion, \=possible
}		1	ł	sequence		nucleotide insertion
1101	2474	A	9173	3	374	GPSPSLLVLLPOEPGGTGTPVRAGAGAGMWL
1124	24/4	l A	91/3		1 - 1 - 1	WEDOGGLLGPFSFLMLMLLLETRNPVNACLL
İ			ļ			TGSLFVLLGVFSFEPVPSCRALQELKPRDRISA
	Į	l .				IAHRGGRHDPPENTLGAIR/QGS**WSNRR
1125	2475	A	9179	704	188	ESSSGLLFQCFQGIHVQKLTLQARPTLFSWWL
1123	24/3	^	1 7.77	,	1	CSKPPKETGELENAESGGDGGRRGGKQDNV
	}		1	1		AWWRRM\QKG\DFPWDDEDFPQSGPFGGQA
1				Į		LPMGFFYLYFRDPGREITWKHFVQYYLARGL
1	1	ì)	j		VDRLEVVNKQSVRVIPAPGTSSEVRGEFKAE
		1				YCRHKFISCKNVVFYFFQ
1126	2476	A	9183	153	233	MEYMAESTDRSPGHILCCECGVPISPN
1127	2477	A	9185	1	321	LTGQLGSILLRVFSKSRAGLGARKLKAYRTM
1121		1	1		<i>'</i>	EYMAESTDRSPGHILCCECGVPISPNPAQY\CV
	1		1		l	ACLRSSFHIYHCIPKLFIHPFSKTSSSAFITPSHY
	1	1				LTFFSTIS
1128	2478	A	9186	183	847	VLKFLLLQTMDEQSQGMQGPPVPQFQPQKAL RPDMGYNTLANFRIEKKIGRGQVFSEVYRAAC
1		1				L/LDGVPVALKKVQIFDLMDAKARADCIKEID
	1		Į			LLKQLNHPNVIKYYASFIEDNELNIVLELADA
1	ì	1	İ		[GDLSRMIKHFKKQKRLIPERTVWKYFVQLCS
·*· '	` i		1			ALEHMHSRRVMHRDIKPANVFITATGVVKLG
i		1	1	i		DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHD
}	1	}	1		1	NG
L					370	GTSWKIPSAAVSESSPNGAAYASGLPCGVRG
1129	2479	A	9190	1	370	PPWAGLALLPSPTLMALLRRPTVSSDLDNIDT
		1		ļ		RATTIKIRVVATITRARIEDMRHSATALTRPD
1	1	1		1		ATTAOIPKLPVTTVCNRRANPGIPPSVL
1100	2480	A	9194	131	487	AYLKRLPVPESITGFARLTVSEWLRLLPFLGV
1130	2480	^	3134	131	1.07	LALLGYLAVRPFLPKKKOOKDSLINLKIQKEN
\		}		1	1	PKVVNEINIEDLCLTKAAYCRCWRSKTPPAC
1		1		1		DGSHNKHNELTGDNVGPLILKKKE
1131	2481	A	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE
11131	2-101	1	1			PLAFLRALELLFAIFAFATCGGYSGGLRLSVD
1				1	[CVNKTESNLSIDIAFAYPFRLHQVTFEG\PTCE
`			1		ì	GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL
	1	'			<u></u>	AATGVYIFFQNKY
1132	2482	A	9206	1	852	GGGRAGAGSRDMGSTDSKLNFRKAVIQLITK
1		1		1	·	TQPVEATDDAFWDQFWADTATSVQDVFALV PAAEIRAVREESPSNLATLCYKAVEKLVQGA
			1		1	PAAEIRAVREESPSNLATICYKAVEKLYQQA ESGCHSEKEKQIVLNCSRLLTRVLPYIFEDPD
1		ŀ	1	ŀ		WRGFFWSTVPGAGRGGQGEEDDEHARPLAE
				1	1	SLLLAIADLLFCPDFTVQSHRRSTVDSAEDVH
	1	-	1		1	SLLSCEYIWEAGVGFAHSPQPNYIHDMNRME
		-	1			LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS
1	1	1		ļ	1	FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY
1		l	{	ł	1	NHLY
				 	1462	GPRARVQGFSGADIVKFMALGSMYLVLTLIV
1133	2483	A	9208	1165	1463	AKVLRGAEPCCGPLKNRVLRPCPLP/VPLPPP
1		1		1	ł	HPQPSRGNPVGCLPTYKVVYKLLSWPLHSNS
	-		i			NVYFIV
		4		- 66	1586	MAGAGPKRRALSAPVAEEKEEAREKIMAAK
1134	2484	A	9210	66	1300	RADGAAPAGEGEGVTLOGNITLLKGVAVIVV
}		1	Ì	[]	AIMGSGIFVTPTGVLKEAGSPGLALVVWAAC
		-		1	1	GVFSIVGALCYAELGTTISKSGGDYAYMLDV
1		- 1	1			VGSLPAFLKLWIELLIIRPSSOYIVALVFATYL
-	1		- [j		LKPLEPTCPVPEEAAKLVACLCVLLLTAVNC
]		[1		YSVKAATRVODAFAAAKLLALALIILLGFVQI
				1		GKGDVSNLDPNFSFEGTKLDVGNIVLALYSG
1		1	1	1		LFAYGGWNYLNFVTEEMINPYRNLPLAIIISLP
L						

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ł		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ .		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	{	1		sequence		nucleotide insertion
		-	 			IVTLVYVLTNLAYFTTLSTEQMLSSEAVAVDF
	l]	ł i			GNYHLGVMSWIIPVFVGLSCFGSVNGSLFTSS
		l				RLFFVGSREGHLPSILSMIHPQLLTPVPSLVFT
· ·	ļ	1	1		ļ '	CVMTLFYAFSKDIFSVINFFSFFNWLCVALAII
	1	ļ	1			GMIWLRHRKPELERPIKVNLALPVFFILACLF
		ļ	1		ì	LIAVSFWKTTPWSVASDFTIILSGLPVYFFGV
1		ļ	l	ł		WWKNKPKWAPPGHLSPRPSCVRSSCMVVPQ
	0.405		9216	40	410	RDRLPPAYFCRPVVCVVTALDVG\SPESQEM
1135	2485	A	9210	40	710	DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV
		}			}	MOETLRNLASIGEKWKDQNIEDQYKNPRNNL
ļ	Į.	ļ	1			RSLLGERVDENTEENHCGETSSQIPDDTLNK
		 	I		007	RRRRSRYRRCSRFPRPGPLAVSMPHAFKPG
1136	2486	A	9223	3	983	DLVFAKMKGYPHWPARIDDIADGAVKPPPN
1		1				KYPIFFFGTHETAFLGPKDLFPYDKCKDKYGK
		1	1		ļ	PNKRKGFNEGLWEIQNNPHASYSAPPPVSSSD
j)	1	1	ļ	1	SEAPEANPADGSDADEDDEG\RGVMAVTAVT
			1	ł	Į.	ATAASDRMESDSDSDKSSDNSGLKRKTPALK
		ı	l		1	MSVSKRARKASSDLDQASVSPSEEENSESSSE
		l.	1	1		SEKTSDQDFTPEKKAAVRAPRRGPLGGRKKK
	1					APSASDSDSKADSDGAKPEPVAMARSASSSSS
1	(i	1	¥ -		SSSSDSDVSVKKPPRGRKPAEKPLPKPRGRK
	Į.	1		1		
		L				PKPERPPSSSSSD LFPRLECRDPVTVNCTLNLPGSKNAPTTASQV
1137	2487	A	9229	21	239	GSTWNYRGGLPHPTNFFVKTGFRCSQAGLKL
1		1	1	1	Į	
j)		1			RGSREPPAWA
1138	2488	A	9231	1664	2	TRSVGVNTCEVGVVTEPECLGPCEPGTSVNL
1						EGIVWHETEEGVLVVNVTWRNKTYVGTLLD
1		1	ì			CTKHDWAPPRFCESPTSDLEMRGGRGRGKR
						ARSAAAAPGSEASFTESRGLQNKNRGGANGK
	1		1			GRRGSLNASGRRTPPNCAAEDIKASPSSTNKR
ì		1		1		KNKPPMELDLNSSSEDNKPGKRVRTNSRSTP
		1	İ	ļ		TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK
	1				1	YKHINGLRYHQAHAHLDPENKLEFEPDSEDK
	1			ľ		ISDCEEGLSNVALECSEPSTSVSAYDQLKAPA
)	1	1	1	ļ	1	SPGAGNPPGTPKGKRELMSNGPGSIIGAKAGK
	1	İ		İ		NSGKKKGLNNELNNLPVISNMTAALDSCSAA
1.	1		1			
1	1	i	l l	1	İ	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK
1						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA
1						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK
1						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNVPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIOPKPTIMGEPITVNPALVSLKDKKKKEKR
						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNVPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK
				,		DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKN\PSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS
						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKYYTFTDNAPSPSIGS
1120	2490		9224	207	443	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGOPWRRRAAAAGILPGREAAACLPSC/AS
1139	2489	A	9234	207	443	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGOPWRRRAAAAGILPGREAAACLPSC/AS
1139	2489	A	9234	207	443	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC
						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEOEMGVSSLVIGALL
1140	2490	A	9238	248	328	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAOGNNYGOTSNGVADESPNMLVYRKV
						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP
1140	2490	A	9238	248	328	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG
1140	2490	A	9238	248	328	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRFDTKCLAA
1140	2490	A	9238	248	328	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRPDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM
1140	2490	A	9238	248	328	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRPDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ
1140	2490	A	9238	248	328 535	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGFDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ NMOEVSRNRCALLHSAAVQEYGYGN
1140	2490 2491	A	9238	248	328	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRFDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ UMQEVSRNRCALLHSAAVQEYGYGN HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD
1140	2490	A	9238 9242	248	328 535	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRFDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ NMQEVSRNRCALHBSAAVQEYGYGN HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD FALGNDFLNITTKAOATKEKLDKLDFIKIKTC
1140	2490 2491	A	9238 9242	248	328 535	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRFDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ UMQEVSRNRCALLHSAAVQEYGYGN HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD
1140	2490 2491	A	9238 9242	248	328 535	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRPDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ NMQEVSRNRCALLHSAAVQEYGYGN HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD FALGNDFLNITTKAQA/TKEKLDKLDFIKIKTC CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF GICKEYSRO
1140	2490 2491 2492	A	9238 9242 9245	248 2	328 535	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRFDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ VMQEVSRNRCALLHSAAVQEYGYGN HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD FALGNDFLNITTKAQATKEKLDKLDFIKIKTC CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF GICKEYSRQ GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPDG
1140	2490 2491	A	9238 9242	248	328 535	DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV FVEAAVKMLGSLVLRRKALAPRLLIRLLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRPDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM WPWAAALVVHCYSKSPSNKDAALLEAARAQ NMQEVSRNRCALLHSAAVQEYGYGN HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD FALGNDFLNITTKAQA/TKEKLDKLDFIKIKTC CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF GICKEYSRO

	OFO TO	N.fat	CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-			correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	i	09/496		acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
		ł	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	İ	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	Í	peptide		nucleotide insertion
				sequence		KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCGP
1144	2494	A	9260	1	401	KKVPGRLSEMSFSLNF1LPAN1155FV1DCGF
			1	}		SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE
1				ţ		AMEESDRPCEISEIDDNPKISENPRRSPTHEKN
		Į.	1			TMGAQEAHIYVKTVAGSEEPVHDRYRPTIEM
		1				ERRR
1145	2495	A	9264	175	411	METIWIYQFRLIEIGDSTVGKSCLLHRFTQGRF
1143	2473	1 **	1 20.			PGLRSPACDPTVGVDFFSRLLEIEPGKRIKLLL
i 1	•	١.	ŀ	·		WDTAGQERFISIT
	0406	A	9277	592	814	MFTYLEGREGIKSOPKMEPHSVT\RLECSGMI
1146	2496	Ι^	3211	1332	011	SAHCSLNLPGTSDSPASASR/VAGTTGMRHHA
1 1		1	1			WLIFAFLVETGF
		1		1000	2	FRRGRRGEEEKEEEEEEEGWYNGMENSHPP
1147	2497	Α	9279	1255	4	HHHHQQPPPQPGPSGERRNHHWRSYKLMIDP
1 1		1	Ì			ALKKGHHKLYRYDGQHFSLAMSSNRPVEIVE
		1				DPRVVGIWTKNKE/LELSVPKFKIDEFYVDQV
	\	1	1	1		PPKQVTFAKLNDNIRENFLRDMCKKYGEVEE
	!	1				VEILYNPKTKKHLGIAKVVFATVRGAKDAVQ
		l	1			HLHSTSVMGNIIHVELDTKGETRMRFYELLLV
1 1	l	1	1	Ì	ľ	HUHSISAMGMIHAETDIKOEIKANG LEDELA
	l	1				TGRYTPQTLPVGELDAVSPIVNETLQLSDALK
1		1		ļ		RLKDGGLSAGCGSGSSSVTPNSGGTPFSQDTA
	1	1	1	.	}	YSSCRLDTPNSYG/QGTPLTPRLGTPFSQDSSY
1			i	1	[SSRQPTPSYLFSQDPAVTFKARRHESKFTDAY
		1	1	1 .		NRRHEHHYVHNSPAVTAVAGATAAFRGSSD
1 1	i	Į.	ĺ		1	LPFGTVGGTGGSSGPPFKAQPQDSATFAHTPP
	1	1				PAQATPAPGFR
1148	2498	A	9302	1026	6	IASIQNADTMPGVGLLVSHFSTLVSRQRCPNY
1140	2470	\ · · ·	120			ADPQNLTDVSIFLLLEVSGDPELQPVLAGLFL
1		1	Ì			SMCLVTVLGNLLIILAISPDSHLHTPMYFFFSN
	1	ł	ł	1	1	LSLPDV\GFTSTTVPK\MIVDI\QSRSRVISYAG
1	ł		1		Ì	CLTQKSLFAIFGGTEE\NMLLSVMAYDRFVAI
i			1			CHPLYHSAIMNPCFCAFLVLLSFFFLSLLDSQL
1		1		1	1	HSWIVLOFTIIKNVEISNFVCDPSQLLKFACSD
1		1	1		1	SIINSIFIYFHKDPERQLVLAGLFLSMCLVTVL
1			1	1	1	GNLIIILDVSPDSHLPTPMYFFLSNLSLPDIGFT
ı		1				STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAIF
1				1)	GGMEERHAPECDGL
4	10:00	 	0202	 , 	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE
1149	2499	A	9303	1	1 057	FRLVAADRSMGRYMLFGVINLICTGFLLMWC
1					1	SSTNSIALT\SYTYLTIFDLFSLMTCLISYWVTL
	1	1				RKPSPVYSFGFERLEVLAVFASTVLAQLGALF
1		1		1		ILKESAERFLEQPEIHTGRLLVGTFVALCFNLF
1	-	[1			TMLSIRNKPFAYVSEAASTSWLQEHVADLSR
			1		1	SLCGIPGLSSIFLPRMNPFVLIDLAGAFALCIT
1		1	1	1	1	1
	1		ļ			YMLIEI
1150	2500	A	9308	797	693	DRSTSVTRAGVQWCSLGSLQPRTPGLLRSSCL
				1		SLP
1151	2501	A	9309	205	406	VAIKELPVLWKWSKPTR\TAKEPPQTQQRAG
1		1 -	1 - 2 - 2			SKTAAPPCQWSRMASEGPNIPCPGARHSDKQ
		1		1	1	FLICTI
1152	2502	A	9314	913	504	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV
1132	2302	1^	7314	1		OGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRR
}	}		1	1		PPPHR\EIFFVFLAETGFHRASQAGPDLPTS/S/I
	1			1		PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL
				1		GTNVSLRAA
				 	 	HPHRPRPGFRSPARSSRPCPVLTSLLPPFPSPSP
1153	2503	A	9315	392	1	PADDLVKAGRDRKDPQVR/ERRLRPNPGRLG
1		1		1		CADADA DA DESCRIPTA A DA CADADA DA CADADA A DA CADADA DA DA CADAD
ı	1	1		1	1	GPR\PRPARARS/CHQPRLTRVCPRSPPPEARA PAPAAPARGRGAPKRNRPRTDTRAPRGSSAR
1						
	1	1	1	1	1	PGNS

	1 000 000	1 1/	CEC	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		ļ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	ļ .		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	10.1	peptide	sequestion	/=possible nucleotide deletion, \=possible
	1	İ	ł	sequence		nucleotide insertion
1154	2504	A	9321	331	433	MPCI/QAQYGTPAPSPGPRDHSASDPLTPEFIK
1154	2504	^	7521	1 33.	'33	PT
1155	2505	A	9324	180	275	MEEPQSDPSVEPPLSQETFSDLWKLLSENNVL
	2506	A	9326	383	619	MISPSRTEGDPLPLPP/EGEGQEVRGFGGGPAK
1156	2500	^	9320	303	""	EAAQRHCRASVSILRMRRPGQGSSRPARVPL
l		1		1		RGPDSHRLREPPPSPP
1167	2507	A	9327	152	292	YERRGRSQGGSHPAGAQPGGRAIGAGWQS
1157	2507	A.	9321	132	2,72	KEPI.WEGLORSGSPLPG
1150	2508	A	9328	1	430	QELKQGPNPLAPSPSAPSTSAGLGDCNHRVD
1158	2300		9320	•	*50	LSKTFSVSSALAMLQERRCLYVVLTDSRCFL
]		1				VCMCFLTFIOALMVSGYLSSVITTIERRYSLKS
	1	1				SESGLLVSCFDIGNLVVVVFVSYFRGRRRRP/
1	Į	1	1		·	RVAAVGGLLDLEGGEMI
1159	2509	A	9334	108	383	KGNOVNGNGNOLKRKHESMCPVSLTQNTVR
1139	2309	^	7554	100		LMEAGLPOKOAERADELFEAGLVIYVKLDER
	Ì	i				VLNAL\YSSVGLOWFKESDLSHLRLLEISFR
1160	2510	A	9338	2	430	FVGRPRGLSDRLEDLFLAGFRVGERLRTAAM
1100	2310	1	7555	~		KRYVRILLLGEGAEHVADPVPGGRGVPRGEA
		1	1	-	Į	DHTDOELREEIHKANVERVVHDVSQEATIEKI
	-) · .		i.		RTKWIPLV/RWGDHA/EGPVGIKSYLPSGRSM
			1	'		EAELPIMSQLTEIETCVEC
1161	2511	A	9341	1	390	NSRVDDFVAPGLSEAGKLLGLEFPERQRLAA
1101	2311		75	1 -		AVG/CSPMSGVISMSAPFFLGKIIDAIYTNPTV
1	ļ		1	1	ļ	DYSDNLTRLCLGLSGVFLCGAAANAIRVYLM
Į	1	1	1			QTSRQRVVKRLRTSLFSSILGQEVAFSDKAGT
j)		1		GELI
1162	2512	A	9343	84	837	QGRFRAFCWQRDFLQPPGMRLSALLALASKV
1102	1	1			,	TLPPHYRYGMSPPGSVADKRKNPPWIRRRPV
ł		1	İ	l .	1	VVEPISDEDWYLFCGDTVEILEGKDAGKQGK
ŀ	1	1	1	i		VVQVIRQRNWVVVGGLNTHYRYIGKTMDYR
		1			Į.	GTMIPSEAPLLHRQVKLVDPMDRKPTEIEWR
	1	1	i	1		FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET
			}	j	,	WIDGPKDTSVEDALERTYVPCLKTLQEEVME
	Í	1			}	AMGIKETR\NTRRSIGIEPGAEQLLPNFCPSLE
		ł			l	G
1163	2513	A	9346	967	616	DSLALSPRIECSGAISAHCNLTPPGFTPFSCLS
1.		1			1	LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ
	İ	ŀ				AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT
į.		1_	1			FSSYQRNNPDLILNDTIMPNIK
1164	2514	A	9347	3	1099	SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI
		1.	1	1	1	HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL
1		1	1		1	FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARNPRYRTEGEACVEFKA
			1		1	MLIAVGIHLLLLMFEVLVCDRVERGTHFWLL
					1	VFMPLFFVSPVSVAACVWGFRHDRSLELEILC
Į.			1			SVNILQFIFIALKLDRIIHWPWLVVFVPLWILM
		1				STLCLVVLYYIVWSLLFLRSLDVVAEQRRTH
1		1			1	VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS
1		1	1	1	ł	YVSIFVPLWLSLLTLMATTFRRKGGNHWWF
1	1	1	1	1		AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA
	1				1	LPLQNKDRGSWPASRGSPRLL
	1	<u> </u>		 	 	DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP
1165	2515	A	9362	547	991	VPEGVRLADGPGHCKGRVEVKHQNQWYTV
					1	COTGWSLRAAKVVCRQLRCGRAVLT\QKRC
1			1	1	1	TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP
		1			1	LGEDTLFHVEYTSVHGRERLSAKD
	<u></u> _				 	PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS
1166	2516	A	9363	201	387	GAISAHLAHCNLCLPGSSDSPASAFQVAS
	1			<u> </u>	1	AVLTPCLSPCSPSRIPRP\SRPYPGRRSLSHTPP
1167	2517	A	9368	707	1087	AVLIPCLOFORIER DRF I PURROLOFITE

	00000	16-4	CEC	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A enartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ŀ		location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		İ		amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
		l	1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	i		peptide	1	nucleotide insertion
		1		sequence		PRPLILYAPAPARPAGTAFIPHSHPPPPDLLRPT
		T				ATPA/TPCPSLPPPPRPLHPTQPSTALLPDPPPW
	ļ	}	1 .	ł		ATPA/IPCPSLPPPPRACHPIQUSTALLIDITI
]		1				PLPFPPPSS/RPPRPDCSTSYSPTFPPPT
1168	2518	A	9375	511	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS
1100	23.0	1				PITVTSAVIIVLMLLMM/IFSPWLATHDPNAID
l	ļ	Ì	İ	[LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS
	1.	ì]	ì	1	QQSILAGLVVVATTGMIGSPLECLFGELGGRA
	[1	1	1	Ì	DAIFMRVMDIMRS/IPSLVLTMEKTAALGPSL
		1				FNAMOASSEH
		↓	0000	42	410	GNGRVAPRDPGAVASAEPGLTTHDSGVNPN
1169	2519	A	9377	42	410	NSARRMEAMASGSNWLSGVNVVLVMAYWS
	1	1	i	1		LVEVLLFIFAKROIMRFAMKSLRGPHGPVGH
l	1	1	1	1		NAPKOLKEEIDILLSRVHNIKYEP\HLLADDDA
		<u> </u>			1202	GVSGFSASVLRQRRMEDELEPSLRPRTQIQGR
1170	2520	Α	9378	302	1303	ILLLTICAAGIGGTFQFGYNLSIINAPTLHIQEF
1				1	1	TNETWQARTGEPLPDHLVLLMWSLIVSLYPL
1	1	1	1	1	1	GGLFGALLAGPLAITLGRKKSLL\VNNIFVVS
}		1	Ì	1	ł	AAILFGFSRKAGSFEMIMLGRLASWGVNAGV
		1	1		ļ	AAILFGFSKKAUSFEINIMLUKLASWUVINAU
1	1	{	{			SMNIQP\MLPGGESAPKELRGAVAMSSAIFTA
1	Į.		1	1	1	LGIVMGQVVGLSTTAATGLRGL\AGELEELEE
	1	1		1		ERAACQGCRARRPWELFQHRALRRQVTSLV
	1	1	ł	1	1	VLGSAMELCGNDSVYAYASSVFRKAGVPEA
		1		i	1	KIQYAIIGTGSCELLTAVVSVSLEGALPPPAL
1	1	ł	i	1	ĺ	WGGTPRSFALNQFTLQKKKK
	0501	A	9381	2	412	RGPASAQEDERARTAPLERVRARGRMTTSSA
1171	2521	I A	3301	1-		1 EDGT I PCGWSTSNKYLAEFRAGKMSLKGTTE
1	1	1	1		ł	TPDKRKGLAY/IOOTDDSLIHFCWKDRTSGNV
		ì	1			EDDLIIFPDDCEFKRLPQCPNGRVYVLKFKAG
1	}	1	ł		1	SKRLFFWMOEP
					355	GWNGRSTEASPAAEAPHVPHKET\KAAMGTQ
1172	2522	Α	9384	20	222	CTHGGKVRPDPHDMLTTVVHKIKLFVLCHSL
	i	}		į	ł	LQLCAIMISDYLKSSIYTVEKRLGLFRPTSGLL
	ì	Ì		1	į.	ASFNEVGNTALIVLESY
		1			100	LCQCIVPGQQKETFSLNPSSATVRFYL*LSLQ
1173	2523	Α	9393	430	87	QRKEDQ*IIL*YHLNKDCLHIFMSAITLYMKI*
		1		1	1	KIFVLFDFNIMFETPFYII*FIFLFSQNLKRIRQV
1		1		}	ļ	WILA TLALIMINE TILL III. LIT THE OCCUPANCE A
				1 <u> </u>		IRPPISFSKINNGP
1174	2524	A	9397	77	374	ERLEIGRLGGERGSGPASCLRVIDVSGMWDQ
1 ** / 7		1		1		RLVKLALLQLLRAFYGIKVKGVRVHRDCGTF
		1		1	1 .	ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF
	1		1			LGMT.
1155	2525	HA-	9399	66	397	HESSRADRDKMDTRGSTYTDADPVNKSGGT
1175	2525	I A	7333	1 55	1	AKMNKWSKGKVRDKLNNLVLFDTATYDKL
1		1		1	1	CKEVPNYKLITLAVVSERLKIPGSLARAALHE
}				1		LLSRGLI*LVIOHIAOVIY
					299	LDLTHVLSLSISLTVTILGTTFGMVIPLLDVVY
1176	2526	A	9408	2	233	GERGYAONGDF*DAOLDDYSFSCYSHAQVN
		1		1]	GAPNSLTRAYDDP*VKISGLECQKVGALVEV
1	İ	1		i		KCLNL
		1				CNFLRSSRIRVHSTPAASTMPPKVDPNEIKVV
1177	2527	A	9416	2	402	YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD
1		1		i	1	TERCHOLEVICATION TOUR TOUR COURTNOOPERCE
	1	1	1	1		FV*ATGDWNVLIISVILTIRILLSHIFVVPPFFCF
	1	- 1	1	1	1	DHLIAFWDLQSLIFLHVIFSLFITLLLFCFFSIF
1100	2528	A	9419	142	426	TPLFDLWPRVVLSWLETVLTSLRTRRAASGPP
1178	2528	^	1717	1		ACRIMPTTVDDVLEHGGEVHFLOKQMLYLL
	1		- 1	1	1	ALI*DTFAPIYVGIVFLGFTPDHRCRSPGVAEL
			0400	1450	1655	I SSAGTKMNI N*KNYWPGASAHACNPSILG
1179	2529	A	9420	1430	1033	GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA
1		1			1	WWRAP
		- 1				

	050 10	1/4	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine O=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid.
nucl-	peptide	поц	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	ucitoc		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ucnoc			,,,	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l	į .	peptide		/=possible nucleotide deletion, \=possible
		ĺ	1	sequence		nucleotide insertion
1180	2530	A	9422	176	375	HRPQTTRPDWKPRT*PQGK*GRLSSEISPASPP
			1	ł		SRFSRSTKPVPPKADPPARQKLTGVLHAPLLK
	l	ì				L
1181	2531	A	9436	2	274	PIAASLRMYNLQPYTEENLICTAFATMVETVP IARTILDRLTGIPHGYCFVE*ADWATADKCVH
		1	}		Į	INGKPLPGATPLLSLQLHQLAHLGS
						VDKCSSKSIVLSEYCPHCMCSLSTDPKPFGQL
1182	2532	A	9442	3	240	SMILK*MGAGDEKISAMGKARVDHRELYLGL
		}	1			LYPTEDYKLTFRARH
						LKDFQPWALHDWPLFCCCTFLLFLVLECFTR
1183	2533	A	9444	384	3	KGCSGWAPWLSLQCQHFGRPRWADHLRSGV
		l			Ì	RDQPGQYSKTTFLPKIQKLAGHSGAHL*S*LL
]	1	1	1		ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT
		1				ERG
		↓ ,	10462	391	655	LSGFKSLMPKIPLOYIYVRVRTTWSFCLPLDG
1184	2534	Α	9462	391		RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV
	ı	[1		IHTCNPSTLGGRAGWIV*AQEFET
1106	2535	A	9467	215	566	RCPMWOGOASRMDPAKAKDREASTCCSLA
1185	2535	A	3407	213	500	WWWGWECWVRALKLSSGPAGPLACWVAK
				1		KKSLSLSGPVYPSEKGAGLYVF*DRVSLCHPG
		1	1			WSAVVQFWLTAASNSCFSLLSSWDYRCA
1186	2536	A	9468	275	452	HIPQLHTKTHYVPTRMVNKI*QIDNSKPWQR
1100	2550	1.			_	GG*TGILTHCW*ESKLVQPLWKIVWHYQ
1187	2537	A	9469	388	3	EVAPGPSQILPRRVTDGGDRPQFSLPGPRLPQ
110,		1				SSRGAEPCLSNCIHSPAPRKQRMGDSDQ*STP
	1	ì		1		NPASPHPEAPQEPWDSASGSVOSFSLGRGAK
ĺ		1		ł		ASS*VPGKGRGPRQGSELLAETILELFLALAN
						S TMDKKNRHGNSLDMASEIHMTGPMCLIENTT
1188	2538	A	9471	124	397	GRLMANPEALKILSAITQPMVEEAIAGLYRAC
				ľ		*FYLTNNLAGMKKGLCLGSTEQAHTIGI
						GHVQSQHFGRPRRADHLRSGDRDHPG*HDET
1189	2539	A	9480	584	769	PSLLKIQKISWAWWRAPVVPATWEAEAEEW
İ	ļ	1		1		R
					100	VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL
1190	2540	Α	9483	463	86	PRQHCTLQTHRHLHPEAPVKV*KT*RLFPGLR
		1				GASSCRRRCNPVLAARKAGSPRSHSTRENC
	1	ı				RRSRCPDTAHRRRRRGRRRNPSCVRSPRWR
				 	411	LADALCLSAAATGAVRPGARAQPSTRRRLSP
1191	2541	Α	9489	1'	411	SVRVCCRAAAASNLLYSSCLQRHSERASEEG
	1	1 .		1	1	ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI
Ì	1	1	1			MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ
1				İ		KEEELTAVNVK
1100	0540		9497	389	161	VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI*
1192	2542	A	747	1 307	1	CEEDERKMAREFLAEFMSTYVMMNIHMIVE
	Ì		1	ļ.		KDTYSDHEEINTS
1102	12542		9509	186	1	TAKSO*KRWORSGAMETLKHGWWECKLVQF
1193	2543	A	7,107	100	1.	FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM
1104	25/4	- A	9512	58	433	PLORSKCLTLRCLRAKPWAWSQSPRACSSAL
1194	2544	I A	7312	1 70	133	LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA
	1	1	1	1		SSKGOOFRR*KEHPFMLKTLNKLRIEGT*LKI
1						RRAIYDNPTANIIVEGOKLEAFPLRTGTRQ
1100	2645	-	9515	595	1223	GHGAPSFOTOVPRTP*ASWPVVPAASESAPAP
1195	2545	A	כוכל	333	-	AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC
	1		-	1		PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP
	1		-	Ì		LPRCSCAPLRSASAPOVS*CV*AVNLLPHNL*
1	1			1	1	I was a second of the
		- 1	1	İ	i	PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP
				1		APGSGPCGATARPSRGGRAGGSRARRPIPPGP
						PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP GTRRTPSGCQNPAASGG

			1 670	Dundinted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence	}	ł	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
1	ļ · · ·			peptide		
	İ]	sequence		nucleotide insertion
1196	2546	A	9518	229	468	RSPTATPAPHAMGPGAPFARGGRPLPLLGAM
						AERVAPGWDLHTPYLPRTNSRRTPHL**EPHA
}		1				GYIGALFPMSGGWPGGQ
1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG
****]	l				HAMRHLTGNTSMAIRFL*ADSRFQVQRARYE
	1	ŀ		ļ	1	APNWKYKYGY*IPVDMLC
1198	2548	A	9524	204	1	KNKKTTKCLSIVTLNISGPNQ*NKRHRVAEWI
1170	25.0	1				VKQEPNICHL*ETHFPFRDTYRLKEREQKKRK
		1				SSYS
1199	2549	A	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA
1199	2349	^	3340	1705	1 -7	V*ORGDGKNPGVTHLNRPVGTX
1000	0.550	 	9548	186	1	VNAEKEF*KIQHYFMTKSQNKLHIEHTYLKPI
1200	2550	Α	9340	100	•	KAIYDKWTSDIMLNLOKL*AFFLRVIVRQI
		<u> </u>	9549	591	2	SSVVEFPRGPRSSLPPLDSTFPCGSSPNWTGGC
1201	2551	Α	9549	291	*	GSCPSGE*LVSPGSEQRKKYSNSNVIMHETSQ
1	1					YHVQHLATFIMDKSEAITSVDDAIRKLVQLSS
		1		1		KEKIWTQEMLLQVNDQSLRLLDIESQEELEDF
ł	1	i	1	Ì	ſ	PLPTVQRSQTVLNQLRYPSVLLLVCQDSEQSK
1	1				ł	PDVHFFHCDEVEAELVHEYMESALTDCRLGK
l	1	1			1	AMRP
		<u> </u>	0.550	100	1	KYGNEGHWSRQCPNPGKPIRPCPLCRGPHWK
1202	2552	A	9552	428	1 1	LDCERPPQGPLPSLPELAKTSYSDLTGLATED
i				1		*WGPGMDAPATTIASSKTRVTLMVAGRPVFF
1					1	LI*YRATYSALPNFSGPTQSSQVSVVGIDGQV
1	1	i	[1	1	SKPRATPPLFCSLHTF
L		<u> </u>		 	738	RRKFERKQKQ*RYREGKQYRQRDKMKEWG
1203	2553	A	9568	517	/38	EKEKRREKGEREERKMRHRERKGESOQRD
		1				TMENWRVERLTEKER
				 _	415	EDKRLRLVDGDSRCAGRV*IYHDGFWGTICD
1204	2554	Α	9573	83	413	DGWDLSDAHVVCQKLGCGVAFNATVSAHFG
		1	1		1	EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ
1	ì	1		i		HDCRHKEDAGVICSEFTALR
					104	ARGSCPTRPRTANGRMGETKDAPQMLVTFK
1205	2555	. A	9577	64	424	DVAVTFFREEWRQLVLVHRTLYR*GMLETC
1	ļ	1				GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE
ł		1		1		VSHSPCAGDMRELFTREATLTPHPYNNGA
					-	TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL
1206	2556	Α	9584	38	476	SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV
	1.	1	1	1	1	NPQPLSTPSWQIETKYSTKVLTGNWMEERRK
1	1	1		1	1	GLPYKHLITHHQEPPHRYLISTYDDHYNRHG
1	ĺ	1			1	YNPGLPPLRTWNGQKLLWL
		_L				LRSSPAALLRALCITTVTGTALALRSRVATTN
1207	2557	A	9586	2	412	LKSSYAALLKALUITI VIUTALALKSKVATIN
		1		1	1	PDGCRNVLRPKYYRLCDKAESWGIALETVPT
	[1.		1		GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP
	1		1	1	1	THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL
		1		L	<u> </u>	FGILFSICFS FGILFSICFS
1208	2558	A	9597	122	3	IKNYWPGMVAHACNPSPLGGRGRWIA*AQK
						FADAWADAW
1209	2559	A	9611	148	558	KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK
1209		1	1			GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ
1		ł	1	1		RIRDHDLLDKRKTVTALKAGEDRAILLGLAM
1		1	1			MVCSIMM*FLLGITLLRSYMQSVWTRESQCT
		1		1		LLNASITETFNC
1012		+	0610	384	2	SLHDMLMLAEQQQKQKWAVNTQNTAWSNA
1210	2560	Α	9618	704	_	DSKFGORILEKMEWSKGRGLGVQEQGGPDDI
1		1				KVQVKNNDLGLQATINNEANWIAHQDDFNW
J		1	1	ł	1	LLAELNTCQRQETADS***WSPKNSHVGKDS
		1	1	İ		GELSAK
	1	1	1			QKHPGGGQLGRSPQEDSRFHNKASSGVSRVR
1211	2561	A	9620	316	610	1 OKHPGGGGULGKSPOEDSKEHNKASSUVSKVK

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	ł	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	l	ł		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ì	ì	residue of	sequence	/=possible nucleotide deletion, \=possible
	Ì	l		peptide		
		ļ	'	sequence		nucleotide insertion
	 					LGRAWWLTPVIPTLWEAKAGGSPE*D*AGRG
		1				GSRL*SQHFGRPRRVDHLRSAVQDQPGQHGE
		}			l	TPSLLKIQKIN*VWGRRL*SSYSEAEAGESL
1212	2562	A	9623	297	344	QFPVDGDYQKIEKITQLFQAQNLSLCLAMTR
12.2	2002	1	1		i	TREL*KGGGKGRHE*AVVPFLKKGGYGVKAP AILNTSNCT*CF*ETKMLSDDPKACVFEVSSA
	ļ	ļ	1		Į.	
	ì	l				DL*NTSFGVIR
1213	2563	A	9624	2	356	AELSLASTACGRNTSGDSLPDYDRAPISSPLA
12.13	1 2000	1		l		TSGTILSAISCLWDLPTPVLRVGLSCQPSMSSQ
1	1	1		ļ	1	IPRMYSTDVEAAVNSLEDLYLQAYYAYLCVG
}		}	1	1	·	LYFHRDDMALEGVSRFL*ELAE
1214	2564	A	9634	776	912	SLSRWVRAKL*VPYNQENCLNPRGGGCSEPR
1214	250.	1 ' '	1		1	SHYCTPAWATEKDS
1215	2565	A	9636	220	426	KPGNFAVSSEY*DITSGQLKTAVRG*IEMTST
[1213	2303	1"	7022	1		EENFGEKLHDIGFGNGFLDKT*KAQATKAKI
į.	1	1		1		DK
1216	2566	A	9637	391	76	CFLEDGCTQAS*AEEAAVSPSMAEEEQGSTSC
1210	2500	1"	700.	1		RERRSIRFKMKNHSPDDTIKENVTISNIRTRKI
, .		1	1	1		NHLPETERNLLEHGLMYIRLNAAFCSLVAHS
İ			1			LFGFILKAT
1217	2567	A	9655	2008	2432	LHCKMGALETQTHPCSQNMLRSLQKCCCKV
1217	2507	1 ^	7020			EEHHLQPVQVLQTLLHSATAGTGCRRPARPP
1				ļ	1	PAPPTPTPWRSRQSGKQSERAS*LKGRGRYGL
1		İ	1	1	1	GALGGRGGRALGGSRWPPPLPGETLFSGCKH
	ļ	1	1			RRRRGSDAAPGEEAGT
1218	2568	A	9658	3	405	HASARALLSPNLSPNNKMAISGGPVLGFFIIA
1218	2500	1.	1	ļ -		VLMSAQEPWAIKEEHVIIQAEFYLNPDQSGEF
1				}	1	MLDFEGEDTFHGDMAKKETVWRLE*LARLD
1	1	1		1	ļ	NFEAQRALANIAADQAALEIMDMGSDYTLIP
)	1	1		1		NVPPKVTVL
1219	2569	A	9662	3	284	PDWTEKRKMQDTGSILPLHWFGFGYAALVA
1213	2507	1 **				YGGIIGYVKAGSVPSLAAGLLFGSLSGLGAYQ
1	1 .	1				LSQDPRNVWVFLATSGTLAGIMGMRFYHSG
1					_	KL
1220	2570	A	9669	200	699	LLLTGYIQTLQNQQLSGNQQEMQAVDNLTSA
1220	2570	1.	7007	1	ļ	PGNTSLCTRDYKITQVLFPLLYTVLFFVGLITN
1	1		- [Į.		GLAMRIFFQIRSKSNFIIFLKNTVISDLLMILTF
	 	1		1	ļ	PFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYI
1		1	1	1	j	SISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
		ĺ				l K
1221	2571	A	9676	164	562	KERDSSTFSAAMTTMQGMEQAMPGAGPGVP
1221	23/1	^	1,0,0	1		QLGNMAVIHSHLWKGLQEKFLKGEPKVLGV
		Į.		Ì	-	VQILTALMSLSMGITMMCMASNTYGSNPISV
	1	1			1	YIGYTIWGSVMFIISGSLSIAAGIRTTKGLVRG
1		.			1 '	SLGMNITSS
1000	2572	HA-	9688	43	412	VAKMVKCCSAIGCASRCLPNSKLKGLTFHVF
1222	2572	A	2000	1.5	1	PTDENIKRKWVLAMKRLDVNAAGIWEPKKG
1	1	1	İ			DVLCSRHFKKTDFDRSAPNIKLKPGVIPSIFDS
İ		- 1			1	PYHLOGKREKLHCRKNFTLKTVPATNYNH
1000	10500	+	9696	308	564	RTSMGILYSEPICOAAYONDFGQVWRWVKE
1223	2573	A	9090	300	1 30.	DSSYANVODGFNGDTPLICACRRGHVRIVSFL
1				1	Į.	1 KKECI COPOKPERENLLALCCE
	4		0500	- 3	632	DAWASGGELGSLFDHHVORAVCDTRAKYRE
1224	2574	A	9700	١٠	1 032	GRRPRAVKVYTINLESOYLLIOGVPAVGVMK
			1	1 .	1	FLVERFALYGAIEOYNALDEYPAEDFTEVYLI
1		1		1	1	KEMNI OSARTAKRKMDEOSFFGGLLHVCYA
1 .	- 1			1		PEFFTVEFTRKKLOMRKAYVVKTTENKDHY
	1			1	i	VTKKKLVTEHKDTEDFRQDFHSEMSGFCKA
		1	- 1	1	1	ALNTSAGNSNPYLPYSCELPLCYFSSK
1	1	1	l l		L	ALNTSAGNSNPYLPYSCELPLCTP33N

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914 9710	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RSGCVLRMTEWETGAPAVAETPDIKLFGKWS TDDVHINDISLQDYIAGVRLILL QGLPSFLPAFGPSGSWLGPAPTLGSSCNTVDT ICHGYSEIRPLFYLSFCDLLLGLCWLTETLLYG ASVANKDIICYNLQAVGQIFYISSFLYTVNYI
1227	2577	Α .	9720	3	416	WYLYTELRMKHTQSGQSTSPLVIDYTCRVCQ MAFVPSSLI GKWKRTQVPLLGEECADMDLARKEFLRGNG
		_				LAAGKMNISIDLDTNYAELVLNVGRVTLGEN NRKKMKDCQLRKQQNENVSRAVCALLNSGG GVIKAEVENKGYSYKKDGIGLDLENSFSNML PFVPNFLDFMQNGNYF
1228	2578	Α	9723	278	411	EASSSNTVASNVADKTDPHSMNSRVFIGNLN TLVLQKSDVEAVF
1229	2579	A	9725	121	902	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDY GGSGGPYSKQYAGYDYSQQGRFVPPDMMQP QQPYTGQIYQPTQAYTPASPQPFYGNNFEDEP PLLEELGINFDHIWQKTLTVLHPLKVADGSIM NETDLAGPMVFCLAFGATLLLAGKIQFGYVY GISAIGCLGMFCLLNLMSMTGVSFGCVASVL GYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMEGQQLLVAYPCALLYG VFALISVF
1230	2580	A	9739	11	247	TFVLNMNTPKEEFQDWPIVRIAAHLPDLIVYG HFSPERPFMDYFDGVLMFVDISGKCKRDVCL MWMSNRLAWEFTCRA
1231	2581	A	9744	37	1100	TPLFDFWPGFVLSWLQPLSASLRARRAASGPP ACRIMPTTVDDVLEHGGEFHFFQKQMFFLLA LLSATFAPIYVGIVFLGFTPDHRCRSPGVAELS LRCGWSPAEELNYTVPGPGPAGEASPRQCRR YEVDWNQSTFDCVDPLASLDTINRSRLPLGPC RDGWVYETPGSSSIVTEFNLVCANSWMLDLFQ SSVNVGFFIGSMSIGYIADRFGRKLCLLTTVLI NAAAGVLMAISPTYTWMLIFRLIQGLVSKAG WLIGYILITEFVGRRYRRTVGIFYQVAYTVGL LVLAGVAYALPHWRWLQFTVALPNFFFLLY YWCIPESPRWLISQNKNAEAMRIIKHIAKKNG KSLPASL
1232	2582	A	9753	164	517	PGPGMQGPPPITPTSWSLPPWRAYVAAAVLC YINLLNYMNWFIIAGVLLDIQEVFQISDNHAG LLQTVFVSCLLLSAPVFGYLGDRHSRKATMS FGILLWSGAGLSSSFISPRYSWLF
1233	2583	A	9757	25	419	LPAPWTERVRKSEGLVGTCLGDPMASPRTVT IVALSVALGLFFVFMGTIKLTPRLSKDAYSEM KRAYKSYVRALPLLKKMGINSILLRKSIGALE VACGIVMTLVPGRPKDVANFFLLLLVLAVLF FHQLV
1234	2584	A	9765	71	456	RLELDWGFSLHFLPVAYLCPLSSGFEMNVQP CSRCGYGVYPAEKISCIDQIWHKACFHCEVC KMMLSVNNFVSHQKKPYCHAHNPKNNTFTS VYHTPLNLNVRTFPEAISGIHDQEDGEQCKSV FHWD
1235	2585	A	9767	52	559	IRSGAMSVDKAELCGSLLTWLQTFHVPSPCA SPQDLSSGLAVAYVLNQIDPSWFNEAWLQGI SEDPGPNWKLKVTSGLLIRGQTGEEMTRDGP ARHMSWVMGRKRDRCLVINHLFIHSSMEYSP CARPGHSARNNTDKNLPHTAIILVTSNTYTTI KINFQAGRSGSCL FRGEALTVRFLTKRFIGEYASNFESIYKKHLC
1236	2586	Α	9770	352	1 000	INCLUDIAL INCLUDIAL CONTROLLEGION

1237 2587 A 9793 266 315 264 2797 2588 A 9793 266 315 2797 2588 A 9802 337 967 266 2798 279				·			Amino acid sequence (A=Alanine C=Cysteine,
NO. of ID NO.	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alainile C=Cystelle,
		NO: of	hod	ID NO:			D=Aspartic Acid, E=Giulainic Acid,
Section	-			in	nucleotide		F=Phenylalanine, G=Glycine, ri=Histidine,
1236 1238 2587 A 9793 266 315 1237 1238 2588 A 9802 537 967 1238 123		1 .		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
1237		1 -	ļ		correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
1237 2387 A 9793 266 315 1260 127 1280 1281 1297 1288 2588 A 9802 537 967 1280		uence	١.			acid residue	O=Glutamine, R=Arginine, S=Serine,
Pepsible Pepsible	uence			714	amino scid		T=Threonine, V=Valine, W=Tryptophan,
Pepsilde Pepsilde]	1			V=Tyrosine X=Unknown, *=Stop codon,
1237 2587 A 9793 266 515 DERENGINELT/DEPSS/TOK/AKFSLTSELHWA DGFVTV/VDISDRSSFATAKALI		l	1			sequence	/
1237 2587 A 9793 266 515 MILHIYPEPSITOKAKPELISELHWA		1	1				
1237 2587 A 9793 266 515			1	l	sequence		nucleotide hiserton
1237 2587 A 9793 266 515 NILAITYFFFFLLENSQSIPKAPALTICHH QKENFQLPVSIDALTPLVVCLVSTHIS RYKPTRPVCTIPGQGCS 1238 2588 A 9802 537 967 ELGAGRSDREAMEAVKEEISVEDEAVDKM FRDCNKLAFYRRQKQULSKKSTYRALLDSYT TDEDSTRFQIINEASK YPLLABIYGEGONIFILK NREFILPKRFEVPDYLTSKFSTYRLISCSGDT GSLLADGKGDLKC VRODPAMVRAGAVGAHLFASGLDIFGDLKK NRRQLYYQVLNFAMIVSSALMIWKGLIVLT GSESPIVVLSGSMPFAHRGDLLFLTNFED PRAGEIVYRK VEGRDIPVHRVIK VHEKDING DIKTLKGDNNEGDDRGSYK TDGRDFLFCAARRGGGECCGAGWVAEW RQFLDPAMLLWMQGFVLEAVACQDNDDYLR YGLLFEDLDCNGDGVYDIBLQGGRNVAEW RQFLDPAMLLWMQGFVLEAVACQDNDDYLR YGLLFEDLDCNGDGVYDIBLQGGRNVAEW TDGRDFLFCAARRGGGECCGAGWVAEW RQFLDPAMLLWMQGFVLEAVACQDNDDYLR YGLLFEDLDCNGDGVYDIBLQGGRNVAEW RQFLDPAMLLWMQGFVLEAVACQDNDDYLR YGLFEDLDCNGDGVYDIBLQGGRNVAEW SPARKSNRTDVMITAPKNKKMTENLAAPEA LDSSTHSSSTATQSRAKMMTPAPTRSTYPAJRR GSSGPPCAPHDRSSVLQCDTQAMDHKTE SSHSVVEFLFKRTKTPSFFFIPAVRENRN TSGGATFPFASLLSSSNDFCKEKTEDRYS LGSSLDSGMRTPLCRICPGGPEGGELLSPCRC CDGSVCTHQPCLLKWISSEGGCWSCLCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAALGS LFLASISWLIWSTFSFSARWGRQDLLSPCRC CDGSVCTHQPCLLKWISSEGGCWSCLCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAALGS LFLASISWLIWSTFSFSARWGRQDLLSPCRC CDGSVCTHQPCLIKWISSEGGCWSCLCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAALGS LFLASISWLIWSTFSFSARWGRQDLLSPCRC CDGSVCTHQPCLIKWISSEGGCWSCLCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAALGS LFLASISWLIWSTFSFSARWGRQDLLSPCRC CDGSVCTHQPCLIKWISGEGGWSCLCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAALGS LFLASISWLIWSTFSFSARWGRQDLLSPCRC CDGSVCTHQPCLIKWIGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA							LERKQLNLEIYDPCSQIQKAKISLISELHWA
1237 256		1	Į	1			DGFVIVYDISDRSSFAFAKALI
1238 2588 A 9802 537 967 ELGAGRSDREAMEAAVKEELSVEDEAVDRN FROKNEAPVERQUEJKSKSTYKALLDSVT TDESTRPOINFASKVPLLARIJGEGONIFRIK NEETPLKPREVPDVJLSKPSTVALLDSVT TDESTRPOINFASKVPLLARIJGEGONIFRIK NEETPLKPREVPDVJLSKPSTVALLDSVT TDESTRPOINFASKVPLLARIJGEGONIFRIK NEETPLKPREVPDVJLSKPSTVALISCSGDT SGLLADOKGDLKC NEETPLKPREVPDVJLSKPSTVALISCSGDT SGLLADOKGDLKC NEETPLKPREVPDVJLSKPSTVALISCSGDT SGLLADOKGDLKC NEETPLKPREVPDVJLSKPSTVALISCSGDT SGLLADOKGDLKC NEETPLKPREVPDVJLSKPSTVALISCSGDT SGLEADOKGDLKC NEETPLKPREVPLVLSGSMEPAFHRGDLLFLITMFRED DRAGEVVKVSGERDPIVHRVKVKHEEDND DRKFLTKGDNNEGDDRGSTYK NEETPLKPREDITH NEETPLKPRED NEETPLKPR	1000	2507	1	0703	266	515	NILAIIYFPFPRLFLLRDSQSNPKAFALTLCHH
1238 2588 A 9802 537 967 ELGAGRSDREAMA-AVERISVEDEAVDKNI FDDCNKIAFYRROKOWLSKSTYRALLDSY TDEDSTRPQINEASY VPLLARIYGEGONIFRIK NEETPLKPRFEVPDVLTSKPSTVRLISCSGDT GSLILADGKGDLKC TDEDSTRPQINEASY VPLLARIYGEGONIFRIK NEETPLKPRFEVPDVLTSKPSTVRLISCSGDT GSLILADGKGDLKC TDEDPAMVRAGAVGAHLPASGLDIFGDLKK MNRQLYYQVLNFAMIVSSALMIWKGLILTINFRED PRAGEIVVYK-VEGRDIPVURVKVHEKDNG DIKFLTKGDNNEGDDRGSYK MNRQLYYGVK-VEGRDIPVURVKVHEKDNG DIKFLTKGDNNEGDDRGSYK TDGRIPPLPCAARRGGGGECGAGWVAEWS POPLLDPAMLL WAMQGVLEAVACQDNDDYLR YGULFEDLDCNGDGVVDIIELQEGLRNWSSAF DPNSEHG SPARKKSNRTDVMITAFKNKKMTENLAND LDSSTHSSSTATQSRAKMTPATPSTYPAPER GGSGGPPCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRENNN TSGGSPPTCAPHRVSSVLQCDTQAMDHKTE SSHSVVERLFKRTKTPSFPHAVRGNCELCYYKY HVIAISTKNPLQWQAISLTVIBKVQVAAALTLATTT TSGSVLWSTFSPSARWQGQCLLCYKYK TVAISTKNPLQWQAISLTVIBKVQVAAALTLATTT SVCALATNGAVQGGACQLQFRWGALLTVISKERGRUNG WAGAGGPGGASARRLSTFLQWVPTVLSMF SIVVERLGFVGGAGGSTVTVVISMFTGVVPTVLSMF SIVVERLGFVGGAGGSTVTVVISMFTGVVPTVLSMF SIVVERLGFVGGAGGSTVTVVISMFTGVVPTVLSMF SIVVERLGFVGGAGGSTVTVVISMSLSLPQDAM AMBLITEDVLAAALADHLPEDK WSAEKRYPL KSLGVETTSLLNPDPKSHDVYNDISKTVANSVLPVRV VYQPFLNALGAAGNFSVDSQLLYYAMLGVAN VYQPFLNALGAAGNFSVDSQLLYYAMLGVAN VYQPFLNALGAAGAGGPGGASAGSTVTVVISSELGSSAA SLYPVLNFLLVVPELAHSPLYIQDKGAPHSVV WEDEAVRA VYQPFLNALGAAGAGGPGGAGGSTVTVVISSELGSSAA SLYPVLNFLLVVPELAHSPLYIQDKGAPHSVV WEDEAVRA VYQPFLNALGAAGAGGGGGAGSTCTVTVSSECGGAGGRTSVTV SAEGGAGGRTSTVTVSSECGGAGGAT VYGNKKMTRSCSAVGGSTRDTVTSSECGGAGAT VAGNKTAN VATAGAGGAG	1237	2307	ΙΑ .	17/73	200		OKIKNFOILPVSIDALTPPLVVCFLVSFLTHFS
1238 2588 A 9802 537 967 ELGAGRSDREAMEAAVKERISVEDEAVDKK			1	1			
FRDCNKIAFYRROKOWLSKKSTYRALLDSY		l		1	505	067	PL GAGRSDREAMEAAVKEEISVEDEAVDKNI
TDEDSTRYQIINEASKYPILAEIYGEGNIPKI	1238	2588	A	9802	537	907	EDDCNIKIAEVPROKOWI SKKSTYRALLDSVT
1239 2589 A 9805 105 540 VFGDPAMYRAGAVCAHLPASGLDIFGDLKK VFGDPAMYRAGAVCAHLPASGLDIFGDLKK VFGDPAMYRAGAVCAHLPASGLDIFGDLKK MNRRQLIVYQVLNFAMIVSSALMIWKGLIVLT GSSSPIVVVLSGSMEPAFHRGDLLFLTNFRED PIRAGEIVVFKVEGRDIPIVHRVIKVHEKDNO DIKFLTKCDNNEGDDRGSYK		1	1		1	·	TRUCINIAL INICAC WEBSICS THE BESSEL
1240 2589 A 9805 105 540 VPGDPAMYRAGAVGAHLPASGLDIFGDLKK VPGDPAMYRAGAVGAHLPASGLDIFGDLKK VPGDPAMYRAGAVGAHLPASGLDIFGDLKK VPGDPAMYRAGAVGAHLPASGLDIFGDLKK VPGRDPAMPARGAVGAHLPASGLDIFTNFRED PIRAGEIVYPKVERGDIPIVHRVIKVHEKDND DIKFLTKGDNNEGDDRGSYK VPGRDPIPFACARRRGGGGECCGAGWVAEWS POGDPAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGLRNWSSAF POFLDPAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGLRNWSSAF POFLDPAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGLRNWSSAF POFLDPAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGRNWSSAF POFLDPAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGRNWSSAF POFLDFAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGRNWSSAF POFLDFAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGRNWSAF POFLDFAMIL WMQGFVLEAVACQDNDDYLR YGLFEDLDCNQDGVVDIIELQEGRAV SSISSVVEFLERKTETPSPFPAVENRN LGSSLDSGMRTPLCRICFQGPEQEGLLSPCC DGSVKCTHQCLIKWISERGCWSCELCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAALGS LFILASISWLIWSTFSPARWQRQDLLFQICVQ MYGFMDVMIVAVDSEDMVQAAKEVGKRWS DIPP MYGFMDVMIVAVDSEDMVQAAKEVGKRWS DIPP DGTHISNFILANQVAKGPIVYCSDGFCELAG FARTEVMQ PARGAGGGGGASARLSTFLGVVVPTVLSMF SIVVFLRIGFVVGHAGLLQALAMLJVAYFILA LTVLSVCAIATIGAVQGGGAYCLQHRWTG VWPVLPAREWMSRTLGFEVGGSICAMFYLA NVCGCAVSLLGLVESVLDVFGA SKCRFFEGISSFOFMYRKERALSSGSVQEAE AMLDEPQEQAEGSLTVYVISEHSSLLFQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQVA AMSLTEDVLAAALADHLPEDKWSAEKRRPL KSSLGYSTIFSLLNPDPKSHDVYWDISENSKLIPODMM SYIGPKRTAVVRGMHREAFMIGRRIVQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQDMM SYIGPKRTAVVRGMHREAFMIGRRIVQDLPKCL LSGFTSEGLMTWEDRLIKWARSVENLATATT TLTSLA PPQLGAGRVEFFRHPDVRAPLKKINDFRC PPQLGAGRVEFFRHPDVRAPLKKINDFRC PPQLGAGRVEFFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFRC PPQLGAGRSWGFRHPDVRAPLKKINDFR			1			1	TDEDSTRIVINGASK VILLAETT ORDORITATION
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Incident Peptide USSN 1987 150 1209 1		SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alaime C-Cysteme,
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1248			1	914			Q=Glutamine, R=Arginine, S=Serule,
1248 2598			1		amino acid		T=Threonine, V=Valine, W=1ryptopnan,
1248 2598 A 9853 58 444 RYDDFYYSKGGKDAGGADVSLACERQSIPEE FRGITVVELIKKEGSTLGLTISGGTDKDGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKVGGKPR YSNLRPGGLARSDLLINGGYTBKYGGKPR YSNLRPGGLARSDLLINGGYTBKYGGKPR YSNLRPGGLARSDLLINGGYTBKYGGKPR YSNLRPGGLARSDLLINGGYTBKYGGKPR YSNLRPGGLARSDLLINGGAGAGAGASASAACHTVAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	i '	ĺ	l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1248	1		1		peptide		/-possible nucleotide deletion, \-possible
1248 2598 A 9853 58	1	Į.	1		sequence		nucleotide insertion
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1255 2605 A 9896 72 386 RPGREQRDCFQAPPLGLGGRQTDMMHHPLT GATCVGLPNVGMCPQLSGALTFMYLQQGNQ EATVAPDTMAQPYASAQFAPPQNGIPGEYTA PHPHPAPEYTGQTT SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEEL		1	- l		1	1	LGAIAGIILLTFEFHPRSKLHL
GATCVGLPNVGMCPQLSGALTFMYLQQGNQ EATVAPDTMAQPYASAQFAPPQNGIPGEYTA PHPHPAPEYTGQTT 1256 2606 A 9902 95 399 SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEEL	1652	0000		0006	172	386	RPGREORDCFQAPPLGLGGRQTDMMHHPLT
EATVAPDTMAQPYASAQFAPPQNGIPGEYTA PHPHPAPEYTGQTT 1256 2606 A 9902 95 399 SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEELE EIT KETPNELGVVAHTCNESTLGGRGGW	1255	2605	A	7070	1"	300	GATCVGLPNVGMCPOLSGALTFMYLQQGNQ
PHPHPAPEYTGQTT 1256 2606 A 9902 95 399 SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEEL **ELL KSTPNPL GVVAHTCNPSTL GGRGGW**		1	-		1		EATVAPDTMAOPYASAOFAPPONGIPGEYTA
1256 2606 A 9902 95 399 SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEELE ENLYSTENDELGVVAHTCNESTLGGRGGW	1	1	-	1	1		
DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEELE EUL STENDELGVVAHTCNESTLGGRGGW	L					300	SGCPAGLI HRPVI PKMGI SGLI PIL VPFILLG
PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH KEELE FULVSTPNPLGVVAHTCNPSTLGGRGGW	1256	2606	A	9902	وم ا	עענ ן	DIOEPGHAEGII GKPCPKIKVECEVEEIDOCTK
KEELE FULL STIPNIPL GUVAHTCNPSTI GGRGGW			{		1		PRICEENMKCCPESRGKKCLDERKVSLTLYH
FULL STEPNING GVVAHTONESTI GGRGGW		1		1	1		l e e e e e e e e e e e e e e e e e e e
	L	L				 	PUT VETDNDI GVVAUTCMPETI GGRGGW
1257 2607 A 9905 374 459 EHLKSTPNRLGVVAHTCNRSTEGGROGW	1257	2607	A	9905	374	459	ETILAST PIAKLUY YAHT CNTST LOGROOW

					S 25. 2 2	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A coartic Acid. F=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	t=tsoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uence ·			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
]	residue of	sequence.	V=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	3cquenee.	/=possible nucleotide deletion, \=possible
		1]	sequence	1	nucleotide insertion
			9911	364	1974	AGPGVPAVGGRWASGPGLGGRTLCSGPPDH
1258	2608	A.	9911	304	1	OPRGPSCGASGDPOCVGSPHPQRARPLLARP
	l	ļ		l .		GARLLPGHLPSPRPPRLPTGOPPAAAFRGPVR
	}	i	ł	İ		POGGGHIHPLPTPGGRPCFAVSEGSGSALLLS
	1	1	1			VI GECGSSSYVTGAACISPVLRCREWFEAGLP
		ł	l		ľ	WPYERGFLLHQKIALSRYATALEDTVDTSRL
	1	l			1	FRSRSLREFEEALFCHTKSFPISWDAYWDRND
•	1	ł	ì	{	ĺ	PLRDVDEAAVPVLCICSADDPVCGPPDHTLTT
	1	}		1		ELFHSNPYFFLLLSRHGGHCGFLRQEPLPAWS
	ł	ł	1	ì	Į.	HEVILESFRALTEFFRTEERIKGLSRHRASFLG
	Ì	1		1		GRRRGGALQRREVSSSSNLEEIFNWKRSYTRL
	ł	1	1	1	1	MAAAAGAAAAPGSREPQDRPECGAGHPGPR
	Į.	ļ	\	1		YYRHPERWLLRPEAFLGPLRTRAPSAEDSQR ERPAARSGPEMRVRYPVVAAVLAPYLALSQD
		1	1			PMYKSSASGQGASGSYNHVREEMLIKAGGA
	}	1.	1	1		MSRRVVRQSKFRHVFGQAAKADQAYEDIRV
	1	1		1		SKVTWDSSFCAVNPKFLAIIVEAGGGGAFIVL
	1	Į.	1 .	1		PLAK
					1026	GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA
1259	2609	A	9919	693	935	TLSKAERLRSQPGPEQGGSSYRPRTPTAAAIL
	·.	1	1	1	1	PPRPGRSHRKRKLVSTK
			 _	155	1082	OPSCI CSATEK DGGDVKALYRRSOALEKLGR
1260	2610	A	9921	455	1002	I DO A VI DI ORCVSI EPKNKVFOEALRNIGGQ
						INDEXIDANGETDAKVEOMFOILLDPEEKGTE
		1			ł	KKOKASONLVVLAREDAGAEKIFRSNGVQLL
		1	1	İ		ORLLDMGETDLMLAALRTLVGICSEHQSRTV
ļ	1	1	}	1		ATLSILGTRRVVSILGVESQAVSLAACHLLQV
		1		1		MFDALKEGVKKGFRGKEGAIIV
1261	2611	A	9928	1	438	GFRGAEAPGAAQAPKKKKPRPTEGGPGAGSG
1201	2011	1^	//20	1		RGKDPYRGPTLLHQPKPPKDEFLSSLESYEIAF
		ì		ł		PTRVDHNGALLAFSPPPPQRQRRGTGATAES
	1					RLFYKEASPSTHFLLNLTRSSRLLAGHVSVEY
			ì	1		WTREGLAWQRADRPHCLYA
1262	2612	A	9931	168	435	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA
1202	20.2	1			1	PPRLPFCLQELQGRHALHTFSLERTCSYQDFL WADEGRLLHVGAQDLATWHTLSPLGLW
		1	1	l		RMSATSVDQRPKGQGNKVSVQNGSIHQKDG
1263	2613	A	9938	247	488	CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY
]	1		1	1	YAPSIGFPYSLGEAAWSQL
		1			1000	ESIGLTALGPRRRPWEHRWSDPITLKMKGWG ESIGLTALGPRRRPWEHRWSDPITLKMKGWG
1264	2614	A	9941	61	277	WLALLGALLGTAWARRSQDLHCGACKAVR
					1	RRVROFNIYDY
			1		1522	FVASEVSKMPVPASWPHPPGPFLLLTLLLGLT
1265	2615	A	9956	2	522	EVAGREELOMIOPEKLLLVTVGKTATLHCTV
		1	1	1	1	TSLLPVGPVLWFRGVGPGRELIYNQKEGHFP
1		1		1		DVTTVSDI.TKRNNMDFSIRISSITPADVGTYY
1	1			1		CVKFRKGSPDHVEFKSGAGTELSVRGEYSVG
1	-		[1		FLSOVWWWLSSHPFMN
			10000	243	387	PKNNACHLLFTAVCQPRCKHGECIGPNKCKC
1266	2616	A	10002	243	307	HPGYAGKTCNOGRKTV
			10004	36	707	I PAPASTWSVARETMASSSVPPATVSAATAG
1267	2617	A	10004	30	1,0,	PGPGFGFASKTKKKHFVOOKVKVFRAADPLV
		}	1	1		GVEL WGVAHSINELSOVPPPVMLLPDDFKAS
		- 1	1	1		CVIV VANNHI FHRENI PSHFKFKEYCPOVFRNL
	1	1	1	1		PORFGIDDODYLVSLTRNPPSESEGSDGRFLIS
		1	1	1	ļ	YDRTLVIKEVSSEDIADMHSNLSNYHQVRPLS
1	1	ı			1	IDKIBVESTORES
						SPILSLSSLLTYSSAIVSNRCQLGRKLIGRENP
1268	2618	A	10005	2	209	SPILSLSSLLTYSSAIVSNRCQLGRKLIGRENP GEGYELFVPSNGVPAVCHMVGRRPHRAVLSP SQDELEHSLGESAAQGAAGVVLWVSWENTR

SEQ ID SEQ ID NO: of N	roline, roline
NO: of nucleotide eotide sequence uence uence users armino acid residue of peptide sequence uenc	roline, c, c, c, c, c, c, c, c, c, c, c, c, c,
nucle obtide sequence USSN location corresponding to last amino acid residue of peptide sequence 1269 2619 A 10010 245 588 RVDDFVRPLPGLMSRSRASHF PFRDVROGSTHRTQVYHSPYDR SGNQLLMLDEDEHPLLIRDRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSFRQILPRFRSADHD 1271 2621 A 10014 7 388 SAVTISWKWRSVMGIQTSPALI LIGLAVGSYLVRRSRRPQVTLI LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDIKVYLKGVHPT	roline, c,
eotide sequence ue	roline, c, c, codon, rsible ALQDHILHD CSLKRDTKAI LDPKPPPLTL CQRSLLQGDS RGSIPAMSYA PGWNPRFCII ESSRNKLLR ERRKSVPGGK LKSSIKRTKS RYRGWSMW
sequence Sequence Post	chan, odon, sible ALQDHILHD CSLKRDTKAI LDPKPPPLTL CQRSLLQGDS RGSIPAMSYA PGWNPRFCII ESSRNKLLR ERRKSVPGGK LKSSIKRTKS PRYRGWSMW
uence amino acid residue of peptide sequence seq	odon, sible ALQDHILHD CSLKRDTKAI LDPKPPPLTL CQRSLLQGDS RGSIPAMSYA PGWNPRFCII ESSRNKLLR RRKSVPGGK LKSSIKRTKS PRYRGWSMW
residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop of /=possible nucleotide deletion, \=pos nucleotide insertion TKVSLGLA	ALQDHILHD CSLKRDTKAI LDPKPPPLTL LQRSLLQGDS RGSIPAMSYA PGWNPRFCII ESSRNKLLR RRKSVPGK LKSSIKRTKS PRYRGWSMW
Peptide sequence Peptide se	ALQDHILHD ALQDHILHD ALQDHILHD ALQRSILQGDS ALGSIPAMSYA PGWNPRFCII BESSRNKLLR RRKSVPGGK LKSSIKRTKS PRYRGWSMW
1269 2619 A 10010 245 688 FGMLKNKGHSSKKDNLAVNAV LQLRNLSVADHSKTQVQKKENN IDTGLKKTTQCPKLEDSEKEYVI AQKLGLIGPPPPPLSDEWEKVK VQPCPICKEEFELRPQVFSIRG	ALQDHILHD ASLKRDTKAI LDPKPPPLTL QRSILLQGDS AGSIPAMSYA PGWNPRFCII ESSRNKLLR RRKSVPGGK LKSSIKRTKS PRYRGWSMW
1269 2619 A 10010 245 688 FGMLKNKGHSSKKDNLAVNAV LQLRNLSVADHSKTQVQKKENI IDTGLKKTTQCPKLEDSEKEYVI AQKLGLIGPPPPPLSSDEWEKVK VQPCPICKEEFELRPQVFSIRG RVDDFVRPLPPGLMSRSRASIHI PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEIHPLLIRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHED DEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDIKVYLKGVHPT SDEDQGYVDIDIKVYLKGVHPT MAAPTI GRGVGRILGSLRGLS	CSLKRDTKAI LDPKPPPLTL LQRSLLQGDS CGSIPAMSYA PGWNPRFCII ESSRNKLLR RRKSVPGGK LKSSIKRTKS PRYRGWSMW
1269 2619 A 10010 245 688 FGMLKNKGHSSKKDNLAVNAV LQLRNLSVADHSKTQVQKKENI IDTGLKKTTQCPKLEDSEKEYVI AQKLGLIGPPPPLSSDEWEKVK VQPCPICKEEFELRPQVFSIRG 1270 2620 A 10011 2 588 RVDDFVRPLPPGLMSRSRASIHI PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEIHPLLIRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHD DEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDIKVYLKGVHPY SDEDQGYVDIDIKVYLKGVHPY	CSLKRDTKAI LDPKPPPLTL LQRSLLQGDS CGSIPAMSYA PGWNPRFCII ESSRNKLLR RRKSVPGGK LKSSIKRTKS PRYRGWSMW
1270 2620 A 10010 2 588 RVDDFVRPLPPGLMSRSRASIHIPFRDVRGPSTHRTQYVHSPYDR SGNULLMLDEDEHPLLIRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHEDDEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDDIKVYLKGVHPT	CSLKRDTKAI LDPKPPPLTL LQRSLLQGDS CGSIPAMSYA PGWNPRFCII ESSRNKLLR RRKSVPGGK LKSSIKRTKS PRYRGWSMW
1270 2620 A 10011 2 588 RVDDFVRPLPPGLMSRSRASIHI PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEHPLLIRDRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRSQGFLSRR QPKLDRTSSFRQILPRFRSADHE DEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDDIKVYLKGVHP	DPKPPPLIL CORSILLOGDS GSIPAMSYA PGWNPRFCII ESSRNKLLR ERRKSVPGGK LKSSIKRTKS PRYRGWSMW PYLTTTGPSHP
AQKLGLIGPPPPPLSSDEWEKVK VQPCPICKEEFELRPQVFSIRG 1270 2620 A 10011 2 588 RVDDFVRPLPPGLMSRSRASIHI PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEIHPLLIRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHD DEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDDIKVYLKGVHPY SDEDQGYDDIKVYLKGVHPY SDEDQGYVDDIKVYLKGVHPY SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIK SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV SDEDQGYDDIKV	GSIPAMSYA PGWNPRFCII ESSRNKLLR ERKSVPGGK LKSSIKRTKS PRYRGWSMW
1270 2620 A 10011 2 588 RVDDFVRPLPPGLMSRSRASHER PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEHPLLIRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHEDEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA 1272 2622 A 10014 7 388 SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYVDIDKSVLKGVHPY SDEDQGYDDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYDDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYDDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYDIDKSVLKGVHPY SDEDQGYDDIDKSVLKGVHPY SDEDQGYDDIDKSVLKGVHPY SDEDQGY SDEDQGYDIDKSVLKGVHPY SDEDQGY SDEDQGY SDEDQGY SDEDQGY SDEDQGY SDEDQGY SDEDQGY SDEDQGY	GSIPAMSYA PGWNPRFCII EESSRNKLLR ERRKSVPGGK LKSSIKRTKS PRYRGWSMW
1270 2620 A 10011 2 588 RVDDFVRPLPPGLMSRSRASHER PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEIHPLLIRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHEDEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA 1272 2622 A 10014 7 388 SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDKVYLKGVHPI SDEDQGYVDIDKVYLKGVHPI	PGWNPRFCII ESSRNKLLR PRRKSVPGGK LKSSIKRTKS PRYRGWSMW
1270 2620 A 10011 2 PFRDVRGPSTHRTQYVHSPYDR SGNQLLMLDEDEHPLLRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHE DEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA 1272 2622 A 10014 7 388 SAVTISWKWRSVMGIQTSPALL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDKVYLKGVHPJ SDEDQGYVDIDKVYLKGVHPJ SDEDQGYVDIDKVYLKGVHPJ SDEDQGYVDIDKVYLKGVHPJ SDEDQGYVDIDKVYLKGVHPJ SDEDQGYVDIJKSLGSLRGLS	PGWNPRFCII ESSRNKLLR PRRKSVPGGK LKSSIKRTKS PRYRGWSMW
SGNQLLMLDEDEIHPLLRDRRS RTVSVPVEGRPHGEHEYHLGRS QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHE DEIDV 1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRRGGRA SAVTISWKWRSVMGIQTSPALL LIGHAVGSYLVRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDIKVYLKGVHPI SDEDQGYVDIDIKVYLKGVHPI	ESSRNKLLK RRKSVPGGK LKSSIKRTKS RYRGWSMW
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QYSMEGAPAAPFRPSQGFLSRR QPKLDRTSSFRQILPRFRSADHE DEIDV	LKSSIKRTKS PRYRGWSMW TYLTTTGPSHP
1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFQFPGGNDN FLSGAEVSQSCRRGGRA 1272 2622 A 10014 7 388 SAVTISWKWRSVMGIQTSPALL LIGLAVGSYLVRRSRRPQVTLL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDKVYLKGVHPY SDEDQGYVDIDKVYLKGVHPY MAAPTI GRGVGRILGSLRGLS	PYLTITGPSHP
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LLGLAVGSYLVRRSRRFQV1LL LIDKTLSARSPCKHIYLSTRIDG SDEDQGYVDIDKVYLKGVHP1 SDEDQGYVDIKVYLKGVHP1 MAAPTI GRGVGRILGSLRGLS	WINDTOWOTAT
SDEDQGYVDIDIKVYLKGVHP	DPNEKULLK
MAARTI GRGVGRLLGSLRGLS	SUSIRPTIPVI
1972 2623 A 10016 1 1339 MAARTLGRGVGRLLGSLRGLS	FPEGGKMSH
	GQPARPPCGV
1 12/3 1 2020 1 1 1 I CADDD A ANTIDOCHNAPA VARAGO	AQPGSYPALS
AQAAREPAAFWGPLARDTLVV	/DTPYHTVW
	NCLDQHVKKS
PESVALIWERDEPGTEVRITYRU	ELLETTCRLA
	PLAVAAMLA
CARIGAVHTVIFAGFSAESLAG	RINDAKCKVV
TTENOGI RGGR VVELKKIVDEA	VKHCPIVQH
I I I I I I I VI VALIR TONK VHMGDLD VPL	EQEMAKEDP
VCAPESMGSEDMI.FMLYTSGS	TOMPROLVET
1	DIFGCVADIG
WITCHSYVVYGPLCNGATSVL	FESTPVYPNA
	VRLLLKYGD .
AWVKKYDRSSLRTLGSVGEPI	NCEAWEWLH
EDDOCTED SPASHVI TMSAPDI	GRRDPPKPKG
1 1274 2024 A 10017 1 VTI GSFFGSI PGFSSARNLVAN	MANARCHA
	HPEQIAPWIE
	NZKYKDY 199
	RSALIGIKEV
	LDISKAALIG
TYDTVSTGI TGAVNVAKGTV	OAGVDITKIV
I TOTE TOTE TO THE TOTE OF THE	GIAGIGAFIS
VANA TOTEDA VSTGLTGAVN	VARGSIQIGV
DTCVTVI TGTKDTVCSGVTGA	MNAKGIIQI
GVDTSKTVLTGTKDTVCSGVTG	GAMNVAKGT
IQTGVDTSKTVLTGTKDTVCS	GVTGAMNVA
KGTIQTGVDTTKTVLTGTKNI	VCSGYTGAVN
LAKEAIQGGLDTTKSMVMGT	KDTMSTGLTG
LAKEAIQGGLDI I KSIM V MIGI AANVAK GAMQT GLNTT QNIA	TGTKDTVCSG
VTGAMNLARGTIQTGVDTTK	IVI.TGTKDTVC
SGVTGAANVAKGAVQGGLD	TKSVI TOTKD
SGVTGAANVAKGAVQGGLD	VDTTKTVI TO
AVSTGLTGAVNVAKGIVQTG	OGGI DTTKSV
TKDTVCSGVTSAVNVAKGAV	CATURATION A
VIGTKDTMSTGLTGAANVAK	UAYCTVOTCM
KTVLTGTKDTVTTGLVGAVN	AUTOTA TOWN
DTTKTVLTGTKDTIYSGVTSA	* * * * * * * * * * * * * * * * * * *
GLKTTQNIATGTKNTFGSGVT	DAYNYAKUAM
OTCVDTAKTVI TGTKDTVI I	GLMGAYNYAN
GTVQTSVDTTKTVLTGTKDT	VCSGVIGAAN

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A-martic Acid E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	neuce		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		. !	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
netter			1. 1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
- 1				residue of	sequence	Y=Tyrosine, X=Unknown, *-Stop codon,
			{	peptide		/=possible nucleotide deletion, \=possible
1		ļ	1	sequence		nucleotide insertion
				55425		VAKGAIQGGLDTTKSVLTGTKDAVSTGLTGA
			1		ļ	VKLAKGTVQTGMDTTKTVLTGTKDAVCSGV
		i	{		ļ	TGAANVAKGAVQMGVDTAKTVLTGTKDTV
	l	1			1	CSGVTGAANVAKGAVQTGLKTTQNIATGTK
	1	1	1		1	NTLGSGVTGAAKVAKGAVQGGLDTTKSVLT
	1]	1	Ì	1	GTEDAVSTGLTGAVNLAKGTVOTGVD15K1
	ľ	1		Į.	1	VI TOTKDTVCSGVTGAVNVAKGTVQ1GVD1
	}	1	1]	j	AVTUI SCAKDAVTTGVTGAVNVAKGI VQIG
)	}	}	ļ		UDACKAVI MGTKDTVFSGVTGAMSMAKGA
	ŀ	1	1	1	}	VOGGI DITKTVI TGTKDAVSAGLMGSGNVA
		1	Į.	Į.	1	TCATUTGL STFONWLPSTPATSWGGLISSKI
	ł	1	1	ļ	l .	TONGGEOTAL SPORAPFSGISTPPDVLSVGPEP
	1	1		1	{	A SURE A A ATTIKGLATOVATETOGAAPGKEDIG
	1)	}		1	I TI ATTUCDEFAPRI AMI ONELEGLEDIFHEM I
		1	ļ	j		NATEGACI AASOPGPKVLSAEQGSYFVKLUD I
		1	ì	1	1	LGPSFRQRAFEHAVSHLQHGQFQARDTLAQL
		1	1			ODCEDI
	1	1				THARKEKTCPCKKEIGRNSRSGMYSRKAM
1275	2625	A	10025	124	415	. vvprvqaantkvekkkkekvlapvikpvGG
				1		DKNGGTRVVKLPTMPRYYPTEDVPRKLLSHG
!		1	Į.	1	1	KKPFS
		1		l		GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMS
1276	2626	A	10030	3	507	ASRPQSPTTPWCLPRRYMKHKRDDGPEKQED
12,0					1	EAVDVTPVMTCVFVVMCCSMLVLLYYFYDL
1	1			1	1	LVYVVIGIFCLASATGLYSCLAPCVRRLPFGK
ł	Į.	- 1	1		j	CRIPNNSLPYFHKRPQARMLLLALFCVAVSV
	1	Ì	1	1		VWGVFRNEDQ
1		1		·		YSRFTVPLPATMASSEVARHLLFQSHMATKT
1277	2627	A	10035	51	869	TCMSSQGSDDEQIKRENIRSLTMSGHVGFESL
12//		1	1	}	ļ	PDQLVNRSIQQGFCFNILCVGETGIGKSTLIDT
	· I	1	- 1	\		LFNTNFEDYESSHFCPNVKLKAQTYELQESN
1	ì	1			l	VQLKLTIVNTVGFGDQINKEERQLGRSQSTEN
}	1	}	ı	1	1	POKYRSEQHPVEPKKCTSFWKGALGKWAGIE
1	}	1		1		SSGQSAQQPYLPINSPPHRLADVADVHLFSSV
1	1	1			1	LSGAFGCYHLDVTVNEFKKQQNRDEQEGYS
		- 1	l	Į.	l l	LSGAFGC TALLY I VILLIAGORIA DE PAGEM
	ł	1	1	ĺ		KGDQEQGSWKHGADPLRGGEM RAFDVRKKSLRPCCPRDFHAGCLTVSGPST
1278	2628	- A	10036	3	457	RAFDVRRKKSLKPCCPRDFHAGCETVBGTGT
12/0	2020	1.	1 22 42	l l		VMGAVGESLSVQCRYEEKYKTFNKYWCRQP VMGAVGESLSVQCRYEEKYKTFNKYWCRQP
1		ł	l l	,	}	CLPIWHEMVETGGSEGVVRSDQVIITDHPGDL CLPIWHEMVETGGSEGVVRSDQVIITDHPGDL
1	•	- 1	1	1	ļ	TFTVTLENLTADDAGKYRCGIATILQEDGLSG
1		- 1		1		FLPDPFFQVQVLVSSASSTENSVKTP
1500	2629	-IA	10039	214	435	NDSLVPMSSWRSCARAPSSESAWRRSAATRR
1279	2029	^	1,000,0	1		SRKCLRTKRKRWSSGKGTQMQSTLSETPRRA
1	1	- 1		1	1	QMPCMWWYPFWG
	-		10043	$\frac{1}{2}$	344	DATWHNAGKEREAVOLMAGAEKRVKASHS
1280	2630	Ā	10043	"	1	FI DGI EGGNTRIEEACEMYTRAANMIKMAN
	}	1	Į	1	- 1	NWSAAGNAFCOAAKLHMQLQSKHDSATSFV
1	1	- 1	1	-		DAGNAYKKADPOGKTARHVACYLCV
L			-+:		818	UIVELDSSI ESYFIYFFIFFTESHFLPLMKWIU
1281	2631	A	10080	620	1 510	DIMAHCSI KII ASRNSADSAFLSAGDI SLSHSI
	1				1640	CASHIRGOKRASGEVGIAPSSRHILIGEPSAKY
1282	2632	A	10084	3	1040	NGTATIST VRGPGILGEVTVFWRIFPPSVGEPA
		- 1	1	1		ETECKI TMRDEOSAVIVVIOALNDDIPEEKSF
	-	- 1	ļ			VEFOI TAVSEGGVLSESSSTANITVVASUSPY
		- 1	1	1	1	GREATSHEOLRVSEAORVNITHRSSGDFGHVK
1	1	1	}	1	- {	I WYKTMSGTAFAGLDFVPAAGELLFEAGEM
,			1	1	l l	RKSLHVEILDDDYPEGPEEFSLTITKVELQGR
-	- 1	ı,				
		1			j	CYDETIOENGI OIDOPPEIGNISIVRIUMKNUN
1						GYDFTIQENGLQIDQPPEIGNISIVRIIIMKNDN AEGIIEFDPKYTAFEVEEDVGLIMIPVVRLHGT

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion YGYVTADFISQSSSASPGGVDYILHGSTVTFQ HGQNLSFINISIIDDNESEFEEPIEILLTGATGG AVLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIA NPNSTMILSLVLERTGGLLGEIQVNWETVGPN SQEALLPQNRDIADPVSGLFYFGEGEGGVRTII LTTYPHEEIEVEETFIIKLHLVKGEAKLDSRAK
1283	2633	A	10088	316	516	DVTLTIQEFGDPNGVVQFAPETLSKKTYSEPL ALEGPLLITFFVRRVKGTFGEIM MGSKTLPAPVPIHPSLQLTNYSFLQAVNGLPT VPSDHLPNLYGFSALHAVHLHQWTLGYPAM
1284	2634	A	10091	2	569	HLXRS FVSPSRAMASALIYVSKFKSFVILVVTPLLLLP LVILMPAKFVRCAYVIILMAIYWCTEVIPLAV TSLMPVLLFPLFQILDSRQVCVQYMKDTNML FLGGLIVAVAVERWNLHKRIALRTLLWVGA KPARLMLGFMGVTALLSMWISNTATTAMMV PIVEAILQQMEATSAATEAGLELVDKGKAKE LP
1285	2635	A	10092	290	728	KQSTRPDVMTLYPLHWQEEMSGESVVSSAVP AAATRTTSFKGTSPSSKYVKLNVGGALYYTT MQTLTKQDTMLKAMFSGRMEVLTDSEGWIL IDRCGKHFGTILNYLRDGAVPLPESRREIEELL AEAKYYLVQGLVEECQAALQV
1286	2636	A	10100	1	574	RPRGRGAWAGPGGDYSGVRRQQRRRTRISGS QRGSDAAGTMGCCTGRCSLICLCALQLVSAL ERQIFDFLGFQWAPILGNFLHIIVVILGLFGTIQ YRPRYIMVYTVWTALWVTWNVFIICFYLEVG GLSKDTDLMTFNISVHRSWWREHGPGCVRR VLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI HSA
1287	2637	A	10103	252	376	RSRMGDKPIWEQIGSSFIQHYYQLFDNDRTQL GALYYSFOL
1288	2638	A	10107	1	478	MEEEDESRGKTEESGEDRGDGPPDRDPTLSPS AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL RWRRCRSPRSEPRSQESGGTDTATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT
1289	2639	A	10113	237	438	LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG
1290	2640	A	10114	367	856	RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRPTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ RTIRETERRSALSCSVLKSEPLPGLQPQASQQR
1291	2641	A	10116	128	591	RTIRETERRSALSCSVLKSEPLFGLOFQASQA RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR
1292	2642	A	10121	1	749	QRRFRAGLWGGHGLTDGLRGATGE VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP MTEKVEELLRVIGPFYEIVEDKKSGRSSDITSD

				Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Mct	SEQ	beginning	nucleotide	D=Acceptic Acid E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	in	location	corresponding	I-Icoleucine K=Lvsine, L=Leucine,
eotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine V=Valine W=Tryptophan,
			}	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
1			l	peptide		nucleotide insertion
i				sequence		LGNVLTSTPNAKTVNGKAESSDSGAESEEEE
					Ì	l ·
		}			l	AC PLMSLVRVVEFVAASSAQKTPSRLENYYMVC
1293	2643	A	10124	2	989	PLMSLVRVVEFVAASSAQKIFSKLENT IMVC
1293	2043 .	۱"		-		KADEKFNOLVHFLRNHKQEKHLVFFRYSSGL
]	1			CGRGIRDSARMCSTCACVEYYGKALEVLVK
		l	1			GVKIMCIHGKMKYKRNKIFMEFRKLQSGILV
		1		1	1	CTDVMARGIDIPEVNWVLQYDPPSNASAFVH
		(1	ļ	ļ	RCGRTARIGHGGSALVFLLPMEESYINFLAIN
		ļ		Į.		QKCPLQEMKPQRNTADLLPKLKSMALADRA
•]	ļ.		1		VEEKGMKAFVSYVOAYAKHECNLIFRLKUL
	1	l	ļ	i	1 .	DFASLARGFALLRMPKMPELRGKQFPDFVPV
		ì	1	1		DVNTDTIPFKDKIREKQRQKLLEQQRREKTEN
		1	İ	ì		FGPPKFIKNKAWSKOKAKKK
			10000	91	1042	VTMVKDCIESTGDYFLLCDAEGPWGILLESLA
1294	2644	A	10129	ا ا	1042	II GIVVTILLLAFLFLMRKIODCSQWNVLPTQ
	Į	ł		į	1	I I FI I SVI GLEGLAFAFIIELNQQTAPVRYFLE
	ļ			ì		GVI RALCESCLLAHASNLVKLVRGCVSFSWI
ı	Ĭ		1	}		TH CLAIGCSLLOHIATEYVTLIMTRGMMFVN
	İ	1		}	· ·	MTPCQLNVDFVVLLVYVLFLMALTFFVSKAT
		1'		1	Į.	FCGPCENWKOHGRLIFITYLFSIIIWVVWISML
		1	1	1	1	LRGNPQFQRQPQWDDPVVCIALVTNAWVFL
	ļ	1			i	LLYIVPELCILYRSCRQECPLQGNACPVTAYQ
}	1	1	1.	1		HSFQVENQELSRDKWKVLLNSDFLSHSGA
	\		·			RPRVVTHNSQWCFLPQDHPGWLPGQSGAPG
1295	2645	A	10133	376	518	GRGAPRQEGPGSSWRQV
					1	EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE
1296	2646	A	10135	3	551	NIQDVLSALPNPDDYFLLRWLQARSFDLQKS
1250	20.0	1		1		EDMLRKHMEFRKQQDLANILAWQPPEVVRL
					1	YNANGICGHDGEGSPVWYHIVGSQDPKGLLL
'	.	1	Ì			YNANGICGHDGEGSPY W THIVOSQUIRGEBS
			ì	1		SASKQELLRDSFRSCELLLRECELQSQKLGKR
1	ł	1	1	1		VEKHAIFGLEGLGLRDLWKPGIELLQE
1297	2647	A	10138	48	407	MVSSCCGSVCSDQGCGQDLCQETCCRPSCCE
1291	2047	1"	.	İ		TTCCRTTCCRPSCCVSSCCRPQCCQSVCCQPT
1	1	-		i		CSRPSCCQTTCCRTTCYRPSCCVSSCCRPQCC
	1	j		}	1	QPVCCQPTCCRPSCCETTCCHPXCC
1000	2648	TA-	10156	94	453	GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG
1298	2048	^	10150	1.		QEMYLRFDQTTRRSPYRMSRILARHQLVTKI
		1	ļ	ĺ	,	QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP
1	ì	1	ľ		1	TAITU A VIKAIDHDET EKDLGEPLCRRLNI
	1		10161	+1	393	DDESEL VDGRGRVSARFGGSPSKAATVRSQF1
1299	2649	A	10161	1'	1 373	A SAOT FNMFRAPKRYSLALULPERUSKURUN
		1		1	1	VPCNCSENPCONGGTCVPGADAHSCDCGPGF
	1	1		1	1	KGRRCELACIKVSRPCTRLFSETKAFPVWEGG
1		- [1	1	1	VCHHV
		L			1201	AKIASI ERIMPANYTCTRPDGDNTDFRYFIYA
1300	2650	A	10162	98	391	VTYTGILGPGLIGNILALWVFYGYMKETKRA
1						VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF
1		-		1	1	
-				 		PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE
1301	2651	A	10165	1	7545	ROLOCMPMEGRGRASSSISDLQGKGFEKGTG
1 ,301	2001	1	1	1		KOLOCAPATORO A SA OCERNIODOR AOT
1		1		1	1	EKHVPGVGSARHSPQASAGGSPWQRGKAQT
1		1		1	1	RWLGKPDPGRKRRRGSPQEEGGLRVSAAAR
]		- 1		1	1	LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP
1	1	1		1	- {	PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA
1	i	1	1			LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP
				1	1	RTLSVEEPGVECNQLCLYADVTDPVLCLGQK
	1	i	1	ļ.	1	KILDADIT QADOL GALLER
		1			1	DPGVEGKHCEKEKISSSKELKHVHAKSEPSKI
						DPGVEGKHCEKEKISSSKELKHVHAKSEPSKI ARRI SESI HVVDENKNESKIEREHKRRTSTPV
						DPGVEGKHCEKEKISSSKELKHVHAKSEPSKI

	one m		OFF	Dundings	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	[in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	[USSN	location	corresponding	1=ISOICIICINE, N=Lysilic, L-Leucine,
seq-	uence	'	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	Į	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
[.	1	1		peptide		/=possible nucleotide deletion, \=possible
1]	1		sequence	ļ	nucleotide insertion
	 	 				KSTLKNEKHLKKDDSETPHLKSLLKKEVKSS
		1	ŀ		1	KEKPEREKTPSEDKLSVKHKYKGDCMHKTG
	1	1]	ĺ	1	DETELHSSEKGLKVEENIQKQSQQTKLSSDDK
1 .	}	1		1	1	TERKSKHRNERKLSVLGKDGKPVSEYIIKTDE
1		1	į	ļ	1	NVRKENNKKERRLSAEKTKAEHKSRRSSDSK
1	1	1	i	(IQKDSLGSKQHGITLQRRSESYSEDKCDMDST
1			1	1		NMDSNLKPEEVVHKEKRRTKSLLEEKLVLKS
1	1	1	1	ŀ	l	KSKTQGKQVKVVETELQEGATKQATTPKPD
}		}	1	1	ŀ	KEKNTEENDSEKQRKSKVEDKPFEETGVEPV
	1		1		l	LETASSSAHSTQKDSSHRAKLPLAKEKYKSD
1	1	1]	1	KDSTSTRLERKLSDGHKSRSLKHSSKDIKKKD
	1			1	1	ENKSDDKDGKEVDSSHEKARGNSSLMEKKL
1	1	1	1	į.		SRRLCENRRGSLSQEMAKGEEKLAANTLSTP
1		1	1	Į.	1	SGSSLQRPKKSGDMTLIPEQEPMEIDSEPGVE
i	· ·			1		NVFEVSKTQDNRNNNSHQDIDSENMKQKTS
1		1	1	1	1	ATVQKDELRTCTADSKATAPAYKPGRGTGV
		ļ	1			NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE
1	1	1	1		ŀ	KEPIHRGTTEVNIDSETVHRMLLSAPSENDRV
	1	1				QKNLKNTAAEEHVAQGDATLEHSTNLDSSPS
	1	1	1	ì	1	LSSVTVVPLRESYDPDVIPLFDKRTVLEGSTA
}	1	1	}	ł	l	STSPADHSALPNQSLTVRESEVLKTSDSKEGG
1		1		ļ		EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ
]]	1	1)	}	GKVIMPLGSKLTGVIVENENITKEGGLVDMA
	1	1			1	KKENDLNAEPNLKQTIKATVENGKKDGIAVD
1		1)	1	HVVGLNTEKYAETVKLKHKRSPGKVKDISID
1	1	1		1		VERRNENSEVDTSAGSGSAPSVLHQRNGQTE
Ī			I	1		DVATGPRRAEKTSVATSTEGKDKDVTLSPVK
	1		}	1	1	AGPATTTSSETRQSEVALPCTSIEADEGLIIGT
1	1	1	1	1		HSRNNPLHVGAEASECTVFAAAEEGGAVVTE
1]	}	1	1	ĺ	GFAESETFLTSTKEGESGECAVAESEDRAADL
	}	1	1	1	1	GRAEDELI LI DI KEUEDUECA VAEDEURAADL
1				1	1	LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE
	1]	1	1	1	KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG
1		1	1		1	TEIRAGSISSEEVDGSQGNMMRMGPKKETEG
1	1	1				TVTCTGAEGRSDNFVICSVTGAGPREERMVT
	1	1	i	1		GAGVVLGDNDAPPGTSASQEGDGSVNDGTE
	1	1	1			GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS
1 .	1	1	1	1		SESEENGESAMDSTVAKEGTNVPLVAAGPCD
	1	i		1		DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH
1	1		1	1 .		ASTCTGLGEESEGVLICESAEGDSQIGTVVEH
1	1	1		1		VEAEAGAAIMNANENNVDSMSGTEKGSKDT
1	1		1		· [DICSSAKGIVESSYTSAVSGKDEVTPVPGGCE
1	1	1	1	1	1	GPMTSAASDQSDSQLEKVEDTTISTGLVGGS
1		1	1	1		YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE
			1	1		NEECDGLMATTASGDITNQNSLAGGKNQGK
1	1	1	1	1		VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE
1	1	1	1	1		ENMEGTRYTTEEFEAPMPSAVSGDDSQLTAS
	1		j	J		RSEEKDECAMISTSIGEEFELPISSATTIKCAES
		1		1		LQPVAAAVEERATGPVLISTADFEGPMPSAPP
	1	ì	1	1	1	EAESPLASTSKEEKDECALISTSIAEECEASVS
1	1	1	ì	1	1	GVVVESENERAGTVMEEKDGSGIISTSSVEDC
		1	1	1	'	EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS
	1	1		1.		TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA
1	1			1	1	AIISTSTAECMPISASIDRHEENQLTADNPEGN
1		1	1	j	1	GDLSATEVSKHKVPMPSLIAENNCRCPGPVR
1	[1		GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH
1				l .	1	PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL
	1	1	1	1	1	HLINAEEKNVLLNSLOKEDKSPETGTAGGSST
ł	1		1	1	1	ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK
1	1		.[DSSVSSIRYLAAVNTGAIKADDMPPVQGTVA
	j	}	1	1	1	EHSFLPAEQQGSEDNLKTSTTKCITGQESKIAP
L						<u>, I </u>

			ODO	Deadists.3	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Mct	SEQ	Predicted beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
- 1			\	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
į]	1 1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	ļ '	peptide		nucleotide insertion
- 1				sequence		SHTMIPPATYSVALLAPKCEQDLTIKNDYSGK
						WTDQASAEKTGDDNSTRKSFPEEGDIMVTVS
			1			SEENVCDIGNEESPLNVLGGLKLKANLKMEA
		l	ł		į .	YVPSEEEKNGEILAPPESLCGKPSGIAELQRE
	l					PLLVNESLNVENSGFRTNEEIHSESYNKGEISS
	ļ	}				GRKDNAEAISGHSVEADPKEVEEEERHMPKR
,	ļ	ì	1		İ	GRKDNAEAISCHSVEADPREVEEERMINI AC
	i					KRKQHYLSSEDEPDDNPDVLDSRIETAQRQC
		1	1	ĺ	1	PETEPHATKEENSRDLEELPKTSSETNSTTSRV
						MEEKDEYSSSETTGEKPEQNDDDTIKSQE
1302	2652	A	10167	321	842	EPSLFPFLRPSPARPPPRPPAPFPSPELAGPEPH
1302	2002	1		i	'	FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG
	1	1	1	1	1	NSTVAGRGTSVRCLSPSPRPLPPLLPLLADLLE
	1	l	1	!	1	DGFGEHPFYHCLVAEVPKEHWTPEGNPSPFP
	İ		1	1		EARETKCYVRSSVGCVEPLTTQAEVTENLDR
	1	1				KNSQQVFKLLKKK
1303	2653	A	10171	206	429	NMILLKKRRLLINSLGEGTINGLLDELLETNV
1303	2033	1^	10	1		LSQEDTEIVKCENVTVIDKARDLLDSVIRKGA
	1	1	ł			RACEICITYI
1004	0054	A	10184	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSFAQNGF
1304	2654] A	10104	1 3/0		VHEAVVIETOALKLNPODHRLFGNRSFCHER
	1			1		I GOPAWALADAOVALTLRPGWPRGLFRLGK
		1		ļ	1 .	ALMGLQRFREAAAVFQETLRGGSQPDAAREL
	i	1	1	1	ł	RSCLIHITLOGORGGICAPPLSPGALQPLPHA
	1	l		1		ELAPSGLPSLRCPRSTALRSPGLSPLLH
	0000		10194	12	394	TOLLGRRERVDGAAMAACEGRRSGALGSSQ
1305	2655	A	10194	2	1 3/4	SDEL TPPVGGAPWAVATTVVMYPPPPPPPPHR
)	1	1	1	DEISVILSEGESYDNSKSWRRRSCWRKWKQL
	1)	1	l		SRLQRNMILFLLAFLLFCGLLFYINLADHWKG
	1	1	Ì	1		TRNTCT
				+1	410	IPGSTISLEGPLSKWTNVMKGWQYRWFVLDY
1306	2656	A	10195	'	410	NAGLLSYYTSKDKMMRGSRRGCVRLRGAVI
i	i	ł			1	GIDDEDDSTFTITVDOKTFHFQARDADEREK
	ì	- {	1	ł	1	WIHALEETILRHTLQLQVRVFTWFPDSSLVGA
l		i	1	·		PERWI VSGFFFK
				105	308	OGI PSTMVKLGCSFSGKPGKDPGDQDGAAM
1307	2657	A	10205	85	300	DSVPLISPLDISQLQPPLPDQVVIKTQTEYQLS
	1		l l			SPDOONYTKSR
					160	ECGGIRQPGPPPALASAPAATMNRVGGSPS
1308	2658	A	10214	2	453	AAANYLLCTNCRKVLRKDKRIRVSQPLTRGP
		1	1	1		SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL
1	1	١		1		DNITQVMSLHTQYLESFLRSQFYMLRMDGPL
1	}	ı	1	1	1	PLPYRHYIAIMAAARHQCSYLINM
	1	1		<u> </u>	<u> </u>	RGWPEQQSTGRPRDVARQPRCQKEEGRRLRP
1309	2659	A	10233	45	421	RALESRTFQGSERSRWGPPLESTKENVQCGH
				1		RALESRIT QGSERSR WGFFLESTREN VQCGIT RPAFPNSSWLPFHERLQVQNGECPWQVSIQM
1		1		1	1	SRKHLCGGSILHWWWVLTAAHCFRRTLLDM
	1	1	1	1	1	
				1		AV CONTROL OF THE CON
1310	2660	A	10241	243	442	AFQLFNAKCESAFLSKRNPLQRNWTVLYRRK
12,0	2000]]		}	HKKGQSAEIQKKRTRRAFKFQRAITGASLADI
	1	- 1				MAK
1311	2661	HA-	10261	751	176	LPGADYGGGHLSLRLFHLLLTSAAWVPDESQ
1211	2001	^	10201	{	1	VTLNSAICVLSTVLIMEFPDLGKHCSEKTCKQ
1		1		1	1	I DEI DVKCDACKODFCKDHFPYAAHKCPFAF
	ı	1	1	-1		OKDARIADA CHILCHTPIPVKKGOIPDVV VGDRI
		1		1	i .	DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML
	- [1	1	I I		DIOCDOIN GRADES
						QMVCAQCHGNFCIQHRHPLDHSCRHGSRPTI
						QMVCAQCHGNFCIQHRHPLDHSCRHGSRP11
1312	2662	A	10270	3	669	QMVCAQCHGNFCIQHRHPLDHSCRHGSRP11

SSQ ID No. of much of peptide general personal process of peptide unco- olide sequence where the personal process of personal		000	N.C.	CEC	Deadicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
mere olde solde sequence were were with the sequence sequence were sequence where sequence se	SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid. E=Glutamic Acid.
uence olide sequence 1944 1946	NO: of		hod				F-Dhenviolanine G-Giveine H-Histidine
USSN	nucl-	peptide					T-Tradevision V-Turing 1-Terring
Sequence 9 44 9 46 9 46 9 46 9 46 9 46 9 46 10 46	entide	Seq-		USSN	location		l=isoleucine, K=Lysine, L-Leucine,
1314 2664 A 10288 536 1890 NVGLAKESELIKALICUPLY ENTRYPROPESSIRE PROSECUE NYTHEORIES RESIDENCE NY		•		09/496	correspondi		M=Methionine, N=Asparagine, P=Proline,
amino acid of peptide residue of peptide residue of peptide sequence per per per per per per per per per pe		uones :	l			acid residue	Q=Glutamine, R=Arginine, S=Serine,
1313	uence		{	***		of peptide	T=Threonine, V=Valine, W=Tryptophan,
Peptide Peptide Peptide Pulceinide deletion, Poposible Pulceinide insertion Pulceinide Pulceinide insertion Pulceinia		1		1			Y=Tyrosine, X=Unknown, *=Stop codon,
1313		ł	ł	1		Joquanos	/=nossible nuclentide deletion. \=possible
1313	1	İ	1	1		\	
1313		1		1	sequence	<u> </u>	nucleonide insertion
LISYISICYYGFICLYTI.FWI.FRIP.KEYSFEKV							LIYKLYVVQIVIKTAKFIFILCYTANFVNAISF
RESSYSDIPUVKNOFAPILHMVDQYTQL/VS	j	1	l	ł		1	EHVCKPKVEHLIGYEVFECTHNMAYMLKKL
RESSYSDIPUVKNDFAFLLHMYDQYDQLYS RFGYFLSEVSBRIKBEISINHEWTEKL	ì			i		1	LISYISIICVYGFICLYTLFWLFRIPLKEYSFEKV
1313 2663 A 10287 1221 266	}	ļ	1		}	ł	REESSESDIPDVKNDFAFLLHMVDOYDQLYS
1313		1			l.	1	VDEGVET SEVSENKI REISLNHEWTEEKL
1315 2665 A 10293 447 1331 SIPPLS-PPRI-NY-PPRI-PPP-PPI-PPP-PP-PP-PP-PP-PP-PP-PP-PP-PP			i				CATENT COLOCAODDI DEA ASVEVENIVOOD
VILLVAPILSOVALISAANITISTUOSITIKEE	1313	2663	A	10287	1221	266	GAHRYLSPAQGAQPRLRSAASVEVSMVOQR
EKSYQVIRWISPEDHOKRIKKHFDSYTALD GRKESBALVKLMERGTOCSYLLSRKDIMDSI KNENYDLYVZAFDFCSFLLABKLVKPYVAIL PTTFOSLDFGLPSPLSYVPYPSLLTDHMDFW GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF PEGSRPVLSHLLLKAEL WFVNSDCAFDFARPL LPNTVYIGGLMERKIKPYPOSSPASFLGFT LPNTVYIGGLMERKIKPYPOSSPASFLGFT NVQLAKFSSTLVFFSCDADPSALAKYVLAL KNESSELSKALCIDOLDYHQKETQIFVEK LPDAYNTKSYLPPFGCPSSGSLKVEFFFPQEK DIKKEEITKEERBEKKSTRSLHSPOSSRYN ENRSDERKKDDRSRKRDVDRNPPRBSYRD RYNRRGRSRSYSRSRSWSKERLRENDRD RSKTRSRSERIKSKERDLVRFYYDLDRTDPLEN NYTPVSSYPSISSGHYVPYTLSSTITVLAPTHIG NYTTESWSETHEDQVDHINSYVRPPMFKKR RDVDEKGFGMRGDMCFFDHGSDPVVVDDVN LPMQFFRAGPVVGCPPFGLPPPPLLTPPPV NLRPFVPPFGPLPSLPPVTGPPPPLPLPPPSG MDAPFNSATSSVPVVTGHPPPPLPLPPPPL NRPPVPPFGPLPSLPPVTGPPPPLPPPPLPPLPPP NLRPFVPPFGPLPSLPPVTGPPPPLPPPLPPLPP NLRPFVPPFGPLPSLPPVTGPPPPLTPPPV NLRPFVPPFGPLPSLPPVTGPPPPLTPPPV NLRPFVPPFGPLPSLPPVTGPPPPLTPPPV NLRPFVPPFGPLPSLPPVTGPPPPLTPPPV NLRPFVPFGGGGAAAAAAAEAAERKIPALRAHL WALLALWLCCATPAHALQCRGYEFCVNEG MCVYTHNGTGYCKCPGGTLGEYCQHRDPCE KNRCONGGTCVAQAMLGKATCKCASGFTGE DCQYSTSHETCYSRPCLNGGTCHMISRDTYE CTQVGFTGRNPKCPGGNLNYQFNGIIVVYS GGSVPPSGTKTSKPAEHNAMGTGSKAFSGT LWVMYSGATSTSTSTL 1316 2666 A 10294 118 572 SILMESNIKSGDGLSGTQKEAALRALVQRTG YSLVQBNGGRKYGGPPPGWDAAPPERGCEIFI GKLPRDLFEDELIPLCEKIGKYYEMRMMDP NGNNRGYAFVTSNIVEAKINGLNNYSER VLYMYSGATSTSTSTL 1317 2667 A 10301 158 1956 LLXSGGVLSGVCIPCEGGGTVKEAALRALVQRTG YSLVQBNGGRKYGGPPFGWDAAPPERGCEIFI GKLPRDLFEDELIPLCEKIGKYYEMRMMDP NGRNRGYAFVTSNIVEAKINGLNNYSERSV PROPSPHKSVSSPTSNINTPIKHLRTPSTKY KQENGGGEKAALESQVRSLLAEAKASDEN RLRSELKKYKEKRTLNAGOHOPDRVRP LPAASSGMKSSKSTSLAFEERSLSLKASSE DTINKFGSTAASGVPLIKATATAGAHSELTES RLRSGGGATTTTKRTGIPAPREFSVTVSRESSY PROPSPHRSSNSSPTSNITTPIKHLRTPSTKY KQENGGGEKAALESQVRSLLAEAKABCDEN RLRSELKKYKEKRTLNAGOHOPDRVRP LPAASSGMKSSSTSSNITGNSSCYPTNTQ ESSGSPTGNGLSSDDEYKKNHIGNALATTSG VSRGDTEPMRRALEENNNFQKELSDLEEENR VLKEKLIVLEHSPNSEGASHTGNSSCYPTNTQ ESSGSPTGNGLSSDDEYKKNHIGNALATTSG VSRGDTEPMRALEENNNFQKELSDLEEENR VLKEKLIVLEHSPNSEGASHTGNSSCYPTNTQ ESSGSPTGNGLSSDDEYKKNHIGNALATTSG VSRGDTEPMRALEENNNFQKELSDLEEENR VLKEKLIVLEHSPNSEGASHTGNSSCYPTNTQ ESSGSPTGNGLOSSDDEYKKKNH							VLLLVAFLLSGVLLSEAAKILTISTLGGSHTLL
GRESSALVKLMEIGTTQCSYLLSRKDIMDSL KNENDTLIVEVEAFDFCSTLARELVKPFVALI PTTFGSLDFGLFSPLSV VPVPFSLLTDHMDFW GRYKNFLMFFSFSSQWDMQSTTDDHTIKEHF PEGSRPVLSHLLIKAELWPVNSDCAFDFARPL LPTTYTIGGLMEKPIKPVPQVSSFASFALGT NVQLAKFSFLVFFSCDADPSALAKYVLAL VKDKSEKELKALCIDQLDVFLQKETIGTVEK LPDAVNTKSYLPPFSCDASSGK VFFFFPQEK DIKKEETIKEEREKKFSRLINHSPPQSSSRYR ENESKDERKKDDRSKRKDDRFNRDSYRD RYNKRRGRSRSYSRSRSSSWKERLREDRD RSRTSSSRTSSSGHYVPTLSTITVLAPTHHG NYTTSSWSEFHEDQVDHNSYVRPMPKKRC RDYDEKGFCMRGMCFPFDLFSPV NLRPPVPPFGPLSPPVTGPFDLPPPV NLRPPVPFPGPLPPPPLPPPLQPSG MDAPPRASTSSVFTVVTTGHHQPPPAPPSLFT ADTYDTDGYNFEAPSITNTSRPMTRHKVHPR AKLG 1315 2665 A 10293 447 1331 SHPLLSCPEKYSAKLRAAAEAAAEERTRGA GSGICAGLRSVAPGFPLKQEGGRREWGSSI GTSPCGSAQAAAAAAEAAEERTRGA GSGICAGLRSVAPGFPLKQEGGRREWGSSI GTSPCGSAQAAAAAAEATEKIPALRPALL WALLALWLCCATPAHALCQCYFECVNEG MCVYTHNGTGYCKCPEGFLGEYCQHRDPCE KNRCQNGGTCVAQAMLGKATCRCASGFTGE DCQYSTSHFCTSSRPAEHNAMGTGSKNPASG GSSYPSGTKTSKPAEHNAMGTGSKNPASG GGSPPSGTKTSKPAEHNAMGTGSKNPASG GGSPPSGTKTSKYPAEHNAMGTGSKNPASG ULVWMVSGATSTSTSTL 1316 2666 A 10294 118 572 SLSMESNIKSGDLSGTGKEAALRALVQRTG TSLVQENGGRKYGGPPOWDAAPPERGCEIFI GKLPRULEDELIPLCEKIGKTYERWRMMPF NGRLIGVCASVDNCELVGGFFKTKK PROSPRKSVSSPTSNNTPTKHLRTPSTKY PROSPRRKSVSSPTSNNTPTKHLRTPSTKY PROSPSPRKSVSSPTSNNTPTKHLRTPSTKY RQPSSPRKSKSSTSAASGVYRLKKTATAGAISELTES RLRSGTGAFTTTKRTGDFAREFSVTYSRERSV PROFSSPRKSVSSPTSNNTPTKHLRTPSTKY KQENEGGEKAALESQVRELLAEAKAKDSEN RLRSELKXYKEKRTINAAGGLRNVDGTS VSRODTEPMRALEEKNKNFQKELSDLEERN VLKEKLIVLEHSPNSSGASHTGDSSCPTSITQ ESSFSSPTGNGCLSSDDFYKKNHGNALRTNS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSPNSVSSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SPECTOR STATEMENT STATEMENT SPRTSP SSCSCTAGGRATTTTKTTGDFTRETSTTT	1	1	ł	ļ	1	ł	LDRVSQILQEHGHNVTMLHQSGKFLIPDIKEE
GRESSALVKLMEIGTTQCSYLLSRKDIMDSL KNENDTLIVEVEAFDFCSTLARELVKPFVALI PTTFGSLDFGLFSPLSV VPVPFSLLTDHMDFW GRYKNFLMFFSFSSQWDMQSTTDDHTIKEHF PEGSRPVLSHLLIKAELWPVNSDCAFDFARPL LPTTYTIGGLMEKPIKPVPQVSSFASFALGT NVQLAKFSFLVFFSCDADPSALAKYVLAL VKDKSEKELKALCIDQLDVFLQKETIGTVEK LPDAVNTKSYLPPFSCDASSGK VFFFFPQEK DIKKEETIKEEREKKFSRLINHSPPQSSSRYR ENESKDERKKDDRSKRKDDRFNRDSYRD RYNKRRGRSRSYSRSRSSSWKERLREDRD RSRTSSSRTSSSGHYVPTLSTITVLAPTHHG NYTTSSWSEFHEDQVDHNSYVRPMPKKRC RDYDEKGFCMRGMCFPFDLFSPV NLRPPVPPFGPLSPPVTGPFDLPPPV NLRPPVPFPGPLPPPPLPPPLQPSG MDAPPRASTSSVFTVVTTGHHQPPPAPPSLFT ADTYDTDGYNFEAPSITNTSRPMTRHKVHPR AKLG 1315 2665 A 10293 447 1331 SHPLLSCPEKYSAKLRAAAEAAAEERTRGA GSGICAGLRSVAPGFPLKQEGGRREWGSSI GTSPCGSAQAAAAAAEAAEERTRGA GSGICAGLRSVAPGFPLKQEGGRREWGSSI GTSPCGSAQAAAAAAEATEKIPALRPALL WALLALWLCCATPAHALCQCYFECVNEG MCVYTHNGTGYCKCPEGFLGEYCQHRDPCE KNRCQNGGTCVAQAMLGKATCRCASGFTGE DCQYSTSHFCTSSRPAEHNAMGTGSKNPASG GSSYPSGTKTSKPAEHNAMGTGSKNPASG GGSPPSGTKTSKPAEHNAMGTGSKNPASG GGSPPSGTKTSKYPAEHNAMGTGSKNPASG ULVWMVSGATSTSTSTL 1316 2666 A 10294 118 572 SLSMESNIKSGDLSGTGKEAALRALVQRTG TSLVQENGGRKYGGPPOWDAAPPERGCEIFI GKLPRULEDELIPLCEKIGKTYERWRMMPF NGRLIGVCASVDNCELVGGFFKTKK PROSPRKSVSSPTSNNTPTKHLRTPSTKY PROSPRRKSVSSPTSNNTPTKHLRTPSTKY PROSPSPRKSVSSPTSNNTPTKHLRTPSTKY RQPSSPRKSKSSTSAASGVYRLKKTATAGAISELTES RLRSGTGAFTTTKRTGDFAREFSVTYSRERSV PROFSSPRKSVSSPTSNNTPTKHLRTPSTKY KQENEGGEKAALESQVRELLAEAKAKDSEN RLRSELKXYKEKRTINAAGGLRNVDGTS VSRODTEPMRALEEKNKNFQKELSDLEERN VLKEKLIVLEHSPNSSGASHTGDSSCPTSITQ ESSFSSPTGNGCLSSDDFYKKNHGNALRTNS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSPNSVSSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SSSSDVTKASLSPDASDFHTTATETSRYLSSTS NPPKSSKCSTAGSSSPNSVSELSLASLTEKQKMS SPECTOR STATEMENT STATEMENT SPRTSP SSCSCTAGGRATTTTKTTGDFTRETSTTT	1	i	1])	}	EKSYOVIRWFSPEDHQKRIKKHFDSYIETALD
ISHNDLVFVEAFDESTLAIRELIVERYVALD PTIFOSLIFOLEPILARELIVERYVALD PTIFOSLIFOLEPILARELIVERYVALD PTIFOSLIFOLEPILARELIVERYVALD PTIFOSLIFOLEPILARELIVERYVALD PTIFOSLIFOLEPILARELIVERY PPEGSRPVLSILLLIKAEL WPVNSCDAFDFARPL LPNTVYIGGLMERYKEVPCOVSEPSAFSLOFT NVQLAKFSSTLVFFFSCDADPSALARYVALD VKKDKSEERIKALCIDQLDVFLQKETQIFVEK LPDAVNTKSYLPPFSCPSOSSIK VEFFPOEK DKKEEITKEEREKKFSRLNHSPPOSSSRYK ENSKDERKKADRSRKODDRSRKODTPORDEN RYNRRGRSRSYSSISSRSWSKEEL RERDID RSRTSSSRTSSREDLVKFYPDLATDHEN RYNRRGRSRSYSSISSRSWSKEEL RERDID RSRTSSSRTSSREDLVKFYDLDRTDFLEN NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVPTLSSTTVAPPHHG NYTPVSSVPSISSGHYPVTLSSTTVAPPHARVHRY AKLG SHPILSCPELPOVPHGSDPVVVEDVN LPGMQPFAQPVVEQPPPGLPPPSLTPLQPSG MDAPFNSATSSVPTVVVTGHHQPPPAPPSLFT ADTYDTOTGYTPAFAPSITTNTSSTPAPHRANKHTRAP AKLG SHPILSCPELYSAKLRAAAEAAEERKTRGA GSRGICAGLRSVAPGPPELPCEPCHROPEC NACCONGRACACAAAAAAAEAATEKLPALPALL WALLALWLCATPAHALQCACPPECVNEG MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCQHRDPE MCVTYHNGTGYCKCPEGFLGEYCYTVLTQTAVPQ GSSYPSGTKTSTCHAPRE MCVTYHNGTGYCKCPEGFLGEYCTVLTQTAVPQ MCVTYHNGTGYCKCPEGFLGEYCTVLTQTAVPQ MCVTYHNGTGYCKCPEGFLGEYCTVLTQTAVPQ MCVTYHNGTGYCKCPEGFLGEYCTVLTQTAVPQ MCVTYHNGTGAASGMKSSTSTALAFSESSISTALKASSE JTINKPGTAASGWKSSTSTALAFSESSISTALKASSE JTINKPGTAASGWKSSTSTALTREGORM MCSCATTTO MCVTYTT MCCATTTO MCVTYTT MCCATTTO MCCATTTO MCCATTTO MCCATTTO M	ĺ	1	1	1	1	l .	GRKESEALVKLMEIFGTOCSYLLSRKDIMDSL
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GRYKNTI,MFFSFSSQWMQSTFDTTIKEHF PEGSRPVLSHLLKAEL WFVNSDCAFDFARPL PEGSRPVLSHLLKAEL WFVNSDCAFDFARPL PEGSRPVLSHLLKAEL WFVNSDCAFDFARPL PHTVYIGGLMEKPIKPVPQVSEPSAFSLGFT NVQLAKFSSTLVFFFSCDADFSALAKYVLAL WKKNSSEKELKALCIDQLOVFLQKETQIFVEK LFDAVNTKSYLPPFEQPSSGSLKVEFFPPQEK DIKKEBITIKBEREKKFSHNSFPQSSSSRV ENRSPERSKENDVENRPPRDSYRD RYNRRGRSRSYSRSRSSWSKERLRSRDBD RSRTRSRSSTSSSSSRSKVEFPPPQEK NYTPVSSVPSISSGHYVPTLSSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTLSTITIVAPTHHG NYTFVSSVPSISSGHYVPTTGHHQPPPAPSLFT ADTYDTDGYNPEAPSITIVAPTHLSPHYLPRA AKLG SPELISCPEKVSSKI KAAAAEAAAEERRTRGA GSRGICAGLRSVAPOPEPLKQEEGRREWGSSI GTSPPCGSAQAAAAAAAEERRTRGA GSRGICAGLRSVAPOPEPLKQEEGREWGSSI GTSPCGSAQAAAAAAAEERRTRGA GSRGICAGLRSVAPOPEPLKQEEGREWGSSI GTSPCGSAQAAAAAAAEERRTRGA GSRGICAGLRSVAPOPEPLKQEEGREWGSSI GTSPCGSAQAAAAAAAEERRTRGA GSRGICAGLRSVAPOPEPLKQEEGREWGSSI CTCQVGFTGENKCCGGGN.NYQCFNGIUVVS GGSVPPSGTKTSKPAEHNAMGTGSKNFASGT LWVMVSGATSTSTSTI. SSSMSMTKASSSSTSTSTI. SSSMSMTKASSSSTSTITICHSKPCTGGGN.NYQCFNGIUVVS GGSVPPSGTKTSKVAEANAIKQLNNYEIR NGRLIGGVCEASCHOPTVAVQ DRYTKSSMRSAAKPWNPARAAGHOPDKVRP LPAASSGMKSSSSTSTISTISTICHSKARASSE DTLNKPGSTAASGVVRLKKTATAGAISELTES RLRSGIGAFTTIKRTOIPAPREFSVTVSRESV PRGSNPRKSSSSTSTNIPTTKHLRTPSTKR QGENEGGEKAALESQVVRLKKTATAGAISELTES RLRSGIGAFTTIKRTOIPAPREFSVTVSRESV PRGSNPRKSSSSTSTNIPTTRHLRTPSTKR QGENEGGEKAALESQVVRLKKATAGAISELTES RLRSGIGAFTTIKRTOIPAPREFSVTVSRESV PRGSNPRKSSSSTTITAGASPNIVSTSNIPTTRHLRTPSTKR QGENEGGEKAALESQVVRLKKATAGASSCTSTITQ SSSSSDVTKASLSPNSEGAASHTGDSSCTSTITQ SSSSSDVTKASLSPNSEGAASHTGDSSCTSTITQ SSSSSDVTKASLSPNSEGAASHTGDSSCTSTITQ SSSSSDVTKASLASSELSIA SALTEKQKM NYFKSSKCTAGSSPNSVESLSLASLTEKQKM NYFKSSKC	1		1	1	Į.		PARTICULAR LIGHT OF COLUMN TO LANGUAGE IN TOUR WENT
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622 FRI CEPCMOSKIYSYMSPNKCSGMRFPI	iP
1324 26/4 A 10000 1	QEE
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1326 2076 A 10344 2 ILLASI GVGLVTLLGLAVGSYLVRRSRR	DLG AAWF ARML FASL YFHS EELE WQG GEE
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I DEDICATED A SECONDA	AAWF ARML FASL YFHS EELE WQG GEE TSPV

			OTO I	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	in No.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	i '	USSN	location	corresponding	I=Icoleucine K=Lvsine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	١	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
}	ł	ł	(residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1		1	peptide	1	/=possible nucleotide deletion, \=possible
}	1	}	1	sequence	1	nucleotide insertion
	 	├──	 			HHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSD
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- 1	\	ł	1	Ì		TDPPNWQQLVSREVLLGLKPCEIKRQEVINEL
	١.		1	1	i Co	FYTERAHVRTLKVLDQVFYQRVSREGILSPSE
	(Į.			1	LRKIFSNLEDILQLHIGLNEQMKAVRKRNETS
1	ł			Į.	1	VIDQIGEDLLTWFSGPGEEKLKHAAATFCSNQ VIDQIGEDLLTWFSGPGEEKLKHAAATFCSNQ
1		- 1	İ	1	1	PFALEMIKSRQKKDSRFQTFVQDAESNPLCRR LQLKDIIPTQMQRLTKYPLLLDNIATYTEWPT
- 1	1		1	1	1	EREKVKKAADHCRQILNYVNQAVKEAENKQ
	}	-	i	1	1	RLEDYQRRLDTSSLKLSEYPNVEELRNLDLTK
1	1	ł				RKMIHEGPLVWKVNRDKTIDLYTLLEDILV
}	}				i	LLQKQDDRLVLRCHSKILASTADSKHTFSPVI
1	- 1	l		1		KLSTVLVRQVATDNKALFVISMSDNGAQIYE
1	1	1			1	LVAQTVSEKTVWQDLICRMAASVKEQSTKPI
1	1	1	1			PLPQSTPGEGDNDEEDPSKLKEEQHGISVTGL
1	1	١		}		OSPORDI GLESTI ISSKPOSHSLSTSGKSEVKD
- 1		1		1	1	LEVARROFAKEOHTDGTLKEVGEDYQIAIPUS
1	1	- 1		1		THE DIVERTE WALDALRNIGLLKOLLY QUULL
.	- 1	Ì		1		EKSVQEDWQHFPRYRTASQGPQTDSVIQNSE
	1	.	1	1		NULL A VIJOGE GHMPFRTGTGDIATCYSPKISIE
	1	1		1	1	CEA PRICEVOLAPODSOASNILVMDHMIMTPE
	1	l		1	1	MPTMEPEGGLDDSGEHFFDAREAHSDENPSE
1		1		1	İ	GDGAVNKEEKDVNLRISGNYLILDGYDPVQE
- }		1	- 1	1	1	SSTDEEVASSLTLQPMTGIPAVESTHQQQHSP
- [- 1	1	1		ONTELISTIC A ISPETPEFL VOORWGAMEY SCIEL
1		1	1	1	1	OSPSSCADSOSOIMEYIHKIEADLEHLKKVEE
1	1		1	1		SYTILCORLAGSALTDKHSDKS
]						1 011 TOOKIO. TOOKIO

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Aimine C-Cysteme,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in I	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence	i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1		7,4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
]	į.	l	1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	ļ	}	1 1	residue of	sequence	/=possible nucleotide deletion, \=possible
1	l.	1		peptide		
			1 1	sequence		nucleotide insertion
1331	2681	Α	10353	1	2100	AVEFAEGALTMAPWPELGDAQPNPDKYLEG
1331	2001	'''				AAGQQPTAPDKSKETNKTDNTEAPVTKIELLP
ľ	ļ	(1			SYSTATLIDEPTEVDDPWNLPTLQDSGIKWSE
1	ì	l	i i			RDTKGKILCFFQGIGRLILLLGFLYFFVCSLDIL
i		1	\			SSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIG
1	1	1	1 !			VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIP
1	ł	ŀ	[l .	TO COLLEGE TO THE PART OF THE
}	1	Ì	}			IIMGANIGTSITNTIVALMQVGDRSEFRRAFA
1	Į.	1	Į.			GATVHDFFNWLSVLVLLPVEVATHYLEIITQL
		İ			ļ	IVESFHFKNGEDAPDLLKVITKPFTKLIVQLDK
1]	1	1.		1	KVISQIAMNDEKAKNKSLVKIWCKTFTNKTQ
1	1		ļ		1	INVTVPSTANCTSPSLCWTDGIQNWTMKNVT
1	1	l	1	l	1	YKENIAKCQHIFVNFHLPDLAVGTILLILSLLV
1	1	1	i	i	ì	LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP
1		1	1	1	ł	FPFAWLTGYLAILVGAGMTFIVQSSSVFTSAL
1	1	1	i	ļ	}	FELY AND THE CONTROL AND THE CONTROL AND AND THE CONTROL AND T
1	1	1	1	ł	1	TPLIGIGVITIERAYPLTLGSNIGTTTTAILAAL
	1	1	1	l	1	ASPGNALRSSLQIALCHFFFNISGILLWYPIPFT
1	1	1		l	1	RLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP
ı		1	1	Į		LTVFGLSLAGWRVLVGVGVPVVFIIILVLCLR
ļ	1	ì	i	ĺ	1	LLQSRCPRVLPKKLQNWNFLPLWMRSLKPW
1		1	1		1	DAVVSKFTGCFQMRCCCCCRVCCRACCLLC
1	ì	1	1	1	100	GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET
1	1	ł	1	i	i	FDNITISREAOGEVPASDSKTECTAL
}	1	1	1		l	FUNITISKEAQGEVPASUSKIECTAL
1332	2682	A	10354	30	1377	SQQGSQPHRQGPPSLLTAPHSLDLPALPPGPR
1332	2002	1		1	ł	GSQGKLRRVLVPMSVKPSWGPGPSEGVTAVP
1	{	1	İ	i	ĺ	TSDLGEIHNWTELLDLFNHTLSECHVELSQST
1	1	1		1		KRVVLFALYLAMFVVGLVENLLVICVNWRG
ì	1	1	١.		l	SGRAGLMNLYILNMAIADLGIVLSLPVWMLE
1	1	١.	.		1	VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF
1	}	1			1	LVCLSVDRYVTLTSASPSWQRYQHRVRRAM
	1) -	1]	1	CACCIONAL CAMPI DESCRIPTION VECOPERMON FM
1	İ	1	1	1	Į.	CAGIWVLSAIIPLPEVVHIQLVEGPEPMCLFM
1	ì	1	1	1 '	i	APFETYSTWALAVALSTTILGFLLPFPLITVFN
1 '	Į.	1	}	}	1	VLTACRLRQPGQPKSRRHCLLLCAYVAVFV
1	İ	Į	ļ		j	MCWLPYHVTLLLTLHGTHISLHCHLVHLLY
1	ì	ì	1			FFYDVIDCFSMLHCVINPILYNFLSPHFRGRLL
1	1	1	1			NAVVHYLPKDOTKAGTCASSSSCSTQHSIIIT
1	1	1	j	}	1	KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP
	1				i	TQPLTPS
	1	1			 	AAGAGADGREPASERASRAEPPAVAMGQND
1333	2683	Α	10358	2	884	ANOMONDORE ROTTON BUILDING OF TOT
						LMGTAEDFADQFLRVTKQYLPHVARLCLIST
1		1	1	l	l	FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA
		1	1	1	1	SSFVFLNLLGQLTGCVLVLSRNFVQYACFGLF
	1	1	! .		1	GIIALOTIAYSILWDLKFLMRNLALGGGLLLL
1		- [LAESRSEGKSMFAGVPTMRESSPKQYMQLGG
ì	1	i		1		RVILVIMEMTLLHEDASFESIVQNIVGTALMI
1	}			1		LVAIGFKTKLAALTLVVWLFAINVYFNAFWT
i		1		1	1	IPVYKPMHDFLKYDFFQTMSVIGGLLLVVAL
	1			1	1	TLA I VENNUTLEW I DILL GIMPA 1000000 A AM
	-			1		GPGGVSMDEKKKEW
1334	2684	A	10367	59	1562	QAWSLQVALSPFFFPASPSNSFAAAVPQLLFP
1,334	2007	1 **	1			ELPLPHVPGQESAKRRSARRFLIMSELTKELM
	[1	1	ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS
	1	1	1	1	1	ALEOFEGGPCAVIAPVQAFLLKKLLFSSEKSS
		-		1	1	WRDCSQEEQKELLCHTLCDILESACCDHSGS
Ì	1	1	1	1	1	YCLVSWLRGKTTEETASISGSPAESSCQVEHS
		- [1	i	[ICTASMTMOUTIEFT WORD CALLED CONTROL
		- 1		1	1	SALAVEELGFERFHALIQKRSFRSLPELKDAV
	1	1	1	1	1	LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN
1	}	1	1	1	[EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN
	1	1	1	1	.[VWDGDRECSGMKLLGIHEOAAVGFLTLMEA
	1		1	1	1	LRYCKVGSYLKISKIPYLDCLASETHLTVFFA
}		1		1	1	KDMALVAPEAPSEQARRVFQTYDPEDNGFIP
1		1		l	1	DSLLEDVMKALDLVSDPEYINLMKNKLDPEG
- 1		}	}			DOLTED AMENTOR A 201 E J HATMAN AND TO

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SEQ ID NO: of nucl- cotide	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of nucl-		hod	ID NO:	beginning	nucleotide	D=Asparuc Acid, L=Oldanino Tiolo,
_					location	F-Phenylalanine, G-Glycine, H-Histidine,
ectide I	pepude		in	nucleotide	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
COUGE	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	į		()	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
1		l		peptide	1 2042-01-0	/=possible nucleotide deletion, \=possible
)]	l		sequence		nucleotide insertion
	<u> </u>		├	Joquenee		LGULLGPFLQEFFPDQGSSGPESFTVYHYNGL
	ì		ł '		Į.	KQSNYNEKVMYVEGTAVVMGFEDPMLQTD
		1				DTPIKRCLQTKWPYIELLWTTDRSPSLN
1335	2685	A	10375	82	2929	TRTKRRLGREKAMASPPRGWGCGELLLPFML
1333	2005	(*	100,00			LGTLCEPGSGQIRYSMPEELDKGSFVGNIAKD
		1			1	LGLEPQELAERGVRIVSRGRTQLFALNPRSGS
	1	1	1	}		LVTAGRIDREELCAQSPLCVVNFNILVENKM KIYGVEVEIIDINDNFPRFRDEELKVKVNENA
			1		{	AAGTRLVLPFARDADVGVNSLRSYQLSSNLH
		1	1	1		FSLDVVSGTDGQKYPELVLEQPLDREKETVH
)	1	1		DLLLTALDGGDPVLSGTTHIRVTVLDANDNA
	}		1]	1	PLETPSEYSVSVPENIPVGTRLLMLTATDPDE
	1		1	1	1	GINGKI TYSFRNEEEKISETFOLDSNLGEISTL
		1			1	LOSI DVEESREYT MEVVAODGGALVASAKVV
					1	VTVODVNDNAPEVILTSLTSSISEDCLPGTVIA
		1				LESVHDGDSGENGEIACSIPRNLPFKLEKSVD
i	1	1	1	1	ì	NYYHLLTTRDLDREETSDYNITLTVMDHGTP
	1	1	1	1	1	PLSTESHIPLKVADVNDNPPNFPQASYSTSVT
	1	1.	1	j	i	ENNPRGVSIFSVTAHDPDSGDNARVTYSLAE
			1	1		DTFQGAPLSSYVSINSDTGVLYALRSFDYEQL
{	1	1		1		RDLQLWVTASDSGNPPLSSNVSLSLFVLDQN DNTPEILYPALPTDGSTGVELAPRSAEPGYLV
[1					TKVVAVDKDSGQNAWLSYRLLKASEPGLFA
1	1	1	1	ì		VGLHTGEVRTARALLDRDALKQSLVVAVED
l	ì	1	į.	Į		HGQPPLSATFTVTVAVADRIPDILADLGSIKTP
ł	1	ì	1	1		IDPEDI.DI.TLYLVVAVAAVSCVFLAFVIVLLV
			ì	l .		I RI RRWHKSRLLOAEGSRLAGVPASHFYGY
)	ì	1		DCVRAFLOTYSHEVSLTADSRKSHLIFPQPNY
		1	}			ADTLLSEESCEKSEPLLMSDKVDANKEERRV
1	}	1		ì	l	LOCAPPNIT DWRFSOAORPGTSGSONGDDIG!
1	1	- 1		1		WPNNQFDTEMLQAMILASASEAADGSSTLGG
ł		-	İ	}	}	GAGTMGLSARYGPQFTLQHVLQGELGSDYR
1	1	i		1	Ì	QNVYIPGSNATLTNAAGKRDGKAPAGGNGN
	1	1	1	1		KKKSGKKEKK RPRRRQPSFSCRVLVLEDPPCFRFTNSMNQEK
1336	2686	A	10379	1	557	LAKLQAQVRIGGKGTARRKKKVVHRTATAD
		1		į	1	DKKLQSSLKKLAVNNIAGIEEVNMIKDDGTVI
1	Į.	ł		l		HFNNPKVQASLSANTFAITGHAEAKPITEMLP
1		1		1	1	GILSQLGADSLTSLRKLAEQFPRQVLDSKAPK
1		•		1		PEDIDEEDDDVPDLVENFDEASKNEAN
		4-	10200	+	1263	TEGSTISWSPAAARGLSVCRCCRLHPASAMUL
1337	2687	A	10380	1	1203	FGDLPEPERSPRPAAGKEAOKGPLLFDDLPPA
1	1	-			Į	ccrpcccccpt.lFDDLPPASSGDSGSLATSISQ
	1				1	MUKTEGKGAKRKTSEEEKNGSEELVEKKVC
1				1	1	KASSVIFGLKGYVAERKGEREEMQDAHVILN
1		1		1		DITEECRPPSSLITRVSYFAVFDGHGGIRASKF
1			1	1 .		AAQNLHQNLIRKFPKGDVISVEKTVKRCLLD
1	1		- 1			TFKHTDEEFLKQASSQKPAWKDGSTATCVLA VDNILYIANLGDSRAILCRYNEESQKHAALSL
1	- {	l l	1	1	1	SKEHNPTQYEERMRIQKAGGNVRDGRVLGV
1	(- [1	LEVSRSIGDGQYKRCGVTSVPDIRRCQLTPND
	l l		- [RFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ
	1					TREGKSAADARYEAACNRLANKAVQRGSAD
	1	1	1		Ì	I KEUKSAADAK I EMACIMEATIKA I QIKOOLE
						NVTVMVVRIGH GPSQSMAAGELEGGKPLSGLLNALAQDTFHG
1338	2688	A	10385	3	589	YPGITEELLRSQLYPEVPPEEFRPFLAKMRGIL
1				1		KSIASADMDFNOLEAFLTAOTKKQGGIISDQ
1						A A VISK FWK SHKTKIRESLMNQSRWNSGLRG
i i			1		1	CM TAULE TO SELECTION OF CALLED
1	ļ	ı		1	ì	I.SWRVDGKSOSRHSAOIHTPVAIIELELGKYG
						LSWRVDGKSQSRHSAQIHTPVAIIELELGKYG QESEFLCLEFDEVKVNQILKTLSEVEESISTLIS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion QPN LGAMAKHHPDLIFCRKQAGVAIGRLCEKCDG KCVICDSYVRPCTLVRICDECNYGSYQGRCVI CGGPGVSDAYYCKECTIQEKDRDGCPKIVNL GSSKTDLFYERKKYGFKKR
1340	2690		10388	113	3472	SQLRKGASATHSSPSRTDCIAQMMDIYVCLK RPSWMVDNKRMRTASNFQWLLSTFILLYLM NQVNSQKKGAPHDLKCVTNNLQVWNCSWK APSGTGRGTDYEVCIENRSSCYQLEKTSIKIP ALSHGDYEITINSLHDFGSSTSKFTLNEQNVSL IPDTPEILNLSADFSTSTLYLKWNDRGSVFPHR SNVIWEIKVLRKESMELVKLVTHNTTLNGKD TLHHWSWASDMPLECAIHFVEIRCYIDNLHFS GLEEWSDWSPVKNISWIPDSQTKVFPQDKVIL VGSDITFCCVSQEKVLSALIGHTNCPLIHLDGE NVAIKIRNISVSASSGTNVVFTTEDNIFGTVIF AGYPPDTPQQLNCETHDLKEIICSWNPGRVTA LVGPRATSYTLVESFSGKYVRLKRAEAPTNES YQLLFQMLPNQEIYNFTLNAHNPLGRSQSTIL VNITEKVYPHTPTSFKVKDINSTAVKLSWHLP GNFAKINFLCEIEIKKSNSVQEQRNVTIKGVE NSSYLVALDKLNPYTLYTFIRCSTETFWKW SKWSNKKQHLTTEASPSKGPDTWREWSSDG KNLIIYWKPLPINEANGKILSYNVSCSSDEETQ SLSEIPDPQHKAEIRLDKNDYIISVVAKNSVGS SPPSKLASMEIPNDDLKIEQVVGMGKGILLTW HYDPNMTCDYVIKWCNSSRSEPCLMDWRKV PSNSTETVIESDEFRPGIRYNFFLYGCRNQGY QLLRSMIGYIEELAPIVAPNFTVEDTSADSILV KWEDIPVEELRGFLRGYLFYFGKGERDTSKM RVLESGRSDIKVKNITDISQKTLRIADLQGKTS YHLVLRAYTDGGVGPEKSMYVVTKENSVGL IIAILIPVAVAVIVGVVTSILCYRKREWIKETFY PDIPNPENCKALQFQKSVCEGSSALKTLEMNP CTPNNVEVLETRSAFPKIEDTEIVSPVAERPEN RSDAKPENHVVESYCPPIIEEEIPNPAADETGG TAQVIYIDVQSMYQPQAKPEEEQENDPVGGA GYKPQMHLPINSTVEDIAAEEDLDKTAGYRP QANVNTWNLVSPDSPRSIDSNSEIVSFGSPCSI NSRQFLIPPKDEDSPKSNGGGWSFTNFFQNKP ND
1341	2691	A .	10392		5057	MLPPKHLSATKPKKSWAPNLYELDSDLTKEP DVIIGEGPTDSEFFHQRFRNLIYVEFVGPRKTL IKLRNLCLDWLQPETRTKEEIIELLVLEQYLTII PEKLKPWVRAKKPENCEKLVTLLENYKEMY QPEGESLHGVLVVSAGLRCPLGLSASTLLTW SGLDNSLSWAAVGMSCVLWDIELHHDFLGV ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRESSPPH SVHSFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRAESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRYYEGNA FRGGFRFNSTLVSRKRVLERKRYHFDTDGK GSIHDQKGCPRKKPFECGSEMRKAMSVSSLS SLSSPSFTESQPIDFGAMPYVCDECGRSFSVIS EFVEHQIMHTRENLYEYGESFIHSVAVSEVQK

	OFO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
QID Or of	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
O: of	peptide	1	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
icl- tide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
q- ence	acioc	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ilice		ĺ	{ }	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
	Ì		1 1	peptide		/=possible nucleonde deletion, \-possible
		1	1	sequence	l	nucleotide insertion SQVGGKRFECKDCGETFNKSAALAEHRKIHA
		 	1			SQVGGKRFECKDCGETFNKSAALAERKNINA
	1	1			Ì	RGYLVECKNQECEEAFMPSPTFSELQKIYGK DKFYECRVCKETFLHSSALIEHQKIHFGDDKD
		1]	NEREHERERERERGETFRPSPALNEFQKMYG
	ł	1			1	KEKMYECKVCGETFLHSSSLKEHQKIHTRGN
	ì	1	}]	PFENKGKVCEETFIPGQSLKRRQKTYNKEKLC
	ì	. [Ì	DFTDGRDAFMQSSELSEHQKIHSRKNLFEGR
	1	1		l	1	GYEKSVIHSGPFTESQKSHTITRPLESDEDEKA
		1			1	FTISSNPYENQKIPTKENVYEAKSYERSVIHSL
	1	1			1	ASVEACKSHSVAGPSKPKVMAESTIQSFDAIN
	1			1	ļ	HORVRAGGNTSEGREYSRSVIHSLVASKPPKS
	i			ĺ	· .	LINCHEL VESNEKGESSTYISDLNDKROKIPAR
	1	Į.	1	1	1	ENDOGGSKNRNYEDSVIOSVFRAKPQKSVP
	1	l	ļ		1	GEGSGEEKKDGEFSVPSSNVREYQKAKAKKK
		1				VIEW SMETSVIHSLPFGEOTFRPRGMLYECQ
		1	İ	1	1	FCGECEAHSSDLTEHOKIHDREKPSGSKNYE
	Ì	1	1	ſ		I WENTEST APTOPOTSYAOEQYAKEQAKNKCK
	1		1	1		DFRQFFATSEDLNTNQKIYDQEKSHGEESQGI
	1		· ·	1		NTDGEETHSEETHGQETIEDPVIQGSDMEDPC
	1	- 1	}	1	1	KDDPDDKIYECEDCGLGFVDLTDLTDHQKVI
	1	1	\ \		i	SRKCLVDSREYTHSVIHTHSISEYQRDYTGEQ
	1	-	1	1	-	LYECPKCGESFIHSSFLFEHQRIHEQDQLYSM KGCDDGFIALLPMKPRRNRAAERNPALAGSA
		1		}	1	RCLLCGQGFIHSSALNEHMRLHREDDLLEQS
	ľ	1		1		QMAEEAIIPGLALTEFQRSQTEERLFECAVCG
	ì	ı		1	1	ESFVNPAELADHVTVHKNEPYEYGSSYTHTS
	1	1	1	1		FLTEPLKGAIPFYECKDCGKSFIHSTVLTKHK
	1					I LIT EFFEEDEAAAAAAAAAOEVEANVHVPQ
		İ	İ	1		VVI RIOGI NVEA AEPEVEA AEPEVEA AEPEV
	1	- (1	1		EAAEDNGEAEGPDGEAAEPIGEAGQPNGEAE
			1 '	1	ì	OPNGDADEPDGAGIEDPEERAEEPEGKAEEP
	1	1			1	CDADEPDGVGIEDPEEGEDOEIQVEEPYYDU
	1	1			1	HECTETETSSTAFSEHLKTHASMIIFEPANAFO
	1	- [l		ECSGYIERASTSTGGANQADEKYFKCDVCGC
	1	- (1		LFNDHLSLARHQNTHTG
12.40	2692	$-\frac{1}{A}$	10393	2	1350	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNS
1342	2092	Α.	10373	-	į.	ASRRSPAARPPVPAPPALPRGRPGTEGSTSLS
	ļ	j	.	1		APAVLVVAVAVVVVVVSAVAWAMANYIH\
	1	ı				PPGSPEVPKLNVTVQDQEEHRCREGALSLLQ
	ł	- 1	1			HLRPHWDPQEVTLQLFTDGITNKLIGCYVGN
	1		1	1		TMEDVVLVRIYGNKTELLVDRDEEVKSFRV
	4	- 1	1	1		QAHGCAPQLYCTFNNGLCYEFIQGEALDPKI
		- 1	1		. [VCNPAIFRLIARQLAKIHAIHAHNGWIPKSNL WLKMGKYFSLIPTGFADEDINKRFLSDIPSSC
		1				WLKMGKYFSLIPIGFADEDINKRFLSDI 33C LQEEMTWMKEILSNLGSPVVLCHNDLLCKN
	1	İ				YNEKQGDVQFIDYEYSGYNYLAYDIGNHFN
		- 1	- [1		FAGVSDVDYSLYPDRELQSQWLRAYLEAYK
	1	- ({	1		EFKGFGTEVTEKEVEILFIQVNQFALASHFFV
	1	- 1	1		1	GLWALIQAKYSTIEFDFLGYAIVRFNQYFKM
	İ	- 1	- 1	1		KPEVTALKVPE
						PEAQTSAVLAREKGHLPTMRHEAPMQMAS
1343	2693	A	10394	102	839	QDARYGQKDSSDQNFDYMFKLLIIGNSSVG
5		- 1	1	1	1	TSFLFRYADDSFTSAFVSTVGIDFKVKTVFKI
- 0		- 1	}		1	EKRIKLQIWDTAGQERYRTITTAYYRGAMG
		-	1	1	1	LMYDITNEESFNAVQDWSTQIKTYSWDNAC
ĺ	-	- 1				VILVGNKCDMEDERVISTERGQHLGEQLGF
		l	i	1		FFETSAKDNINVKQTFERLVDIICDKMSESLI
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		1			1:00	DEPRWASE VODEVINI THI SSK GHISPAKDI
1344	2694	A	10395	2	4136	DRPPWNSRVDDFVTNLIHLSSKGHISPAKD LQQRTPAEMSPVLHFYVRPSGHEGAASGH

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SEQ ID	SEQ ID	Met	~~ (Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide			nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l i	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	1 1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
)	1		peptide	Sequence	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
<u> </u>		ļ		sequence	 	RKLQGKLPELQGVETELCYNVNWTAEALPSA
	ļ		, ,		1	FETKKLMWLFGCPLLLDDVARESWLLPGSN
	1	1			1	DILLEVOPRLNFSTPTSTNIVSVCRATGLGPV
	ļ	1			1	DRVETTRRYRLSFAHPPSAEVEAIALATLHDR
	ŀ	1				MTEQHFPHPIQSFSPESMPEPLNGPINILGEGR
			1			LALEKANQELGLALDSWDLDFYTKRFQELQR
	1	1	1 1			NPSTVEAFDLAQSNSEHSRHWFFKGQLHVDG
		i			ì	QKLVHSLFESIMSTQESSNPNNVLKFCDNSSA
	}	1			i	IQGKEVRFLRPEDPTRPSRFQQQQGLRHVVFT AETHNFPTGVCPFSGATTGTGGRIRDVQCTG
	1	1	1			RGAHVVAGTAGYCFGNLHIPGYNLPWEDLSF
	1	1	1		1	QYPGNFARPLEVAIEASNGASDYGNKFGEPV
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	Ì	1	ł		.	PTPPPTPVDLELEWVLGKMPRKEFFLQRKPP
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1	}	1 '		ļ	ŀ	FRGVAFVGGFSYADVLGSAKGWAAAVTFHP RAGAELRRFRKRPDTFSLGVCNGCQLLALLG
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SEQ ID No: of No: of No: of nucleotide sequence No: of nucleotide No: of nu	WCV IDS LYY PDFV LTQ DLPI	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrossine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LMNKLAGKNKGFSLGSTVKSHTKGIWMV PHPKKPEHTLVLLDTEGLGDVKKGDNQN WHETLAVILSSTLVYNSMGTINOQAMDQI	nucleotide location corresponding to last amino acid residue of peptide	beginning nucleotide location correspondi ng to first amino acid residue of peptide	ID NO: in USSN 09/496	hod	NO: of peptide seq-	NO: of nucl- eotide seq-
NO: of nucleoted peptide cotide sequence NO: of nucleoted peptide sequence NO: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleoted sequence No: of nucleotide	NDS LYY PDFV LTQ DLPI	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LMNKLAGKNKGFSLGSTVKSHTKGIWMV PHPKKPEHTLVLLDTEGLGDVKKGDNQN WHET! AVI LSSTLVYNSMGTINOQAMDQI	location corresponding to last amino acid residue of peptide	nucleotide location correspondi ng to first amino acid residue of peptide	in USSN 09/496		peptide seq-	NO: of nucl- eotide seq-
nucle eotide sequence e Sequenc	NDS LYY PDFV LTQ DLPI	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LMNKLAGKNKGFSLGSTVKSHTKGIWMV PHPKKPEHTLVLLDTEGLGDVKKGDNQN WHETI AVI LSSTLVYNSMGTINQQAMDQI	corresponding to last amino acid residue of peptide	location correspondi ng to first amino acid residue of peptide	USSN 09/496		seq-	eotide seq-
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sequence Sequence	NDS LYY PDFV LTQ DLPI	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LMNKLAGKNKGFSLGSTVKSHTKGIWMV PHPKKPEHTLVLLDTEGLGDVKKGDNQN WHETI AVI LSSTLVYNSMGTINQQAMDQI	acid residue of peptide	ng to first amino acid residue of peptide			- 1	seq-
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WO 01/57188

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
- A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).
- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

Pages 340 to 1963 of this application contain amino acid sequence listings. They can be obtained at the address given below.

Les pages 340 to 1963 de cette demande contiennent des listages des séquences d'acides aminés. Elles peuvent être obtenues à l'adresse indiquée ci-dessous.

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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